



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 12, 2024 – 01:18 AM EDT

PDB ID : 1RQ0
Title : Crystal structure of peptide releasing factor 1
Authors : Shin, D.H.; Brandsen, J.; Jancarik, J.; Yokota, H.; Kim, R.; Kim, S.-H.;
Berkeley Structural Genomics Center (BSGC)
Deposited on : 2003-12-03
Resolution : 2.65 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

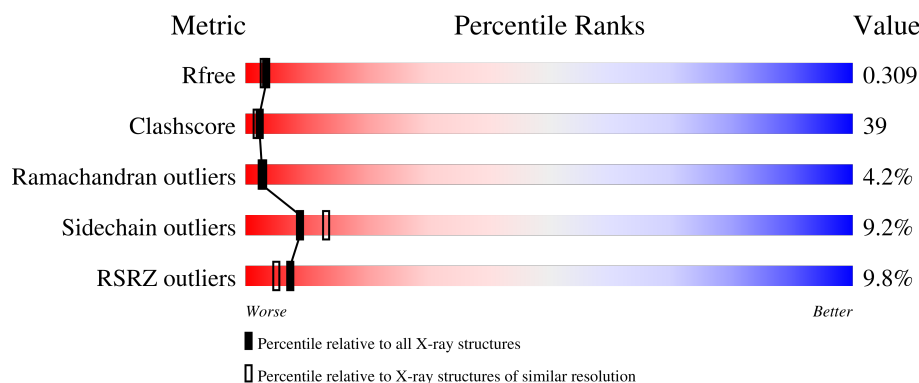
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	342	
1	B	342	
1	C	342	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8002 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	319	Total	C	N	O	S	0	0	0
			2628	1649	459	515	5			
1	B	314	Total	C	N	O	S	0	0	0
			2585	1621	452	507	5			
1	C	314	Total	C	N	O	S	0	0	0
			2585	1621	452	507	5			

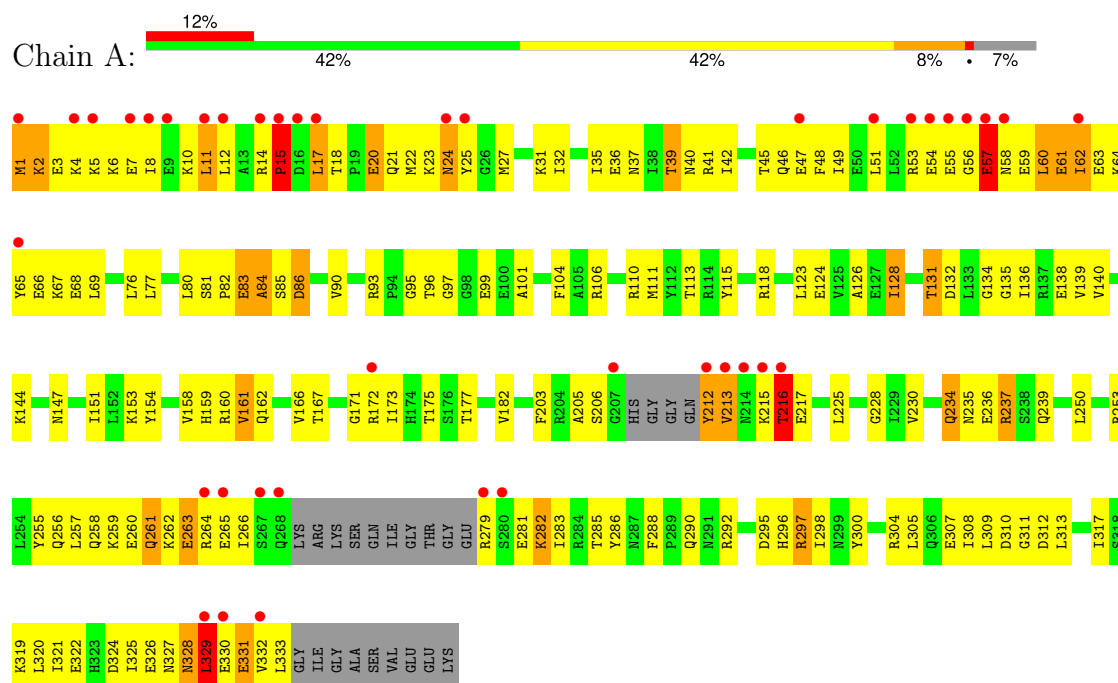
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	78	Total	O	0	0
			78	78		
2	B	70	Total	O	0	0
			70	70		
2	C	56	Total	O	0	0
			56	56		

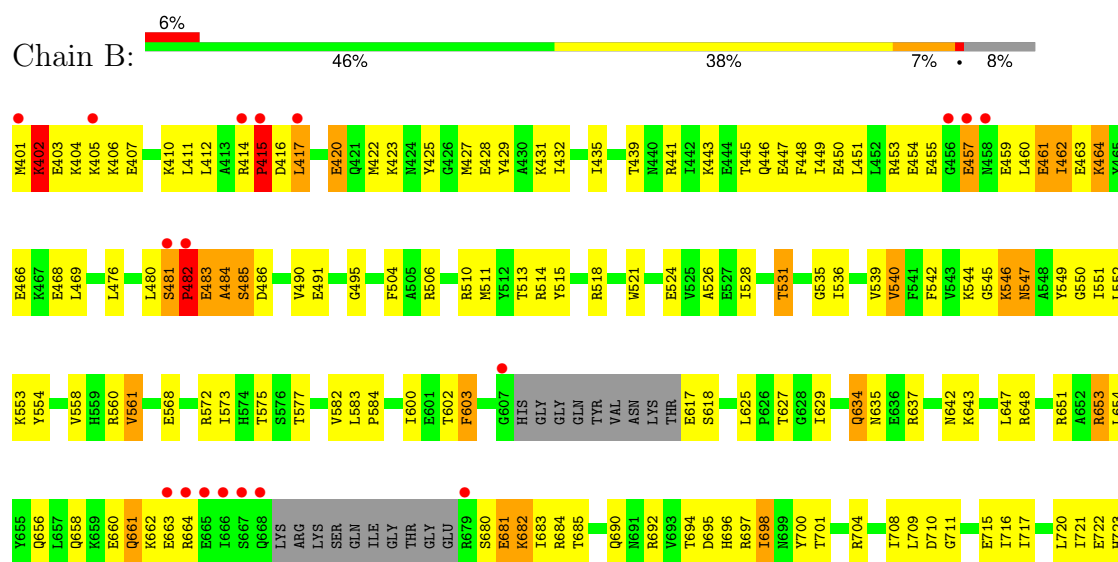
3 Residue-property plots

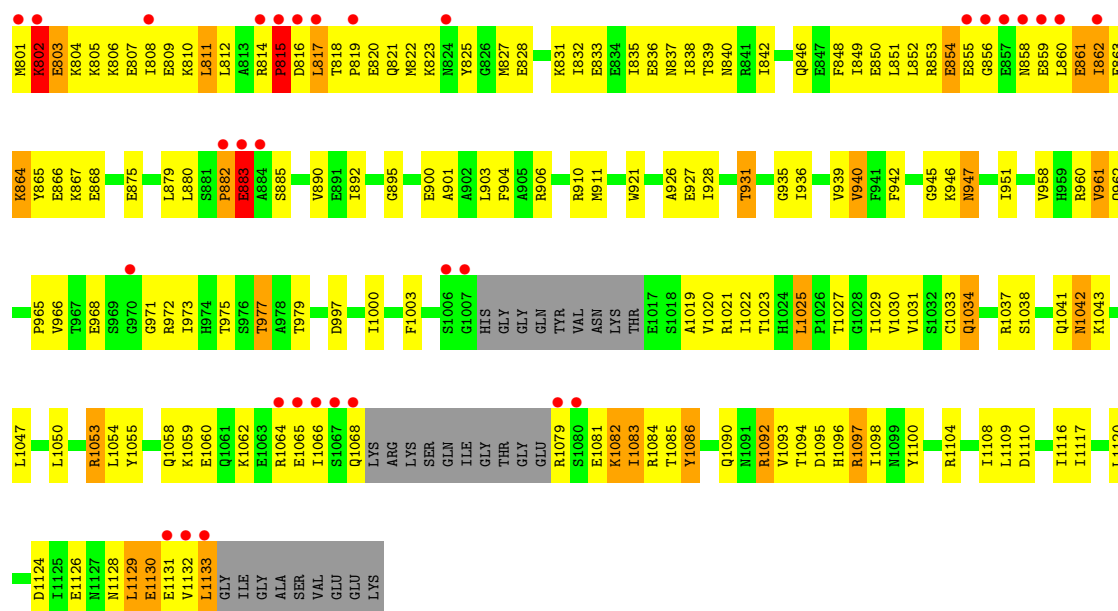
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Peptide chain release factor 1



• Molecule 1: Peptide chain release factor 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.90Å 137.23Å 80.93Å 90.00° 106.00° 90.00°	Depositor
Resolution (Å)	19.89 – 2.65 68.62 – 2.65	Depositor EDS
% Data completeness (in resolution range)	84.8 (19.89-2.65) 93.1 (68.62-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.65Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.216 , 0.294 0.231 , 0.309	Depositor DCC
R_{free} test set	3040 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å ²)	30.1	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 63.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.035 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	8002	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.88% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.44	2/2664 (0.1%)	0.70	3/3581 (0.1%)
1	B	0.41	1/2620 (0.0%)	0.69	2/3521 (0.1%)
1	C	0.39	0/2620	0.70	3/3521 (0.1%)
All	All	0.42	3/7904 (0.0%)	0.70	8/10623 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	213	VAL	N-CA	-6.13	1.34	1.46
1	A	212	TYR	C-N	-6.07	1.20	1.34
1	B	482	PRO	N-CA	5.11	1.55	1.47

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	213	VAL	N-CA-C	-9.87	84.34	111.00
1	C	883	GLU	N-CA-C	8.22	133.19	111.00
1	C	802	LYS	N-CA-C	-6.89	92.40	111.00
1	A	216	THR	N-CA-C	-6.65	93.05	111.00
1	B	482	PRO	CA-N-CD	-6.59	102.28	111.50
1	A	2	LYS	N-CA-C	-6.58	93.23	111.00
1	B	402	LYS	N-CA-C	-6.45	93.58	111.00
1	C	882	PRO	C-N-CA	5.05	134.34	121.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2628	0	2633	238	0
1	B	2585	0	2587	186	0
1	C	2585	0	2587	183	0
2	A	78	0	0	11	0
2	B	70	0	0	1	0
2	C	56	0	0	4	0
All	All	8002	0	7807	601	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 39.

All (601) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MET:CE	1:A:32:ILE:HG12	1.26	1.59
1:A:1:MET:HE2	1:A:32:ILE:CG1	1.41	1.47
1:A:1:MET:HE2	1:A:32:ILE:CD1	1.49	1.39
1:A:1:MET:CE	1:A:32:ILE:CG1	2.00	1.31
1:A:1:MET:N	1:A:6:LYS:HB2	1.49	1.26
1:B:482:PRO:O	1:B:483:GLU:HG2	1.40	1.18
1:A:1:MET:HE1	1:A:32:ILE:HG12	1.21	1.17
1:C:931:THR:HG22	1:C:935:GLY:H	1.04	1.12
1:B:482:PRO:O	1:B:483:GLU:CG	1.99	1.11
1:A:1:MET:CE	1:A:32:ILE:CD1	2.27	1.09
1:C:911:MET:HE3	1:C:1109:LEU:HA	1.38	1.01
1:C:1129:LEU:O	1:C:1133:LEU:HG	1.60	1.00
1:A:111:MET:HE3	1:A:309:LEU:HA	1.46	0.98
1:B:417:LEU:HD11	1:B:422:MET:HG3	1.46	0.98
1:A:131:THR:HG22	1:A:135:GLY:H	1.29	0.96
1:A:1:MET:H2	1:A:6:LYS:HB2	1.08	0.95
1:A:1:MET:N	1:A:6:LYS:CB	2.30	0.94
1:C:960:ARG:HB3	1:C:1082:LYS:HD2	1.47	0.94
1:A:1:MET:H2	1:A:6:LYS:CB	1.82	0.93
1:A:1:MET:HE2	1:A:32:ILE:HD13	1.47	0.93
1:C:972:ARG:HE	1:C:973:ILE:H	1.13	0.92
1:C:1090:GLN:NE2	1:C:1092:ARG:HE	1.70	0.90
1:A:95:GLY:HA3	1:A:177:THR:HG22	1.53	0.90
1:C:951:ILE:HG23	1:C:1117:ILE:HG21	1.54	0.89
1:C:931:THR:HG22	1:C:935:GLY:N	1.88	0.89

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1060:GLU:O	1:C:1064:ARG:HG2	1.72	0.88
1:A:36:GLU:HG2	2:A:2542:HOH:O	1.74	0.88
1:C:803:GLU:O	1:C:807:GLU:HG3	1.73	0.86
1:B:495:GLY:HA3	1:B:577:THR:HG22	1.56	0.86
1:B:690:GLN:NE2	1:B:692:ARG:HE	1.74	0.86
1:A:1:MET:H1	1:A:6:LYS:HB2	1.35	0.85
1:B:526:ALA:HB3	1:B:540:VAL:HG22	1.57	0.85
1:B:403:GLU:O	1:B:407:GLU:HG3	1.77	0.84
1:B:572:ARG:HE	1:B:573:ILE:H	1.24	0.84
1:B:560:ARG:HB2	1:B:682:LYS:HD2	1.60	0.84
1:B:572:ARG:NE	1:B:573:ILE:H	1.76	0.83
1:A:1:MET:HE3	1:A:5:LYS:NZ	1.93	0.83
1:A:14:ARG:HB3	1:A:15:PRO:HD2	1.60	0.82
1:B:528:ILE:HD12	1:B:528:ILE:O	1.77	0.82
1:C:972:ARG:HE	1:C:973:ILE:N	1.77	0.82
1:C:972:ARG:NE	1:C:973:ILE:H	1.78	0.81
1:C:911:MET:HE2	1:C:1108:ILE:HG22	1.61	0.81
1:B:410:LYS:HE3	1:B:429:TYR:OH	1.81	0.81
1:C:1079:ARG:HE	1:C:1081:GLU:HB3	1.46	0.81
1:A:17:LEU:HD11	1:A:22:MET:HG3	1.60	0.80
1:A:81:SER:N	1:A:82:PRO:HD3	1.96	0.80
1:C:806:LYS:O	1:C:810:LYS:HG2	1.81	0.79
1:C:801:MET:C	1:C:802:LYS:O	2.11	0.79
1:A:128:ILE:HG23	1:A:139:VAL:HG23	1.64	0.79
1:B:401:MET:C	1:B:402:LYS:O	2.18	0.79
1:B:401:MET:HB2	1:B:405:LYS:HD3	1.66	0.78
1:C:817:LEU:HD11	1:C:822:MET:HG3	1.64	0.78
1:A:3:GLU:O	1:A:7:GLU:HG3	1.84	0.78
1:A:1:MET:CE	1:A:32:ILE:HD11	2.14	0.77
1:C:1027:THR:HG21	1:C:1029:ILE:HG13	1.66	0.77
1:A:1:MET:HE3	1:A:5:LYS:HZ2	1.48	0.76
1:A:6:LYS:O	1:A:10:LYS:HG2	1.85	0.76
1:A:39:THR:OG1	2:A:2541:HOH:O	2.01	0.76
1:C:904:PHE:CE1	1:C:961:VAL:HG13	2.19	0.76
1:A:32:ILE:O	1:A:36:GLU:HG3	1.84	0.76
1:C:802:LYS:HA	2:C:2560:HOH:O	1.84	0.76
1:A:36:GLU:HA	2:A:2541:HOH:O	1.85	0.76
1:B:411:LEU:HA	1:B:414:ARG:HG3	1.66	0.76
1:B:550:GLY:HA2	1:B:553:LYS:HE3	1.67	0.76
1:A:329:LEU:HD12	1:A:329:LEU:H	1.50	0.76
1:B:629:ILE:HD13	1:B:653:ARG:HB3	1.68	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:ARG:HG3	1:A:285:THR:HG23	1.68	0.75
1:B:441:ARG:O	1:B:445:THR:HG23	1.86	0.75
1:A:1:MET:HE1	1:A:32:ILE:CG1	1.90	0.75
1:A:131:THR:HG22	1:A:135:GLY:N	2.01	0.74
1:C:835:ILE:O	1:C:839:THR:HG23	1.88	0.74
1:B:647:LEU:O	1:B:651:ARG:HG3	1.87	0.74
1:C:820:GLU:HA	1:C:823:LYS:HE2	1.70	0.74
1:A:1:MET:SD	1:A:32:ILE:HG12	2.27	0.74
1:A:126:ALA:HB3	1:A:140:VAL:HG13	1.70	0.73
1:A:158:VAL:HG13	1:A:177:THR:HG23	1.70	0.73
1:A:1:MET:N	1:A:6:LYS:N	2.36	0.73
1:A:172:ARG:HA	1:A:172:ARG:HE	1.52	0.73
1:C:931:THR:CG2	1:C:935:GLY:H	1.95	0.73
1:A:111:MET:HE2	1:A:308:ILE:HG22	1.69	0.72
1:A:325:ILE:O	1:A:331:GLU:HB2	1.88	0.72
1:B:690:GLN:HE21	1:B:692:ARG:HE	1.36	0.72
1:B:729:LEU:H	1:B:729:LEU:HD12	1.53	0.72
1:B:627:THR:CG2	1:B:629:ILE:HG13	2.19	0.72
1:B:547:ASN:ND2	1:B:550:GLY:H	1.88	0.72
1:A:1:MET:HB2	1:A:32:ILE:HD13	1.70	0.71
1:C:1000:ILE:HD13	1:C:1043:LYS:HE3	1.73	0.71
1:A:159:HIS:HB3	1:A:286:TYR:HE2	1.55	0.71
1:A:1:MET:CE	1:A:5:LYS:NZ	2.53	0.70
1:A:172:ARG:HA	1:A:172:ARG:NE	2.04	0.70
1:A:213:VAL:HG12	1:A:217:GLU:OE1	1.91	0.70
1:C:802:LYS:NZ	1:C:804:LYS:HB2	2.06	0.70
1:C:1090:GLN:HE21	1:C:1092:ARG:HE	1.39	0.70
1:C:1027:THR:CG2	1:C:1029:ILE:HG13	2.21	0.70
1:B:526:ALA:HB2	1:B:542:PHE:CE1	2.26	0.70
1:C:1108:ILE:HD13	1:C:1116:ILE:HD11	1.74	0.70
1:C:817:LEU:HD11	1:C:822:MET:CG	2.21	0.70
1:B:449:ILE:HG23	1:B:462:ILE:HB	1.72	0.70
1:A:11:LEU:HA	1:A:14:ARG:HG3	1.74	0.70
1:B:572:ARG:HE	1:B:573:ILE:N	1.88	0.70
1:B:617:GLU:HB2	1:B:635:ASN:O	1.92	0.70
1:B:428:GLU:HA	1:B:431:LYS:HD2	1.72	0.69
1:B:412:LEU:O	1:B:417:LEU:HD23	1.91	0.69
1:A:1:MET:H3	1:A:6:LYS:N	1.91	0.69
1:A:162:GLN:HG2	1:A:175:THR:HG22	1.74	0.69
1:A:32:ILE:HG22	1:A:36:GLU:OE2	1.93	0.68
1:B:504:PHE:CZ	1:B:561:VAL:HG13	2.28	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1126:GLU:O	1:C:1131:GLU:HG2	1.93	0.68
1:B:461:GLU:C	1:B:463:GLU:H	1.93	0.68
1:A:324:ASP:O	1:A:328:ASN:HB2	1.93	0.67
1:C:802:LYS:HE3	1:C:804:LYS:HZ2	1.60	0.67
1:C:1038:SER:OG	1:C:1041:GLN:HG3	1.94	0.67
1:C:911:MET:CE	1:C:1108:ILE:HG22	2.25	0.67
1:A:160:ARG:HG2	1:A:282:LYS:HD2	1.78	0.66
1:B:518:ARG:HD2	2:B:2463:HOH:O	1.94	0.66
1:C:890:VAL:O	1:C:940:VAL:HA	1.96	0.66
1:B:402:LYS:HE3	1:B:404:LYS:HZ2	1.60	0.66
1:B:698:ILE:HD11	1:B:723:HIS:CG	2.31	0.66
1:A:1:MET:HE3	1:A:5:LYS:HD3	1.78	0.66
1:A:166:VAL:O	1:B:600:ILE:HG21	1.96	0.65
1:C:849:ILE:HG23	1:C:862:ILE:HB	1.77	0.65
1:A:329:LEU:H	1:A:329:LEU:CD1	2.10	0.65
1:A:282:LYS:HA	1:A:282:LYS:HZ2	1.61	0.65
1:B:551:ILE:HG23	1:B:717:ILE:HG21	1.78	0.65
1:B:627:THR:HG21	1:B:629:ILE:HG13	1.78	0.65
1:C:802:LYS:HZ1	1:C:804:LYS:HB2	1.60	0.65
1:A:298:ILE:HD13	1:A:320:LEU:HD23	1.79	0.65
1:A:106:ARG:HA	1:A:136:ILE:HD12	1.77	0.65
1:B:445:THR:O	1:B:449:ILE:HG13	1.96	0.65
1:B:683:ILE:HG13	1:B:697:ARG:HD2	1.79	0.65
1:B:461:GLU:C	1:B:463:GLU:N	2.50	0.65
1:A:4:LYS:NZ	1:A:4:LYS:HB3	2.12	0.64
1:A:104:PHE:CE1	1:A:161:VAL:HG13	2.32	0.64
1:A:1:MET:N	1:A:6:LYS:CA	2.60	0.64
1:A:118:ARG:NH1	1:A:312:ASP:HB2	2.12	0.64
1:B:435:ILE:O	1:B:439:THR:HG23	1.97	0.64
1:B:427:MET:O	1:B:431:LYS:HG3	1.97	0.64
1:A:329:LEU:O	1:A:333:LEU:HB2	1.97	0.64
1:A:1:MET:CE	1:A:5:LYS:HZ2	2.10	0.64
1:A:31:LYS:O	1:A:35:ILE:HG13	1.98	0.64
1:C:1098:ILE:HD13	1:C:1120:LEU:HD23	1.80	0.63
1:B:416:ASP:CG	1:B:417:LEU:N	2.51	0.63
1:B:417:LEU:HD11	1:B:422:MET:CG	2.25	0.63
1:C:802:LYS:HB3	1:C:802:LYS:HZ2	1.62	0.63
1:A:42:ILE:O	1:A:46:GLN:HG3	1.98	0.63
1:C:1129:LEU:O	1:C:1131:GLU:N	2.31	0.63
1:A:59:GLU:O	1:A:61:GLU:N	2.31	0.63
1:B:428:GLU:HA	1:B:431:LYS:CD	2.28	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:911:MET:HE3	1:C:1109:LEU:CA	2.24	0.63
1:A:282:LYS:HZ3	1:A:282:LYS:HB2	1.64	0.63
1:B:404:LYS:NZ	1:B:404:LYS:HB3	2.13	0.63
1:B:684:ARG:HG3	1:B:695:ASP:HA	1.79	0.63
1:C:802:LYS:HE3	1:C:804:LYS:NZ	2.13	0.63
1:B:729:LEU:H	1:B:729:LEU:CD1	2.12	0.62
1:C:814:ARG:HB3	1:C:815:PRO:HD2	1.81	0.62
1:B:528:ILE:CG2	1:B:539:VAL:HG23	2.29	0.62
1:A:260:GLU:O	1:A:264:ARG:HG2	2.00	0.62
1:C:1055:TYR:CE2	1:C:1059:LYS:HE3	2.35	0.62
1:B:414:ARG:O	1:B:416:ASP:N	2.32	0.62
1:B:572:ARG:HE	1:B:572:ARG:HA	1.63	0.62
1:C:804:LYS:HA	1:C:807:GLU:OE1	1.99	0.62
1:C:926:ALA:HB2	1:C:942:PHE:CE1	2.34	0.62
1:B:511:MET:HE2	1:B:709:LEU:HD23	1.82	0.61
1:A:285:THR:OG1	1:A:296:HIS:CE1	2.54	0.61
1:C:802:LYS:NZ	1:C:804:LYS:CB	2.63	0.61
1:C:926:ALA:HA	1:C:1037:ARG:HH21	1.64	0.61
1:B:451:LEU:O	1:B:455:GLU:HB3	2.00	0.61
1:B:486:ASP:O	1:B:544:LYS:HA	2.00	0.61
1:C:1083:ILE:HG13	1:C:1097:ARG:NE	2.15	0.61
1:A:11:LEU:HD23	1:A:11:LEU:H	1.65	0.61
1:A:205:ALA:HB1	1:A:215:LYS:HB3	1.82	0.61
1:B:726:GLU:O	1:B:731:GLU:HG2	2.00	0.61
1:C:910:ARG:NH2	1:C:1110:ASP:OD2	2.33	0.61
1:A:257:LEU:HD13	1:A:257:LEU:O	2.01	0.61
1:B:404:LYS:HZ2	1:B:404:LYS:HB3	1.66	0.61
1:B:698:ILE:HD11	1:B:723:HIS:CD2	2.35	0.61
1:B:401:MET:CB	1:B:405:LYS:HD3	2.31	0.60
1:B:725:ILE:O	1:B:731:GLU:HB2	2.01	0.60
1:A:1:MET:HE3	1:A:5:LYS:CD	2.31	0.60
1:C:1133:LEU:N	1:C:1133:LEU:HD23	2.16	0.60
1:B:401:MET:HB3	1:B:405:LYS:HB3	1.83	0.60
1:C:838:ILE:HD12	1:C:879:LEU:HD12	1.83	0.60
1:B:482:PRO:O	1:B:483:GLU:CD	2.39	0.60
1:B:511:MET:HE2	1:B:709:LEU:HA	1.84	0.60
1:A:329:LEU:HA	1:A:333:LEU:HD23	1.84	0.60
1:C:804:LYS:HZ2	1:C:804:LYS:HB3	1.66	0.60
1:C:900:GLU:HA	1:C:903:LEU:HD12	1.83	0.60
1:B:445:THR:OG1	1:B:469:LEU:HD21	2.01	0.60
1:B:459:GLU:O	1:B:461:GLU:N	2.34	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:504:PHE:CD1	1:B:561:VAL:HG11	2.37	0.59
1:A:263:GLU:HG3	1:A:264:ARG:N	2.17	0.59
1:B:414:ARG:HB3	1:B:415:PRO:HD2	1.82	0.59
1:C:801:MET:CB	1:C:805:LYS:HD3	2.33	0.59
1:A:215:LYS:HD3	1:A:234:GLN:HE22	1.66	0.59
1:C:928:ILE:HD12	1:C:928:ILE:O	2.03	0.59
1:C:802:LYS:NZ	1:C:802:LYS:HB3	2.15	0.59
1:A:76:LEU:O	1:A:80:LEU:HG	2.01	0.59
1:A:285:THR:OG1	1:A:296:HIS:HE1	1.86	0.59
1:C:838:ILE:HD13	1:C:875:GLU:HG3	1.83	0.59
1:A:1:MET:O	1:A:2:LYS:C	2.41	0.59
1:A:41:ARG:O	1:A:45:THR:HG23	2.03	0.59
1:A:215:LYS:HD3	1:A:234:GLN:NE2	2.17	0.59
1:B:654:LEU:O	1:B:658:GLN:HG3	2.02	0.59
1:C:801:MET:HB2	1:C:805:LYS:HD3	1.84	0.58
1:B:627:THR:HG22	1:B:629:ILE:HG13	1.85	0.58
1:C:1038:SER:O	1:C:1042:ASN:HB2	2.03	0.58
1:B:637:ARG:HB2	1:B:642:ASN:ND2	2.18	0.58
1:B:731:GLU:HG3	1:B:732:VAL:N	2.18	0.58
1:C:861:GLU:C	1:C:863:GLU:H	2.05	0.58
1:B:402:LYS:HE3	1:B:404:LYS:NZ	2.18	0.58
1:B:690:GLN:NE2	1:B:692:ARG:NE	2.48	0.58
1:A:80:LEU:C	1:A:82:PRO:HD3	2.24	0.58
1:A:263:GLU:HG3	1:A:264:ARG:H	1.67	0.58
1:A:123:LEU:HD23	1:A:124:GLU:N	2.18	0.58
1:A:317:ILE:O	1:A:321:ILE:HG13	2.04	0.58
1:B:416:ASP:CG	1:B:417:LEU:H	2.07	0.57
1:B:685:THR:OG1	1:B:696:HIS:HE1	1.87	0.57
1:A:295:ASP:OD1	1:A:297:ARG:HD3	2.04	0.57
1:A:1:MET:HG3	1:A:32:ILE:HG23	1.86	0.57
1:C:1020:VAL:HG12	1:C:1021:ARG:N	2.19	0.57
1:B:528:ILE:HG22	1:B:539:VAL:HG23	1.87	0.57
1:C:972:ARG:HE	1:C:972:ARG:HA	1.69	0.57
1:C:1128:ASN:O	1:C:1129:LEU:C	2.42	0.57
1:C:1129:LEU:C	1:C:1133:LEU:HG	2.25	0.57
1:B:704:ARG:NH2	1:B:715:GLU:OE1	2.34	0.57
1:C:801:MET:O	1:C:802:LYS:C	2.37	0.57
1:C:802:LYS:HZ2	1:C:804:LYS:CB	2.18	0.57
1:A:90:VAL:HG22	1:A:182:VAL:HG22	1.85	0.57
1:A:283:ILE:HG13	1:A:297:ARG:NE	2.20	0.57
1:B:405:LYS:HZ2	1:B:432:ILE:HD11	1.70	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:5:LYS:HZ2	1:A:32:ILE:HD11	1.69	0.56
1:B:661:GLN:HG2	1:B:664:ARG:HH11	1.70	0.56
1:B:690:GLN:HE21	1:B:692:ARG:NE	2.02	0.56
1:C:972:ARG:HE	1:C:972:ARG:CA	2.17	0.56
1:B:406:LYS:O	1:B:410:LYS:HG2	2.05	0.56
1:B:572:ARG:HE	1:B:572:ARG:CA	2.17	0.56
1:C:828:GLU:HA	1:C:831:LYS:HD2	1.88	0.56
1:A:216:THR:OG1	1:A:234:GLN:NE2	2.38	0.56
1:C:1000:ILE:CD1	1:C:1043:LYS:HE3	2.36	0.56
1:C:802:LYS:CE	1:C:804:LYS:HZ2	2.18	0.56
1:C:1053:ARG:NH1	2:C:2402:HOH:O	2.37	0.56
1:B:661:GLN:HA	1:B:664:ARG:HG2	1.87	0.56
1:B:729:LEU:O	1:B:733:LEU:HD23	2.05	0.56
1:C:811:LEU:O	1:C:814:ARG:HG3	2.06	0.56
1:B:401:MET:O	1:B:402:LYS:C	2.43	0.55
1:B:490:VAL:O	1:B:540:VAL:HA	2.05	0.55
1:A:96:THR:H	1:A:177:THR:HB	1.70	0.55
1:C:859:GLU:O	1:C:861:GLU:N	2.39	0.55
1:C:1085:THR:OG1	1:C:1096:HIS:HE1	1.90	0.55
1:B:491:GLU:OE1	1:B:653:ARG:NH1	2.40	0.55
1:A:81:SER:N	1:A:82:PRO:CD	2.66	0.55
1:B:560:ARG:CB	1:B:682:LYS:HD2	2.35	0.55
1:C:1090:GLN:NE2	1:C:1092:ARG:NE	2.47	0.55
1:A:206:SER:O	1:A:215:LYS:HD2	2.06	0.55
1:B:690:GLN:HE22	1:B:692:ARG:HH21	1.55	0.55
1:A:85:SER:HB2	1:A:147:ASN:HD22	1.72	0.55
1:A:1:MET:HE3	1:A:5:LYS:CE	2.36	0.55
1:A:95:GLY:HA3	1:A:177:THR:CG2	2.34	0.55
1:C:1130:GLU:HG3	2:C:2568:HOH:O	2.07	0.55
1:B:511:MET:CE	1:B:709:LEU:HD23	2.35	0.55
1:C:811:LEU:HA	1:C:814:ARG:NE	2.21	0.55
1:C:818:THR:OG1	1:C:821:GLN:HG3	2.07	0.55
1:C:951:ILE:HG22	1:C:1117:ILE:HD13	1.88	0.54
1:A:77:LEU:HD12	1:A:147:ASN:OD1	2.06	0.54
1:B:464:LYS:HD2	1:B:464:LYS:O	2.07	0.54
1:A:282:LYS:HA	1:A:282:LYS:NZ	2.23	0.54
1:C:1050:LEU:HD23	1:C:1050:LEU:C	2.28	0.54
1:C:1066:ILE:C	1:C:1068:GLN:N	2.60	0.54
1:B:404:LYS:HA	1:B:407:GLU:OE1	2.08	0.54
1:B:729:LEU:O	1:B:731:GLU:N	2.40	0.54
1:C:817:LEU:HD11	1:C:822:MET:CB	2.37	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:THR:HA	1:B:600:ILE:CG2	2.38	0.54
1:B:403:GLU:O	1:B:403:GLU:HG3	2.07	0.53
1:B:482:PRO:O	1:B:483:GLU:OE2	2.26	0.53
1:C:1060:GLU:HB3	1:C:1064:ARG:HD3	1.90	0.53
1:A:167:THR:HA	1:B:600:ILE:HG22	1.91	0.53
1:A:49:ILE:HG23	1:A:62:ILE:HB	1.91	0.53
1:C:842:ILE:O	1:C:846:GLN:HG3	2.08	0.53
1:B:504:PHE:CE1	1:B:561:VAL:CG1	2.92	0.53
1:A:166:VAL:HG21	1:B:602:THR:HG21	1.91	0.53
1:B:510:ARG:NH2	1:B:710:ASP:OD2	2.42	0.53
1:A:1:MET:HE2	1:A:32:ILE:HG12	1.08	0.53
1:B:462:ILE:O	1:B:466:GLU:HB2	2.08	0.53
1:A:85:SER:O	1:A:147:ASN:HA	2.09	0.53
1:B:729:LEU:O	1:B:733:LEU:HB2	2.08	0.53
1:C:1090:GLN:HE22	1:C:1092:ARG:HH21	1.57	0.53
1:B:528:ILE:HG22	1:B:539:VAL:CG2	2.39	0.53
1:C:880:LEU:O	1:C:882:PRO:HD3	2.10	0.53
1:C:928:ILE:HG23	1:C:939:VAL:HG23	1.90	0.52
1:A:160:ARG:HB3	1:A:282:LYS:CE	2.39	0.52
1:A:172:ARG:HE	1:A:173:ILE:H	1.57	0.52
1:C:837:ASN:O	1:C:840:ASN:HB3	2.10	0.52
1:C:848:PHE:CE1	1:C:852:LEU:HD11	2.44	0.52
1:A:147:ASN:O	1:A:151:ILE:HG13	2.10	0.52
1:A:45:THR:O	1:A:49:ILE:HG13	2.09	0.52
1:C:861:GLU:C	1:C:863:GLU:N	2.63	0.52
1:C:972:ARG:NE	1:C:972:ARG:HA	2.24	0.52
1:C:1090:GLN:HE22	1:C:1092:ARG:HE	1.55	0.52
1:B:405:LYS:NZ	1:B:432:ILE:HD11	2.24	0.52
1:B:648:ARG:HA	1:B:651:ARG:NH1	2.24	0.52
1:A:4:LYS:HA	1:A:7:GLU:HG3	1.90	0.52
1:A:62:ILE:HD13	1:A:62:ILE:H	1.74	0.52
1:A:62:ILE:HD13	1:A:62:ILE:N	2.25	0.52
1:A:99:GLU:HA	1:A:99:GLU:OE1	2.10	0.52
1:C:875:GLU:HA	1:C:875:GLU:OE2	2.10	0.52
1:A:12:LEU:O	1:A:17:LEU:HD23	2.09	0.52
1:A:250:LEU:O	1:A:250:LEU:HD23	2.09	0.52
1:A:290:GLN:NE2	1:A:292:ARG:HE	2.08	0.52
1:A:263:GLU:C	1:A:265:GLU:H	2.13	0.51
1:B:549:TYR:CE1	1:B:584:PRO:HD3	2.45	0.51
1:C:1060:GLU:HB3	1:C:1064:ARG:CD	2.40	0.51
1:A:1:MET:HG2	2:A:2544:HOH:O	2.09	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:LYS:HA	1:A:7:GLU:CD	2.31	0.51
1:C:951:ILE:CG2	1:C:1117:ILE:HG21	2.35	0.51
1:C:997:ASP:O	1:C:1025:LEU:HD22	2.09	0.51
1:A:4:LYS:HA	1:A:7:GLU:OE1	2.10	0.51
1:A:56:GLY:O	1:A:57:GLU:HB2	2.10	0.51
1:C:1000:ILE:HG23	1:C:1022:ILE:HG12	1.92	0.51
1:B:554:TYR:HB3	1:B:720:LEU:HD13	1.91	0.51
1:C:833:GLU:O	1:C:837:ASN:ND2	2.43	0.51
1:C:868:GLU:HA	1:C:868:GLU:OE1	2.11	0.51
1:A:110:ARG:NH2	1:A:310:ASP:OD2	2.39	0.51
1:A:2:LYS:HE3	1:A:4:LYS:HZ2	1.76	0.51
1:A:20:GLU:HG2	1:A:20:GLU:O	2.10	0.51
1:A:283:ILE:HG13	1:A:297:ARG:CZ	2.41	0.51
1:B:511:MET:HG3	1:B:708:ILE:O	2.11	0.50
1:B:504:PHE:CE1	1:B:561:VAL:HG13	2.46	0.50
1:B:660:GLU:HA	1:B:663:GLU:HG3	1.93	0.50
1:B:724:ASP:O	1:B:728:ASN:HB2	2.10	0.50
1:C:1132:VAL:O	1:C:1132:VAL:HG12	2.11	0.50
1:B:401:MET:HE3	1:B:435:ILE:HD12	1.92	0.50
1:A:7:GLU:O	1:A:10:LYS:N	2.45	0.50
1:A:12:LEU:HD13	1:A:25:TYR:CE1	2.45	0.50
1:A:23:LYS:O	1:A:27:MET:HB2	2.11	0.50
1:B:462:ILE:HD13	1:B:462:ILE:N	2.27	0.50
1:B:524:GLU:OE1	1:B:637:ARG:NH2	2.37	0.50
1:A:68:GLU:OE1	1:A:68:GLU:HA	2.11	0.50
1:A:128:ILE:HG23	1:A:139:VAL:CG2	2.40	0.50
1:A:154:TYR:O	1:A:297:ARG:NH2	2.25	0.50
1:C:862:ILE:O	1:C:866:GLU:HB2	2.12	0.50
1:B:510:ARG:NH1	1:B:514:ARG:HD2	2.27	0.50
1:B:547:ASN:HD21	1:B:550:GLY:HA3	1.76	0.50
1:C:1066:ILE:C	1:C:1068:GLN:H	2.14	0.50
1:C:817:LEU:HD12	1:C:817:LEU:C	2.31	0.50
1:C:966:VAL:HG13	2:C:2415:HOH:O	2.11	0.50
1:A:11:LEU:O	1:A:14:ARG:HB2	2.12	0.50
1:C:904:PHE:CD2	1:C:961:VAL:HG22	2.47	0.50
1:A:85:SER:HB2	1:A:147:ASN:ND2	2.27	0.50
1:B:572:ARG:NE	1:B:572:ARG:HA	2.26	0.49
1:C:804:LYS:NZ	1:C:804:LYS:HB3	2.27	0.49
1:A:159:HIS:HB3	1:A:286:TYR:CE2	2.43	0.49
1:A:279:ARG:HE	1:A:281:GLU:HB3	1.77	0.49
1:B:682:LYS:HB2	1:B:682:LYS:NZ	2.26	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:812:LEU:HD13	1:C:825:TYR:CZ	2.47	0.49
1:A:104:PHE:HZ	1:A:286:TYR:CD2	2.30	0.49
1:A:329:LEU:HA	1:A:333:LEU:CD2	2.41	0.49
1:B:483:GLU:O	1:B:485:SER:N	2.45	0.49
1:A:118:ARG:HH12	1:A:312:ASP:HB2	1.77	0.49
1:B:708:ILE:HD13	1:B:716:ILE:HD11	1.94	0.49
1:C:1093:VAL:HG11	1:C:1116:ILE:HD13	1.95	0.49
1:A:151:ILE:HG23	1:A:317:ILE:HG21	1.93	0.49
1:C:895:GLY:N	1:C:977:THR:O	2.46	0.49
1:C:1086:TYR:N	1:C:1086:TYR:CD2	2.80	0.49
1:B:404:LYS:HZ2	1:B:404:LYS:CB	2.24	0.49
1:C:819:PRO:O	1:C:823:LYS:HG2	2.13	0.49
1:C:958:VAL:HG13	1:C:977:THR:HG23	1.95	0.49
1:B:558:VAL:HG13	1:B:577:THR:HG23	1.95	0.49
1:C:812:LEU:O	1:C:817:LEU:HD23	2.13	0.49
1:C:927:GLU:OE2	1:C:1033:CYS:HA	2.13	0.49
1:C:895:GLY:HA3	1:C:977:THR:HG22	1.95	0.49
1:C:911:MET:CE	1:C:1109:LEU:HD23	2.43	0.49
1:C:1108:ILE:HD13	1:C:1116:ILE:CD1	2.42	0.49
1:C:1094:THR:HG22	1:C:1096:HIS:CD2	2.48	0.48
1:A:104:PHE:CD2	1:A:161:VAL:HG22	2.48	0.48
1:A:304:ARG:NH1	1:A:307:GLU:OE1	2.46	0.48
1:C:1050:LEU:HD23	1:C:1050:LEU:O	2.12	0.48
1:A:216:THR:HG21	1:A:235:ASN:HA	1.95	0.48
1:A:295:ASP:OD2	1:A:297:ARG:NH1	2.46	0.48
1:C:1098:ILE:HD13	1:C:1120:LEU:CD2	2.43	0.48
1:A:283:ILE:HG13	1:A:297:ARG:HD2	1.95	0.48
1:B:660:GLU:O	1:B:663:GLU:HG3	2.12	0.48
1:C:808:ILE:HG22	1:C:812:LEU:CD1	2.44	0.48
1:C:852:LEU:O	1:C:858:ASN:HA	2.14	0.48
1:A:172:ARG:HE	1:A:172:ARG:CA	2.22	0.48
1:A:298:ILE:HD13	1:A:320:LEU:CD2	2.42	0.48
1:B:439:THR:O	1:B:443:LYS:HG3	2.14	0.48
1:C:1019:ALA:HB2	1:C:1034:GLN:HG2	1.95	0.48
1:C:1104:ARG:O	1:C:1108:ILE:HG13	2.14	0.48
1:A:1:MET:O	1:A:3:GLU:N	2.46	0.48
1:A:4:LYS:HA	1:A:7:GLU:CG	2.44	0.48
1:A:14:ARG:HB3	1:A:15:PRO:CD	2.38	0.48
1:A:115:TYR:HD1	1:A:311:GLY:O	1.97	0.48
1:A:172:ARG:NE	1:A:172:ARG:CA	2.76	0.48
1:A:290:GLN:HE22	1:A:292:ARG:HE	1.60	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:921:TRP:CD1	1:C:945:GLY:HA3	2.48	0.48
1:A:1:MET:CE	1:A:5:LYS:HZ1	2.27	0.47
1:A:81:SER:O	1:A:83:GLU:HG2	2.13	0.47
1:B:531:THR:HG22	1:B:535:GLY:H	1.79	0.47
1:A:93:ARG:NH2	1:A:138:GLU:OE2	2.47	0.47
1:A:327:ASN:OD1	1:A:328:ASN:N	2.47	0.47
1:C:928:ILE:CG2	1:C:939:VAL:HG23	2.44	0.47
1:C:892:ILE:HA	1:C:979:THR:O	2.14	0.47
1:A:18:THR:OG1	1:A:21:GLN:HG3	2.14	0.47
1:A:212:TYR:N	1:A:213:VAL:O	2.48	0.47
1:C:802:LYS:HZ2	1:C:804:LYS:HB3	1.79	0.47
1:A:166:VAL:HG13	2:A:2478:HOH:O	2.15	0.47
1:B:480:LEU:O	1:B:481:SER:O	2.33	0.47
1:B:660:GLU:O	1:B:664:ARG:HG2	2.14	0.47
1:C:863:GLU:O	1:C:867:LYS:HG3	2.13	0.47
1:A:93:ARG:HE	1:A:138:GLU:HG3	1.80	0.47
1:A:153:LYS:NZ	1:A:154:TYR:CZ	2.83	0.47
1:A:288:PHE:HA	1:A:305:LEU:CD2	2.45	0.47
1:A:300:TYR:CE1	1:A:319:LYS:HE3	2.50	0.47
1:B:660:GLU:C	1:B:662:LYS:H	2.18	0.47
1:C:848:PHE:HE1	1:C:865:TYR:CZ	2.32	0.47
1:C:1043:LYS:O	1:C:1047:LEU:HG	2.15	0.47
1:B:504:PHE:CE2	1:B:561:VAL:HG13	2.49	0.47
1:B:511:MET:CE	1:B:709:LEU:HA	2.44	0.47
1:C:801:MET:HB3	1:C:805:LYS:HB3	1.95	0.47
1:C:1094:THR:HA	1:C:1100:TYR:O	2.14	0.47
1:B:526:ALA:CB	1:B:540:VAL:HG22	2.37	0.47
1:B:547:ASN:ND2	1:B:550:GLY:N	2.61	0.47
1:A:255:TYR:CE2	1:A:259:LYS:HE3	2.50	0.47
1:B:447:GLU:O	1:B:451:LEU:HG	2.15	0.47
1:A:1:MET:H1	1:A:6:LYS:CB	2.10	0.46
1:A:62:ILE:H	1:A:62:ILE:CD1	2.28	0.46
1:C:811:LEU:O	1:C:814:ARG:CG	2.63	0.46
1:C:853:ARG:O	1:C:858:ASN:HB3	2.15	0.46
1:C:1082:LYS:HB2	1:C:1082:LYS:NZ	2.30	0.46
1:C:1093:VAL:HG11	1:C:1116:ILE:CD1	2.45	0.46
1:B:461:GLU:O	1:B:463:GLU:N	2.48	0.46
1:B:661:GLN:HG2	1:B:664:ARG:NH1	2.31	0.46
1:C:972:ARG:NE	1:C:972:ARG:CA	2.78	0.46
1:A:115:TYR:CE1	1:A:313:LEU:HB3	2.51	0.46
1:A:228:GLY:O	1:A:230:VAL:HG23	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:GLN:HE22	1:C:903:LEU:CD2	2.29	0.46
1:A:283:ILE:HG13	1:A:297:ARG:CD	2.46	0.46
1:A:1:MET:HE1	1:A:5:LYS:HZ1	1.81	0.46
1:B:401:MET:HB2	1:B:401:MET:HE2	1.61	0.46
1:B:401:MET:HE3	1:B:435:ILE:CD1	2.46	0.46
1:B:476:LEU:CD2	1:B:725:ILE:HD13	2.46	0.46
1:B:660:GLU:O	1:B:662:LYS:N	2.49	0.46
1:C:1062:LYS:HA	1:C:1062:LYS:HD3	1.75	0.46
1:A:1:MET:H2	1:A:6:LYS:N	2.10	0.46
1:A:7:GLU:O	1:A:11:LEU:HD23	2.15	0.46
1:A:166:VAL:HG23	1:A:167:THR:N	2.30	0.45
1:B:412:LEU:HD13	1:B:425:TYR:CE2	2.50	0.45
1:B:618:SER:O	1:B:634:GLN:HA	2.16	0.45
1:A:298:ILE:CD1	1:A:320:LEU:HD23	2.45	0.45
1:A:97:GLY:HA3	1:A:101:ALA:HB2	1.98	0.45
1:B:698:ILE:HD11	1:B:723:HIS:CB	2.46	0.45
1:C:817:LEU:HD13	1:C:818:THR:O	2.17	0.45
1:B:417:LEU:C	1:B:417:LEU:HD12	2.37	0.45
1:B:521:TRP:CD1	1:B:545:GLY:HA3	2.51	0.45
1:A:20:GLU:O	1:A:24:ASN:HB2	2.17	0.45
1:A:20:GLU:HA	1:A:23:LYS:NZ	2.31	0.45
1:B:406:LYS:HG2	1:B:410:LYS:HD3	1.99	0.45
1:B:545:GLY:O	1:B:546:LYS:C	2.55	0.45
1:C:831:LYS:O	1:C:835:ILE:HG13	2.17	0.45
1:C:864:LYS:HD2	1:C:864:LYS:O	2.17	0.45
1:C:1019:ALA:CB	1:C:1034:GLN:HG2	2.46	0.45
1:A:257:LEU:HD13	1:A:257:LEU:C	2.37	0.45
1:A:288:PHE:CD2	1:A:305:LEU:HD21	2.51	0.45
1:C:962:GLN:HG2	1:C:975:THR:HG22	1.98	0.45
1:A:239:GLN:HB2	2:A:2525:HOH:O	2.16	0.45
1:B:510:ARG:HH12	1:B:514:ARG:NH1	2.15	0.45
1:B:637:ARG:HD2	1:B:642:ASN:OD1	2.17	0.45
1:A:81:SER:HB2	1:A:83:GLU:OE2	2.16	0.45
1:B:483:GLU:O	1:B:484:ALA:C	2.55	0.45
1:A:53:ARG:HH11	1:A:53:ARG:HG2	1.82	0.45
1:C:1020:VAL:HG21	1:C:1042:ASN:HB3	1.98	0.45
1:A:8:ILE:O	1:A:12:LEU:HG	2.17	0.44
1:A:332:VAL:HG12	1:A:332:VAL:O	2.17	0.44
1:B:404:LYS:NZ	1:B:404:LYS:CB	2.81	0.44
1:A:1:MET:CG	2:A:2544:HOH:O	2.63	0.44
1:A:131:THR:N	1:A:135:GLY:O	2.44	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:528:ILE:HG23	1:B:539:VAL:HG23	1.98	0.44
1:B:683:ILE:HG13	1:B:697:ARG:CD	2.44	0.44
1:C:1079:ARG:NE	1:C:1081:GLU:HB3	2.24	0.44
1:A:23:LYS:O	1:A:27:MET:N	2.44	0.44
1:A:37:ASN:O	1:A:40:ASN:HB3	2.16	0.44
1:A:60:LEU:O	1:A:61:GLU:HG2	2.18	0.44
1:A:158:VAL:CG1	1:A:177:THR:HG23	2.44	0.44
1:C:816:ASP:O	1:C:817:LEU:CB	2.65	0.44
1:A:51:LEU:O	1:A:55:GLU:HB3	2.18	0.44
1:B:583:LEU:HD21	1:B:656:GLN:HG2	1.99	0.44
1:C:1029:ILE:CD1	1:C:1054:LEU:HA	2.47	0.44
1:A:258:GLN:O	1:A:262:LYS:HG2	2.17	0.44
1:B:401:MET:CE	1:B:435:ILE:HD12	2.47	0.44
1:B:476:LEU:HG	1:B:480:LEU:HD12	1.98	0.44
1:C:812:LEU:HD13	1:C:825:TYR:CE2	2.53	0.44
1:C:801:MET:N	1:C:832:ILE:HD13	2.33	0.44
1:A:37:ASN:O	1:A:40:ASN:N	2.49	0.44
1:B:600:ILE:HD13	1:B:643:LYS:HE3	1.98	0.44
1:B:717:ILE:O	1:B:721:ILE:HG13	2.17	0.44
1:A:256:GLN:O	1:A:260:GLU:HG3	2.17	0.44
1:B:429:TYR:O	1:B:432:ILE:HB	2.18	0.44
1:A:236:GLU:HG3	1:A:237:ARG:N	2.33	0.44
1:B:662:LYS:HA	1:B:662:LYS:HD3	1.78	0.44
1:B:722:GLU:O	1:B:726:GLU:HB2	2.18	0.44
1:A:77:LEU:HD13	1:A:81:SER:OG	2.18	0.43
1:A:160:ARG:CG	1:A:282:LYS:HD2	2.46	0.43
1:A:282:LYS:NZ	1:A:282:LYS:CB	2.81	0.43
1:B:549:TYR:CZ	1:B:584:PRO:HD3	2.53	0.43
1:A:1:MET:HB3	1:A:5:LYS:HB3	1.99	0.43
1:B:680:SER:O	1:B:681:GLU:C	2.56	0.43
1:C:1130:GLU:H	1:C:1130:GLU:CD	2.21	0.43
1:A:1:MET:HE2	1:A:1:MET:HB2	1.74	0.43
1:B:455:GLU:OE1	1:B:459:GLU:HG3	2.19	0.43
1:B:697:ARG:O	1:B:698:ILE:HD12	2.18	0.43
1:A:322:GLU:O	1:A:326:GLU:HB2	2.18	0.43
1:B:506:ARG:HB2	1:B:536:ILE:HG13	1.99	0.43
1:C:816:ASP:CG	1:C:817:LEU:N	2.72	0.43
1:C:828:GLU:HA	1:C:831:LYS:CD	2.48	0.43
1:A:307:GLU:HG3	2:A:2575:HOH:O	2.18	0.43
1:B:410:LYS:HE3	1:B:429:TYR:CZ	2.54	0.43
1:B:453:ARG:HG2	1:B:453:ARG:HH11	1.84	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:811:LEU:HA	1:C:814:ARG:HE	1.83	0.43
1:A:4:LYS:HB3	1:A:4:LYS:HZ3	1.83	0.43
1:B:401:MET:CB	1:B:405:LYS:HB3	2.47	0.43
1:C:1065:GLU:HA	1:C:1065:GLU:OE1	2.18	0.43
1:C:811:LEU:HA	1:C:814:ARG:HG3	2.00	0.43
1:C:817:LEU:HD11	1:C:822:MET:HB2	2.00	0.43
1:C:1034:GLN:HE21	1:C:1034:GLN:HB3	1.63	0.43
1:A:83:GLU:CG	1:A:84:ALA:H	2.30	0.43
1:A:86:ASP:O	1:A:144:LYS:HA	2.18	0.43
1:A:328:ASN:O	1:A:329:LEU:C	2.57	0.43
1:A:331:GLU:HG3	1:A:332:VAL:N	2.34	0.43
1:C:1098:ILE:CD1	1:C:1120:LEU:HD23	2.47	0.43
1:B:698:ILE:CG2	1:B:700:TYR:HB2	2.49	0.43
1:C:809:GLU:OE2	1:C:825:TYR:HB3	2.19	0.43
1:A:4:LYS:O	1:A:7:GLU:HB2	2.18	0.43
1:A:12:LEU:HD13	1:A:25:TYR:CZ	2.53	0.43
1:A:115:TYR:CD1	1:A:313:LEU:HB3	2.54	0.43
1:B:603:PHE:CD1	1:B:603:PHE:N	2.87	0.43
1:C:1084:ARG:HG3	1:C:1095:ASP:HA	1.99	0.43
1:B:547:ASN:HD21	1:B:550:GLY:H	1.62	0.42
1:B:420:GLU:HA	1:B:423:LYS:NZ	2.34	0.42
1:C:895:GLY:H	1:C:901:ALA:HB1	1.84	0.42
1:A:36:GLU:CD	2:A:2543:HOH:O	2.57	0.42
1:A:255:TYR:CZ	1:A:259:LYS:HE3	2.54	0.42
1:A:263:GLU:C	1:A:265:GLU:N	2.73	0.42
1:A:261:GLN:HA	1:A:264:ARG:HD3	2.00	0.42
1:B:547:ASN:HD21	1:B:550:GLY:CA	2.32	0.42
1:A:132:ASP:C	1:A:134:GLY:H	2.22	0.42
1:A:261:GLN:HG2	1:A:264:ARG:NH1	2.35	0.42
1:B:504:PHE:CD1	1:B:561:VAL:CG1	3.02	0.42
1:C:965:PRO:O	1:C:968:GLU:HB3	2.19	0.42
1:A:47:GLU:O	1:A:51:LEU:HG	2.19	0.42
1:A:66:GLU:OE1	1:A:69:LEU:HD12	2.18	0.42
1:C:805:LYS:NZ	1:C:828:GLU:OE2	2.46	0.42
1:A:8:ILE:HG22	1:A:12:LEU:CD1	2.49	0.42
1:A:161:VAL:O	1:A:175:THR:HA	2.19	0.42
1:A:11:LEU:O	1:A:14:ARG:CB	2.68	0.42
1:A:59:GLU:O	1:A:60:LEU:C	2.58	0.42
1:B:547:ASN:HD21	1:B:550:GLY:N	2.18	0.42
1:B:552:LEU:O	1:B:582:VAL:HG21	2.20	0.42
1:B:731:GLU:HA	1:B:731:GLU:OE2	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:906:ARG:HA	1:C:936:ILE:HD12	2.02	0.42
1:A:18:THR:O	1:A:21:GLN:HB2	2.19	0.42
1:A:282:LYS:HZ3	1:A:282:LYS:CB	2.31	0.41
1:B:463:GLU:O	1:B:463:GLU:HG2	2.18	0.41
1:C:851:LEU:O	1:C:855:GLU:HB3	2.20	0.41
1:B:446:GLN:C	1:B:448:PHE:N	2.73	0.41
1:A:260:GLU:C	1:A:262:LYS:H	2.24	0.41
1:A:329:LEU:HD12	1:A:329:LEU:N	2.27	0.41
1:C:1020:VAL:CG1	1:C:1021:ARG:N	2.82	0.41
1:A:4:LYS:HB3	1:A:4:LYS:HZ2	1.85	0.41
1:A:160:ARG:HE	1:A:285:THR:CG2	2.33	0.41
1:C:816:ASP:O	1:C:817:LEU:HB3	2.19	0.41
1:C:823:LYS:O	1:C:827:MET:HB2	2.20	0.41
1:C:1054:LEU:O	1:C:1058:GLN:HG3	2.20	0.41
1:A:48:PHE:HE1	1:A:65:TYR:CE2	2.38	0.41
1:B:482:PRO:O	1:B:483:GLU:CB	2.53	0.41
1:B:482:PRO:C	1:B:484:ALA:H	2.22	0.41
1:B:515:TYR:HD1	1:B:711:GLY:O	2.04	0.41
1:C:832:ILE:O	1:C:836:GLU:HB2	2.21	0.41
1:B:694:THR:HG23	1:B:701:THR:OG1	2.21	0.41
1:C:802:LYS:NZ	1:C:804:LYS:HB3	2.35	0.41
1:C:904:PHE:CG	1:C:961:VAL:HG22	2.55	0.41
1:A:85:SER:HA	2:A:2409:HOH:O	2.21	0.41
1:A:167:THR:HG22	1:B:600:ILE:O	2.21	0.41
1:C:947:ASN:HD22	1:C:947:ASN:HA	1.63	0.41
1:A:1:MET:H3	1:A:5:LYS:C	2.25	0.41
1:A:297:ARG:C	1:A:298:ILE:HD12	2.42	0.41
1:B:466:GLU:HA	1:B:466:GLU:OE1	2.19	0.41
1:B:661:GLN:HA	1:B:664:ARG:CG	2.50	0.41
1:C:1066:ILE:O	1:C:1068:GLN:N	2.54	0.41
1:A:14:ARG:CB	1:A:15:PRO:HD2	2.41	0.41
1:C:807:GLU:O	1:C:811:LEU:HD23	2.20	0.41
1:C:854:GLU:C	1:C:856:GLY:H	2.24	0.41
1:C:1023:THR:HG23	1:C:1030:VAL:HG22	2.03	0.41
1:A:67:LYS:NZ	2:A:2432:HOH:O	2.54	0.40
1:B:682:LYS:HB2	1:B:682:LYS:HZ3	1.86	0.40
1:C:801:MET:HB3	1:C:805:LYS:HD3	2.03	0.40
1:C:814:ARG:HB3	1:C:815:PRO:CD	2.51	0.40
1:A:4:LYS:O	1:A:7:GLU:N	2.49	0.40
1:C:1090:GLN:HE21	1:C:1092:ARG:NE	2.12	0.40
1:A:83:GLU:HG3	1:A:84:ALA:H	1.87	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:282:LYS:HB2	1:A:282:LYS:NZ	2.35	0.40
1:C:1021:ARG:HA	1:C:1031:VAL:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	313/342 (92%)	266 (85%)	31 (10%)	16 (5%)	2	2
1	B	308/342 (90%)	265 (86%)	29 (9%)	14 (4%)	2	2
1	C	308/342 (90%)	266 (86%)	33 (11%)	9 (3%)	4	6
All	All	929/1026 (90%)	797 (86%)	93 (10%)	39 (4%)	3	3

All (39) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	15	PRO
1	A	57	GLU
1	A	60	LEU
1	A	329	LEU
1	B	415	PRO
1	B	460	LEU
1	B	485	SER
1	B	730	GLU
1	C	817	LEU
1	C	860	LEU
1	C	1130	GLU
1	A	61	GLU
1	A	237	ARG
1	A	328	ASN
1	A	330	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	331	GLU
1	B	417	LEU
1	B	457	GLU
1	B	484	ALA
1	B	661	GLN
1	B	681	GLU
1	C	1129	LEU
1	A	58	ASN
1	A	261	GLN
1	B	402	LYS
1	B	481	SER
1	C	815	PRO
1	C	861	GLU
1	C	971	GLY
1	A	84	ALA
1	A	171	GLY
1	A	266	ILE
1	B	461	GLU
1	B	546	LYS
1	C	883	GLU
1	C	946	LYS
1	A	17	LEU
1	A	24	ASN
1	B	482	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	287/303 (95%)	262 (91%)	25 (9%)	10	15
1	B	282/303 (93%)	256 (91%)	26 (9%)	9	13
1	C	282/303 (93%)	255 (90%)	27 (10%)	8	12
All	All	851/909 (94%)	773 (91%)	78 (9%)	9	13

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	11	LEU
1	A	15	PRO
1	A	20	GLU
1	A	39	THR
1	A	54	GLU
1	A	57	GLU
1	A	62	ILE
1	A	63	GLU
1	A	64	LYS
1	A	83	GLU
1	A	86	ASP
1	A	113	THR
1	A	128	ILE
1	A	131	THR
1	A	161	VAL
1	A	203	PHE
1	A	216	THR
1	A	225	LEU
1	A	234	GLN
1	A	253	ARG
1	A	263	GLU
1	A	282	LYS
1	A	297	ARG
1	A	329	LEU
1	B	402	LYS
1	B	415	PRO
1	B	420	GLU
1	B	450	GLU
1	B	454	GLU
1	B	457	GLU
1	B	462	ILE
1	B	464	LYS
1	B	468	GLU
1	B	483	GLU
1	B	513	THR
1	B	531	THR
1	B	540	VAL
1	B	547	ASN
1	B	561	VAL
1	B	568	GLU
1	B	575	THR
1	B	603	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	625	LEU
1	B	634	GLN
1	B	653	ARG
1	B	682	LYS
1	B	698	ILE
1	B	724	ASP
1	B	728	ASN
1	B	729	LEU
1	C	802	LYS
1	C	803	GLU
1	C	811	LEU
1	C	815	PRO
1	C	850	GLU
1	C	854	GLU
1	C	862	ILE
1	C	864	LYS
1	C	883	GLU
1	C	885	SER
1	C	931	THR
1	C	940	VAL
1	C	947	ASN
1	C	961	VAL
1	C	977	THR
1	C	1003	PHE
1	C	1025	LEU
1	C	1034	GLN
1	C	1042	ASN
1	C	1053	ARG
1	C	1082	LYS
1	C	1083	ILE
1	C	1086	TYR
1	C	1092	ARG
1	C	1097	ARG
1	C	1124	ASP
1	C	1133	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	122	ASN
1	A	174	HIS
1	A	234	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	261	GLN
1	A	268	GLN
1	A	290	GLN
1	A	296	HIS
1	A	323	HIS
1	A	328	ASN
1	B	547	ASN
1	B	661	GLN
1	B	668	GLN
1	B	690	GLN
1	B	696	HIS
1	B	727	ASN
1	C	837	ASN
1	C	840	ASN
1	C	974	HIS
1	C	1034	GLN
1	C	1068	GLN
1	C	1090	GLN
1	C	1096	HIS
1	C	1127	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	212:TYR	C	213:VAL	N	1.20

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	319/342 (93%)	0.56	40 (12%) 3 2	8, 37, 130, 170	0
1	B	314/342 (91%)	0.39	21 (6%) 17 14	10, 36, 118, 183	0
1	C	314/342 (91%)	0.52	32 (10%) 6 4	8, 35, 127, 179	0
All	All	947/1026 (92%)	0.49	93 (9%) 7 5	8, 36, 128, 183	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1132	VAL	13.3
1	A	17	LEU	11.1
1	B	664	ARG	9.9
1	C	1066	ILE	9.6
1	A	56	GLY	9.5
1	C	856	GLY	9.4
1	B	668	GLN	8.9
1	B	456	GLY	7.6
1	C	857	GLU	7.3
1	A	215	LYS	7.0
1	A	8	ILE	6.9
1	B	663	GLU	6.8
1	B	666	ILE	6.7
1	C	1067	SER	6.5
1	C	1068	GLN	6.2
1	A	212	TYR	6.1
1	A	213	VAL	5.9
1	C	1006	SER	5.8
1	B	732	VAL	5.4
1	A	57	GLU	5.4
1	B	457	GLU	5.3
1	B	667	SER	5.2
1	A	264	ARG	5.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	1079	ARG	5.1
1	C	1007	GLY	5.0
1	A	15	PRO	4.9
1	C	802	LYS	4.8
1	B	679	ARG	4.8
1	C	1064	ARG	4.8
1	A	267	SER	4.5
1	B	607	GLY	4.5
1	A	329	LEU	4.4
1	A	216	THR	4.4
1	A	51	LEU	4.3
1	C	814	ARG	4.3
1	C	883	GLU	4.3
1	A	4	LYS	4.0
1	C	1065	GLU	4.0
1	B	415	PRO	3.9
1	A	268	GLN	3.9
1	A	1	MET	3.9
1	C	1131	GLU	3.9
1	A	330	GLU	3.8
1	C	970	GLY	3.8
1	C	808	ILE	3.8
1	C	855	GLU	3.8
1	C	1133	LEU	3.8
1	C	1080	SER	3.7
1	A	25	TYR	3.7
1	B	401	MET	3.6
1	B	482	PRO	3.6
1	C	858	ASN	3.6
1	A	9	GLU	3.5
1	C	815	PRO	3.4
1	B	665	GLU	3.3
1	C	817	LEU	3.2
1	A	265	GLU	3.2
1	A	5	LYS	3.2
1	A	65	TYR	3.2
1	A	279	ARG	3.2
1	A	332	VAL	3.1
1	A	12	LEU	3.1
1	A	16	ASP	3.0
1	A	62	ILE	3.0
1	A	24	ASN	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	819	PRO	2.9
1	A	172	ARG	2.8
1	C	801	MET	2.8
1	A	55	GLU	2.8
1	C	862	ILE	2.7
1	A	53	ARG	2.7
1	C	860	LEU	2.7
1	B	414	ARG	2.7
1	A	47	GLU	2.7
1	A	54	GLU	2.6
1	C	882	PRO	2.6
1	B	733	LEU	2.6
1	A	58	ASN	2.5
1	C	884	ALA	2.5
1	A	14	ARG	2.4
1	A	280	SER	2.4
1	C	824	ASN	2.4
1	A	207	GLY	2.4
1	C	859	GLU	2.4
1	A	214	ASN	2.4
1	B	417	LEU	2.3
1	A	7	GLU	2.3
1	B	731	GLU	2.3
1	B	481	SER	2.2
1	A	11	LEU	2.2
1	B	405	LYS	2.1
1	C	816	ASP	2.1
1	B	458	ASN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.