



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 6, 2024 – 12:04 AM EDT

PDB ID : 1SQ4
Title : Crystal Structure of the Putative Glyoxylate Induced Protein from *Pseudomonas aeruginosa*, Northeast Structural Genomics Target PaR14
Authors : Forouhar, F.; Chen, Y.; Xiao, R.; Acton, T.B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2004-03-17
Resolution : 2.70 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

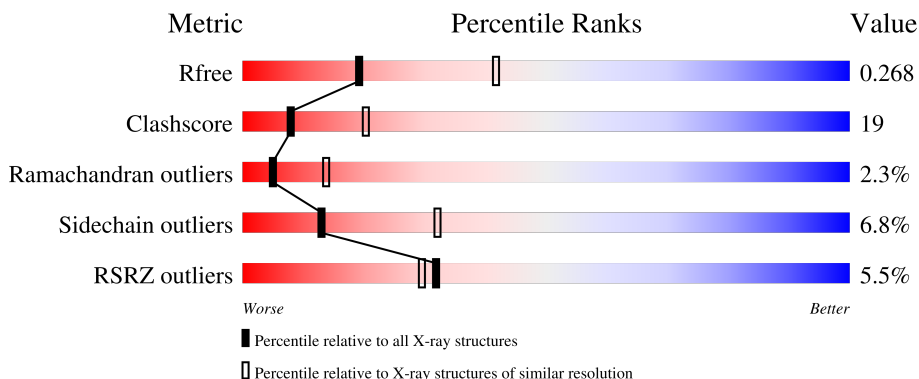
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (2.70-2.70)

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	278	
1	B	278	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4412 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 Glyoxylate-induced Protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	270	Total	C	N	O	S	Se	0	0	0
			2167	1387	377	389	2	12			
1	B	267	Total	C	N	O	S	Se	0	0	0
			2144	1371	374	385	2	12			

There are 26 discrepancies between the modelled and reference sequences:

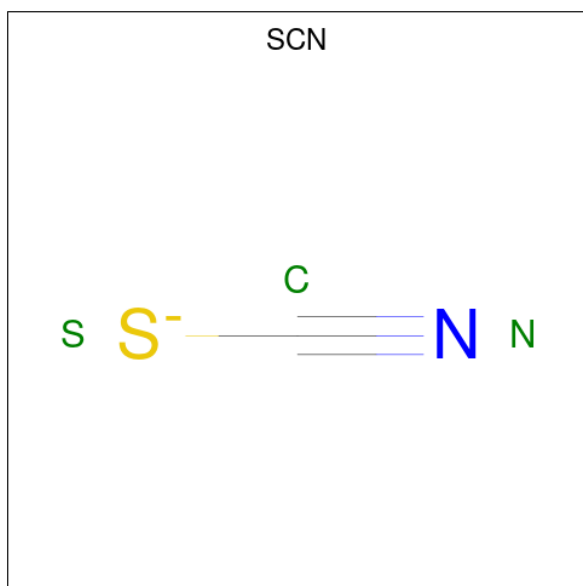
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP Q9I4J5
A	25	MSE	MET	modified residue	UNP Q9I4J5
A	38	MSE	MET	modified residue	UNP Q9I4J5
A	52	MSE	MET	modified residue	UNP Q9I4J5
A	54	MSE	MET	modified residue	UNP Q9I4J5
A	112	MSE	MET	modified residue	UNP Q9I4J5
A	169	MSE	MET	modified residue	UNP Q9I4J5
A	184	MSE	MET	modified residue	UNP Q9I4J5
A	187	MSE	MET	modified residue	UNP Q9I4J5
A	191	MSE	MET	modified residue	UNP Q9I4J5
A	212	MSE	MET	modified residue	UNP Q9I4J5
A	240	MSE	MET	modified residue	UNP Q9I4J5
A	270	MSE	MET	modified residue	UNP Q9I4J5
B	1	MSE	MET	modified residue	UNP Q9I4J5
B	25	MSE	MET	modified residue	UNP Q9I4J5
B	38	MSE	MET	modified residue	UNP Q9I4J5
B	52	MSE	MET	modified residue	UNP Q9I4J5
B	54	MSE	MET	modified residue	UNP Q9I4J5
B	112	MSE	MET	modified residue	UNP Q9I4J5
B	169	MSE	MET	modified residue	UNP Q9I4J5
B	184	MSE	MET	modified residue	UNP Q9I4J5
B	187	MSE	MET	modified residue	UNP Q9I4J5
B	191	MSE	MET	modified residue	UNP Q9I4J5
B	212	MSE	MET	modified residue	UNP Q9I4J5
B	240	MSE	MET	modified residue	UNP Q9I4J5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	270	MSE	MET	modified residue	UNP Q9I4J5

- Molecule 2 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	S	0	0
			3	1	1	1		
2	A	1	Total	C	N	S	0	0
			3	1	1	1		
2	B	1	Total	C	N	S	0	0
			3	1	1	1		
2	B	1	Total	C	N	S	0	0
			3	1	1	1		

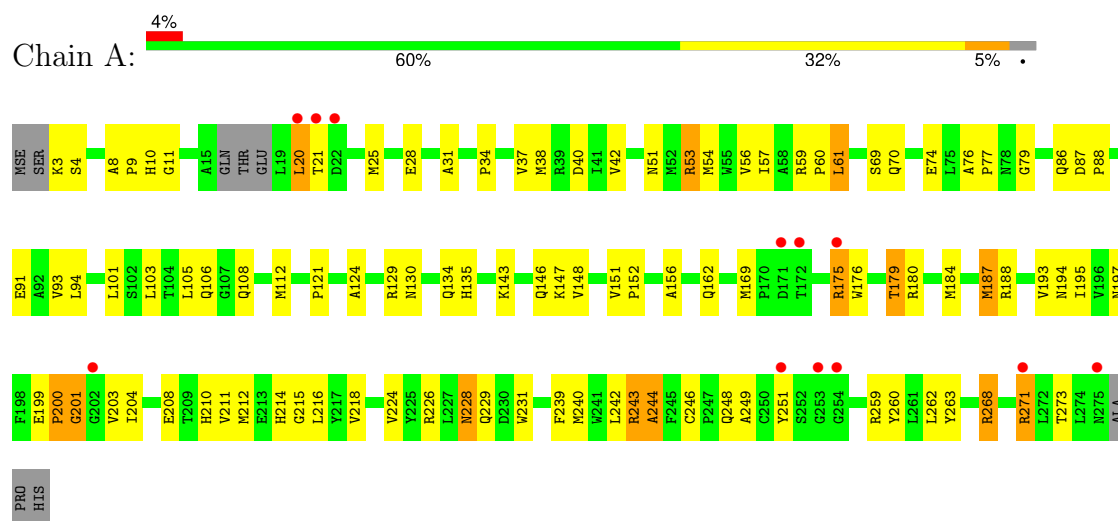
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	52	Total	O	0	0
			52	52		
3	B	37	Total	O	0	0
			37	37		

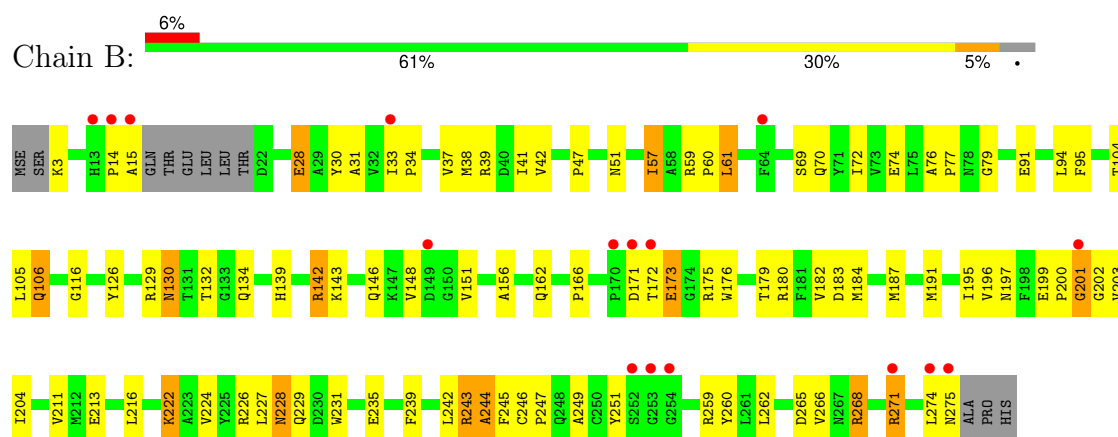
3 Residue-property plots [i](#)

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: Glyoxylate-induced Protein



• Molecule 1: Glyoxylate-induced Protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α , β , γ	106.86Å 106.86Å 107.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.75 – 2.70 29.75 – 2.70	Depositor EDS
% Data completeness (in resolution range)	9.7 (29.75-2.70) 98.5 (29.75-2.70)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.79 (at 2.68Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.213 , 0.262 0.203 , 0.268	Depositor DCC
R_{free} test set	1724 reflections (9.77%)	wwPDB-VP
Wilson B-factor (Å ²)	24.8	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 32.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.017 for -h,l,k 0.000 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4412	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SCN

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	0.42	0/2222	0.62	0/3002
1	B	0.41	0/2199	0.60	0/2970
All	All	0.41	0/4421	0.61	0/5972

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2167	0	2076	85	1
1	B	2144	0	2047	80	0
2	A	6	0	0	1	0
2	B	6	0	0	1	0
3	A	52	0	0	3	0
3	B	37	0	0	3	0
All	All	4412	0	4123	164	1

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 19.

All (164) 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:B:226:ARG:HB3	1:B:249:ALA:HB3	1.51	0.93
1:B:180:ARG:HD3	1:B:184:MSE:HE3	1.48	0.93
1:B:179:THR:HG23	1:B:197:ASN:HD21	1.34	0.92
1:A:31:ALA:HB2	1:A:61:LEU:HD13	1.52	0.90
1:B:57:ILE:HG23	1:B:70:GLN:HB3	1.53	0.89
1:A:226:ARG:HB3	1:A:249:ALA:HB3	1.58	0.85
1:A:268:ARG:HG3	2:A:301:SCN:S	2.18	0.83
1:B:271:ARG:HD2	1:B:271:ARG:H	1.44	0.82
1:A:179:THR:HG22	1:A:197:ASN:HD21	1.44	0.81
1:A:180:ARG:HD3	1:A:184:MSE:HE3	1.66	0.76
1:B:31:ALA:HB2	1:B:61:LEU:HD13	1.71	0.72
1:B:148:VAL:HG13	1:B:151:VAL:HB	1.70	0.72
1:A:148:VAL:HG13	1:A:151:VAL:HB	1.72	0.72
1:A:103:LEU:HB2	1:A:112:MSE:HE2	1.72	0.71
1:A:242:LEU:HD23	1:A:246:CYS:HB3	1.72	0.70
1:A:216:LEU:HD23	1:A:240:MSE:HE3	1.72	0.69
1:B:175:ARG:HD3	1:B:202:GLY:H	1.58	0.69
1:A:243:ARG:O	1:A:244:ALA:HB2	1.94	0.68
1:A:4:SER:H	1:A:162:GLN:NE2	1.93	0.67
1:B:33:ILE:HG13	1:B:33:ILE:O	1.93	0.67
1:B:166:PRO:HB3	1:B:179:THR:HG22	1.76	0.66
1:B:79:GLY:O	1:B:129:ARG:HD3	1.96	0.66
1:A:231:TRP:HB2	1:B:231:TRP:HB2	1.79	0.65
1:B:176:TRP:HE1	1:B:196:VAL:CG1	2.10	0.65
1:A:3:LYS:HG3	1:A:162:GLN:HE22	1.63	0.64
1:B:130:ASN:ND2	1:B:132:THR:H	1.96	0.64
1:B:142:ARG:HH11	1:B:142:ARG:HG3	1.62	0.64
1:B:213:GLU:HB3	1:B:243:ARG:O	1.99	0.62
1:A:57:ILE:HG23	1:A:70:GLN:HB3	1.81	0.62
1:A:28:GLU:H	1:A:28:GLU:CD	2.03	0.61
1:A:101:LEU:HD23	1:A:112:MSE:HE3	1.81	0.61
1:A:53:ARG:HD3	1:A:74:GLU:CD	2.20	0.61
1:B:228:ASN:HB2	1:B:247:PRO:HD2	1.81	0.61
1:B:216:LEU:HG	1:B:260:TYR:CE2	2.35	0.61
1:A:215:GLY:O	1:A:216:LEU:HD12	2.01	0.61
1:A:31:ALA:HB2	1:A:61:LEU:CD1	2.27	0.60
1:B:28:GLU:H	1:B:28:GLU:CD	2.06	0.59
1:A:121:PRO:HG2	1:A:124:ALA:HB2	1.84	0.59
1:A:175:ARG:HG2	1:A:201:GLY:HA3	1.86	0.58
1:B:175:ARG:CD	1:B:201:GLY:HA3	2.34	0.58
1:A:184:MSE:HG3	3:A:320:HOH:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:33:ILE:CG1	1:B:239:PHE:HB3	2.35	0.57
1:B:39:ARG:O	1:B:42:VAL:HG12	2.04	0.57
1:B:59:ARG:N	1:B:60:PRO:HD3	2.19	0.57
1:B:3:LYS:HE3	1:B:162:GLN:HE22	1.70	0.57
1:A:77:PRO:HD3	1:A:135:HIS:CD2	2.40	0.57
1:A:146:GLN:CD	1:A:268:ARG:HG2	2.25	0.57
1:A:218:VAL:HA	1:A:260:TYR:HB3	1.86	0.57
1:B:106:GLN:HE21	1:B:106:GLN:HA	1.70	0.57
1:B:31:ALA:HB2	1:B:61:LEU:CD1	2.34	0.57
1:B:57:ILE:HD11	1:B:239:PHE:CE2	2.40	0.56
1:A:146:GLN:NE2	1:A:268:ARG:HG2	2.19	0.56
1:A:4:SER:H	1:A:162:GLN:HE21	1.52	0.56
1:A:169:MSE:HG3	1:A:176:TRP:CD2	2.41	0.56
1:A:203:VAL:C	1:A:204:ILE:HD12	2.26	0.55
1:A:204:ILE:HD12	1:A:204:ILE:N	2.22	0.55
1:B:142:ARG:HG3	1:B:142:ARG:NH1	2.22	0.55
1:B:224:VAL:HG12	1:B:231:TRP:HE3	1.72	0.54
1:B:146:GLN:CD	1:B:268:ARG:HG2	2.29	0.53
1:A:91:GLU:HG2	1:A:143:LYS:O	2.08	0.53
1:B:173:GLU:HB3	1:B:175:ARG:NH1	2.24	0.53
1:B:105:LEU:HD21	1:B:156:ALA:HB1	1.90	0.53
1:A:262:LEU:C	1:A:262:LEU:HD23	2.28	0.52
1:B:51:ASN:HB3	1:B:76:ALA:HB3	1.91	0.52
1:A:243:ARG:O	1:A:244:ALA:CB	2.55	0.52
1:B:274:LEU:HD12	1:B:274:LEU:N	2.24	0.52
1:B:243:ARG:O	1:B:244:ALA:HB2	2.10	0.52
1:B:179:THR:OG1	1:B:195:ILE:HB	2.09	0.52
1:B:226:ARG:NH1	1:B:229:GLN:H	2.08	0.52
1:A:57:ILE:HD11	1:A:239:PHE:CD2	2.45	0.51
1:A:179:THR:O	1:A:194:ASN:HB3	2.10	0.51
1:B:38:MSE:HA	1:B:38:MSE:HE2	1.92	0.51
1:B:47:PRO:HD2	2:B:304:SCN:N	2.26	0.51
1:A:199:GLU:C	1:A:201:GLY:H	2.13	0.51
1:A:226:ARG:HE	1:A:229:GLN:CA	2.24	0.51
1:B:199:GLU:C	1:B:201:GLY:H	2.14	0.50
1:B:244:ALA:C	1:B:246:CYS:H	2.15	0.50
1:B:175:ARG:HD3	1:B:201:GLY:HA3	1.92	0.50
1:A:226:ARG:HE	1:A:229:GLN:HA	1.75	0.50
1:B:204:ILE:HD12	1:B:204:ILE:N	2.27	0.49
1:B:203:VAL:HG22	1:B:251:TYR:CE1	2.47	0.49
1:B:176:TRP:HE1	1:B:196:VAL:HG13	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:ASN:HB3	1:A:76:ALA:HB3	1.95	0.49
1:B:242:LEU:HD12	1:B:242:LEU:N	2.28	0.48
1:A:9:PRO:O	1:A:10:HIS:HD2	1.95	0.48
1:A:152:PRO:HG2	1:A:188:ARG:HD3	1.95	0.48
1:B:33:ILE:HG13	1:B:239:PHE:HB3	1.95	0.48
1:A:203:VAL:HG22	1:A:251:TYR:CE1	2.48	0.48
1:A:226:ARG:HH21	1:A:229:GLN:HA	1.79	0.48
1:A:216:LEU:HD23	1:A:240:MSE:CE	2.43	0.48
1:B:61:LEU:HD23	1:B:243:ARG:HH11	1.77	0.48
1:A:211:VAL:HG13	1:A:212:MSE:HE3	1.96	0.47
1:B:15:ALA:HA	3:B:325:HOH:O	2.15	0.47
1:A:57:ILE:HD11	1:A:239:PHE:CE2	2.50	0.47
1:A:216:LEU:HG	1:A:260:TYR:CE2	2.49	0.47
1:B:72:ILE:HG12	1:B:139:HIS:CE1	2.50	0.47
1:A:208:GLU:HG3	1:A:248:GLN:HE21	1.80	0.46
1:B:130:ASN:HD22	1:B:132:THR:H	1.63	0.46
1:A:34:PRO:O	1:A:37:VAL:HG23	2.15	0.46
1:A:211:VAL:HG13	1:A:212:MSE:CE	2.46	0.46
1:A:11:GLY:HA3	1:A:40:ASP:OD2	2.16	0.46
1:A:271:ARG:H	1:A:271:ARG:HD2	1.80	0.46
1:B:14:PRO:HG2	1:B:39:ARG:NH2	2.31	0.46
1:B:262:LEU:C	1:B:262:LEU:HD23	2.35	0.46
1:B:57:ILE:HD11	1:B:239:PHE:CD2	2.51	0.46
1:A:59:ARG:N	1:A:60:PRO:HD3	2.32	0.45
1:A:31:ALA:CB	1:A:61:LEU:HD13	2.35	0.45
1:A:79:GLY:O	1:A:129:ARG:HD3	2.17	0.45
1:B:130:ASN:HD22	1:B:130:ASN:C	2.20	0.45
1:A:57:ILE:O	1:A:57:ILE:HG13	2.17	0.45
1:A:208:GLU:HG3	1:A:248:GLN:NE2	2.32	0.44
1:A:228:ASN:O	1:A:229:GLN:HB2	2.16	0.44
1:B:244:ALA:O	1:B:245:PHE:HB2	2.16	0.44
1:A:54:MSE:HE3	1:A:56:VAL:HG22	2.00	0.44
1:B:226:ARG:CZ	1:B:229:GLN:HA	2.47	0.44
1:A:226:ARG:HG3	3:A:321:HOH:O	2.17	0.44
1:A:210:HIS:HB3	1:A:214:HIS:CE1	2.53	0.44
1:B:30:TYR:CD2	1:B:227:LEU:HD13	2.53	0.44
1:B:91:GLU:HG3	1:B:191:MSE:HE2	2.00	0.44
1:A:105:LEU:HD21	1:A:156:ALA:HB1	1.99	0.44
1:B:187:MSE:O	1:B:268:ARG:NH1	2.46	0.44
1:A:242:LEU:HD23	1:A:246:CYS:CB	2.46	0.43
1:A:4:SER:HB2	1:A:162:GLN:HE21	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:LEU:HD23	1:A:112:MSE:CE	2.45	0.43
1:A:187:MSE:O	1:A:268:ARG:NH1	2.49	0.43
1:A:224:VAL:HG12	1:A:231:TRP:HE3	1.83	0.43
1:A:3:LYS:CG	1:A:162:GLN:HE22	2.31	0.43
1:A:94:LEU:HD23	1:A:112:MSE:HE1	2.00	0.43
1:B:34:PRO:O	1:B:37:VAL:HG23	2.18	0.43
1:B:95:PHE:HA	1:B:116:GLY:O	2.17	0.43
1:B:106:GLN:HE21	1:B:106:GLN:CA	2.31	0.43
1:B:182:VAL:HG12	1:B:183:ASP:N	2.33	0.43
1:B:265:ASP:C	1:B:266:VAL:HG13	2.40	0.43
1:A:203:VAL:HG12	1:A:204:ILE:N	2.34	0.42
1:A:244:ALA:C	1:A:246:CYS:H	2.21	0.42
1:B:274:LEU:HD12	1:B:274:LEU:H	1.84	0.42
1:B:76:ALA:O	1:B:77:PRO:C	2.56	0.42
1:A:169:MSE:HG3	1:A:176:TRP:CE3	2.54	0.42
1:B:61:LEU:HD12	1:B:61:LEU:HA	1.82	0.42
1:A:42:VAL:HG22	1:A:42:VAL:O	2.20	0.42
1:A:86:GLN:HA	1:A:86:GLN:OE1	2.19	0.42
1:A:8:ALA:HA	1:A:9:PRO:HD3	1.92	0.42
1:B:172:THR:HG21	1:B:176:TRP:HB3	2.02	0.42
1:B:211:VAL:CG2	1:B:245:PHE:CE1	3.02	0.42
1:B:57:ILE:O	1:B:57:ILE:HG13	2.20	0.42
1:B:222:LYS:HG3	1:B:235:GLU:HB3	2.02	0.42
1:B:104:THR:O	1:B:126:TYR:HA	2.20	0.41
1:B:129:ARG:HB2	3:B:339:HOH:O	2.20	0.41
1:A:184:MSE:CG	3:A:320:HOH:O	2.65	0.41
1:B:179:THR:CG2	1:B:197:ASN:HD21	2.19	0.41
1:A:224:VAL:HG12	1:A:231:TRP:CE3	2.56	0.41
1:A:20:LEU:HD12	1:A:20:LEU:O	2.21	0.41
1:B:91:GLU:HG2	1:B:143:LYS:O	2.20	0.41
1:B:199:GLU:O	1:B:201:GLY:N	2.54	0.41
1:A:93:VAL:HG21	1:A:193:VAL:HG21	2.01	0.41
1:A:179:THR:HG23	1:A:195:ILE:O	2.21	0.40
1:A:87:ASP:HA	1:A:88:PRO:HD2	1.93	0.40
1:A:262:LEU:HD23	1:A:263:TYR:N	2.37	0.40
1:B:244:ALA:C	1:B:246:CYS:N	2.74	0.40
1:A:200:PRO:O	1:A:201:GLY:O	2.40	0.40
1:B:74:GLU:HG2	3:B:331:HOH:O	2.21	0.40
1:A:147:LYS:NZ	1:A:148:VAL:O	2.54	0.40
1:A:25:MSE:HA	1:A:25:MSE:HE2	2.03	0.40
1:B:226:ARG:CB	1:B:249:ALA:HB3	2.35	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:GLN:OE1	1:A:108:GLN:OE1[8_666]	1.88	0.32

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	266/278 (96%)	243 (91%)	17 (6%)	6 (2%)	5	14
1	B	263/278 (95%)	239 (91%)	18 (7%)	6 (2%)	5	14
All	All	529/556 (95%)	482 (91%)	35 (7%)	12 (2%)	5	14

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	244	ALA
1	A	38	MSE
1	A	201	GLY
1	A	21	THR
1	B	201	GLY
1	B	228	ASN
1	B	244	ALA
1	A	228	ASN
1	B	171	ASP
1	B	41	ILE
1	B	200	PRO
1	A	200	PRO

5.3.2 Protein sidechains [i](#)

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	229/223 (103%)	214 (93%)	15 (7%)	14	33
1	B	226/223 (101%)	210 (93%)	16 (7%)	12	30
All	All	455/446 (102%)	424 (93%)	31 (7%)	13	32

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	LEU
1	A	53	ARG
1	A	61	LEU
1	A	69	SER
1	A	106	GLN
1	A	130	ASN
1	A	134	GLN
1	A	175	ARG
1	A	179	THR
1	A	187	MSE
1	A	243	ARG
1	A	259	ARG
1	A	268	ARG
1	A	271	ARG
1	A	273	THR
1	B	28	GLU
1	B	57	ILE
1	B	61	LEU
1	B	69	SER
1	B	94	LEU
1	B	106	GLN
1	B	130	ASN
1	B	134	GLN
1	B	142	ARG
1	B	173	GLU
1	B	222	LYS
1	B	243	ARG
1	B	259	ARG
1	B	268	ARG
1	B	271	ARG
1	B	275	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	HIS
1	A	113	GLN
1	A	130	ASN
1	A	134	GLN
1	A	135	HIS
1	A	146	GLN
1	A	162	GLN
1	A	192	HIS
1	A	248	GLN
1	B	10	HIS
1	B	86	GLN
1	B	106	GLN
1	B	130	ASN
1	B	134	GLN
1	B	146	GLN
1	B	192	HIS
1	B	248	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SCN	A	302	-	1,2,2	0.40	0	0,1,1	-	-
2	SCN	B	304	-	1,2,2	0.40	0	0,1,1	-	-
2	SCN	B	303	-	1,2,2	0.33	0	0,1,1	-	-
2	SCN	A	301	-	1,2,2	0.51	0	0,1,1	-	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	304	SCN	1	0
2	A	301	SCN	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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	258/278 (92%)	-0.02	12 (4%) 37 35	2, 13, 39, 63	0
1	B	255/278 (91%)	0.07	16 (6%) 27 25	3, 17, 44, 74	0
All	All	513/556 (92%)	0.03	28 (5%) 32 29	2, 15, 43, 74	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	172	THR	5.6
1	B	15	ALA	5.4
1	B	14	PRO	4.9
1	B	171	ASP	4.1
1	B	13	HIS	3.9
1	A	253	GLY	3.7
1	A	21	THR	3.6
1	A	172	THR	3.6
1	B	275	ASN	3.5
1	A	202	GLY	3.5
1	A	20	LEU	3.2
1	A	171	ASP	3.1
1	A	251	TYR	3.0
1	A	254	GLY	3.0
1	B	253	GLY	2.9
1	A	175	ARG	2.8
1	B	201	GLY	2.7
1	A	275	ASN	2.7
1	B	170	PRO	2.6
1	B	274	LEU	2.5
1	A	22	ASP	2.4
1	A	271	ARG	2.3
1	B	254	GLY	2.3
1	B	271	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	149	ASP	2.2
1	B	33	ILE	2.2
1	B	252	SER	2.1
1	B	64	PHE	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SCN	B	304	3/3	0.91	0.11	32,32,33,34	0
2	SCN	A	301	3/3	0.93	0.11	24,24,25,25	0
2	SCN	A	302	3/3	0.96	0.07	21,21,21,22	0
2	SCN	B	303	3/3	0.97	0.11	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.