



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 2, 2024 – 09:41 AM EST

PDB ID : 1HPL
Title : HORSE PANCREATIC LIPASE. THE CRYSTAL STRUCTURE AT 2.3
ANGSTROMS RESOLUTION
Authors : Bourne, Y.; Cambillau, C.
Deposited on : 1993-01-27
Resolution : 2.30 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)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

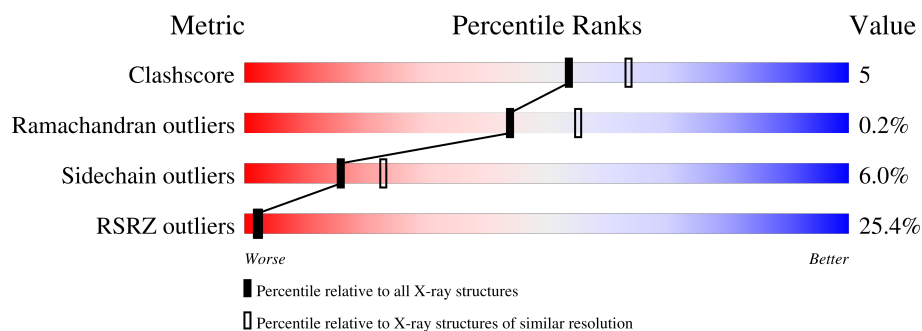
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	449	<div> <div>14%</div> <div>83%</div> <div>13%</div> <div>.</div> </div>
1	B	449	<div> <div>37%</div> <div>78%</div> <div>18%</div> <div>..</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7709 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 LIPASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	449	Total	C	N	O	S	0	0	0
			3501	2205	601	676	19			
1	B	449	Total	C	N	O	S	0	0	0
			3501	2205	601	676	19			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		

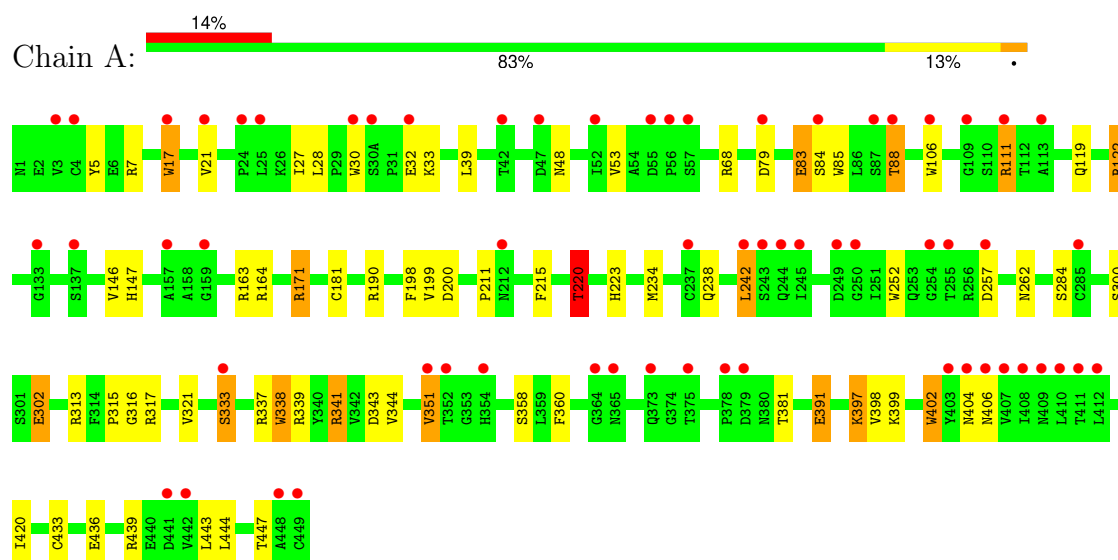
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	397	Total	O	0	0
			397	397		
3	B	308	Total	O	0	0
			308	308		

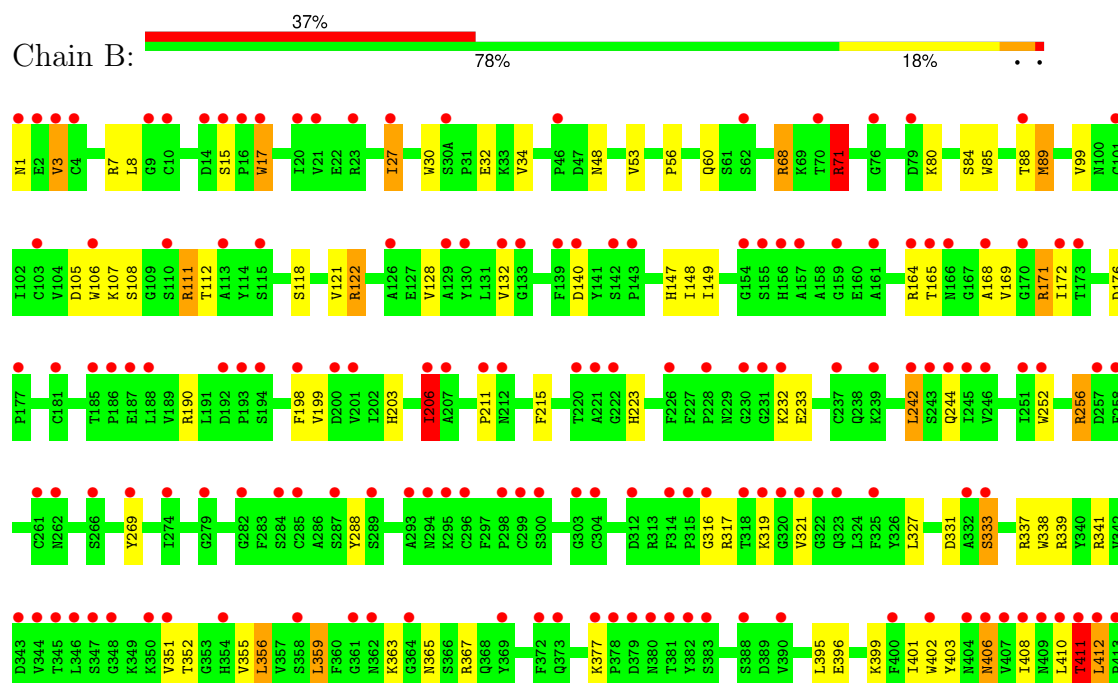
3 Residue-property plots [i](#)

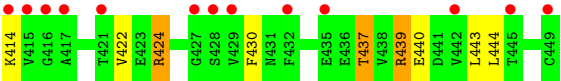
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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: LIPASE



• Molecule 1: LIPASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.80Å 97.20Å 145.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.30 6.00 – 2.31	Depositor EDS
% Data completeness (in resolution range)	(Not available) (6.00-2.30) 81.3 (6.00-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.159 , (Not available) 0.331 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	18.9	Xtriage
Anisotropy	0.244	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 102.7	EDS
L-test for twinning ¹	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.81	EDS
Total number of atoms	7709	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 30.58 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2770e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Theoretical 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: CA

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	0.83	1/3587 (0.0%)	1.60	52/4867 (1.1%)
1	B	0.83	0/3587	1.71	67/4867 (1.4%)
All	All	0.83	1/7174 (0.0%)	1.65	119/9734 (1.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	3
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	146	VAL	CA-CB	5.60	1.66	1.54

All (119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	333	SER	O-C-N	-21.47	88.34	122.70
1	A	333	SER	O-C-N	-19.70	91.19	122.70
1	B	122	ARG	NE-CZ-NH1	19.23	129.91	120.30
1	A	339	ARG	NE-CZ-NH2	-17.82	111.39	120.30
1	B	171	ARG	NE-CZ-NH1	17.45	129.03	120.30
1	B	164	ARG	NE-CZ-NH2	-16.29	112.16	120.30
1	B	122	ARG	NE-CZ-NH2	-15.84	112.38	120.30
1	B	7	ARG	NE-CZ-NH2	-14.68	112.96	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	164	ARG	NE-CZ-NH2	-14.28	113.16	120.30
1	B	7	ARG	NE-CZ-NH1	12.68	126.64	120.30
1	A	339	ARG	NE-CZ-NH1	11.96	126.28	120.30
1	B	71	ARG	NE-CZ-NH2	-11.72	114.44	120.30
1	A	164	ARG	NE-CZ-NH1	11.68	126.14	120.30
1	A	122	ARG	NE-CZ-NH1	11.17	125.88	120.30
1	B	171	ARG	NE-CZ-NH2	-10.76	114.92	120.30
1	B	339	ARG	NE-CZ-NH1	10.76	125.68	120.30
1	B	317	ARG	NE-CZ-NH2	-10.41	115.09	120.30
1	A	171	ARG	NE-CZ-NH2	-10.37	115.11	120.30
1	B	337	ARG	NE-CZ-NH2	-10.04	115.28	120.30
1	B	68	ARG	NE-CZ-NH2	-9.86	115.37	120.30
1	A	171	ARG	NE-CZ-NH1	9.63	125.11	120.30
1	B	30	TRP	CD1-CG-CD2	9.54	113.93	106.30
1	B	71	ARG	NE-CZ-NH1	9.47	125.04	120.30
1	B	317	ARG	NE-CZ-NH1	9.39	125.00	120.30
1	B	333	SER	CA-C-N	9.28	137.62	117.20
1	B	339	ARG	NE-CZ-NH2	-9.27	115.67	120.30
1	A	333	SER	CA-C-N	9.17	137.38	117.20
1	B	68	ARG	NE-CZ-NH1	9.07	124.84	120.30
1	A	122	ARG	NE-CZ-NH2	-8.99	115.81	120.30
1	B	17	TRP	CD1-CG-CD2	8.78	113.32	106.30
1	A	439	ARG	NE-CZ-NH1	8.34	124.47	120.30
1	B	164	ARG	NE-CZ-NH1	8.24	124.42	120.30
1	A	313	ARG	NE-CZ-NH2	-8.19	116.21	120.30
1	A	5	TYR	CB-CG-CD1	-8.16	116.10	121.00
1	B	439	ARG	NE-CZ-NH1	8.16	124.38	120.30
1	A	252	TRP	CD1-CG-CD2	8.12	112.80	106.30
1	B	17	TRP	CE2-CD2-CG	-8.02	100.88	107.30
1	A	17	TRP	CD1-CG-CD2	8.00	112.70	106.30
1	B	85	TRP	CD1-CG-CD2	7.95	112.66	106.30
1	B	111	ARG	NE-CZ-NH1	7.92	124.26	120.30
1	B	337	ARG	NE-CZ-NH1	7.80	124.20	120.30
1	A	402	TRP	CD1-CG-CD2	7.69	112.45	106.30
1	A	30	TRP	CD1-CG-CD2	7.67	112.44	106.30
1	A	17	TRP	CE2-CD2-CG	-7.64	101.19	107.30
1	A	341	ARG	NE-CZ-NH1	7.61	124.11	120.30
1	A	85	TRP	CD1-CG-CD2	7.61	112.39	106.30
1	B	402	TRP	CD1-CG-CD2	7.58	112.36	106.30
1	A	17	TRP	CG-CD2-CE3	7.57	140.71	133.90
1	B	30	TRP	CE2-CD2-CG	-7.49	101.31	107.30
1	B	85	TRP	CE2-CD2-CG	-7.47	101.32	107.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	190	ARG	NE-CZ-NH1	7.46	124.03	120.30
1	B	424	ARG	NE-CZ-NH2	-7.43	116.59	120.30
1	A	338	TRP	CD1-CG-CD2	7.36	112.18	106.30
1	A	163	ARG	NE-CZ-NH1	7.21	123.91	120.30
1	A	85	TRP	CE2-CD2-CG	-7.16	101.57	107.30
1	A	30	TRP	CE2-CD2-CG	-7.12	101.60	107.30
1	B	256	ARG	NE-CZ-NH1	7.09	123.84	120.30
1	B	338	TRP	CD1-CG-CD2	7.00	111.90	106.30
1	A	7	ARG	NE-CZ-NH1	6.95	123.78	120.30
1	B	402	TRP	CE2-CD2-CG	-6.95	101.74	107.30
1	B	3	VAL	CB-CA-C	-6.93	98.23	111.40
1	A	252	TRP	CE2-CD2-CG	-6.92	101.76	107.30
1	A	317	ARG	NE-CZ-NH2	-6.80	116.90	120.30
1	B	106	TRP	CE2-CD2-CG	-6.77	101.88	107.30
1	B	424	ARG	CB-CG-CD	-6.72	94.14	111.60
1	B	111	ARG	NE-CZ-NH2	-6.65	116.97	120.30
1	B	206	ILE	CA-CB-CG1	-6.64	98.38	111.00
1	B	288	TYR	CB-CG-CD1	-6.62	117.03	121.00
1	A	17	TRP	CB-CG-CD1	-6.62	118.39	127.00
1	B	252	TRP	CD1-CG-CD2	6.52	111.52	106.30
1	B	269	TYR	CB-CG-CD2	-6.45	117.13	121.00
1	B	30	TRP	CG-CD1-NE1	-6.42	103.67	110.10
1	B	411	THR	CA-C-N	-6.40	103.12	117.20
1	B	256	ARG	NE-CZ-NH2	-6.38	117.11	120.30
1	A	300	SER	N-CA-CB	-6.29	101.06	110.50
1	A	338	TRP	CE2-CD2-CG	-6.28	102.28	107.30
1	B	338	TRP	CE2-CD2-CG	-6.27	102.28	107.30
1	A	337	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	B	190	ARG	NE-CZ-NH1	6.25	123.42	120.30
1	B	17	TRP	CB-CG-CD1	-6.25	118.88	127.00
1	B	8	LEU	CA-C-N	6.23	128.66	116.20
1	B	252	TRP	CE2-CD2-CG	-6.21	102.33	107.30
1	B	367	ARG	CA-CB-CG	6.19	127.02	113.40
1	A	106	TRP	CE2-CD2-CG	-6.17	102.36	107.30
1	B	17	TRP	CG-CD2-CE3	6.14	139.43	133.90
1	A	315	PRO	CA-C-N	6.11	128.42	116.20
1	B	8	LEU	O-C-N	-6.10	112.84	123.20
1	A	337	ARG	NE-CZ-NH2	-6.07	117.27	120.30
1	A	402	TRP	CE2-CD2-CG	-6.07	102.45	107.30
1	B	356	LEU	CA-CB-CG	6.05	129.23	115.30
1	A	402	TRP	CG-CD1-NE1	-5.97	104.13	110.10
1	B	106	TRP	CD1-CG-CD2	5.85	110.98	106.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	242	LEU	CA-CB-CG	5.80	128.64	115.30
1	A	190	ARG	NE-CZ-NH2	-5.77	117.42	120.30
1	B	176	ASP	CB-CG-OD1	5.75	123.47	118.30
1	A	397	LYS	CA-CB-CG	5.72	125.99	113.40
1	B	171	ARG	CB-CG-CD	5.67	126.34	111.60
1	A	106	TRP	CD1-CG-CD2	5.66	110.83	106.30
1	B	17	TRP	CG-CD1-NE1	-5.65	104.45	110.10
1	B	333	SER	CA-C-O	5.63	131.92	120.10
1	B	341	ARG	CG-CD-NE	-5.57	100.11	111.80
1	A	68	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	A	30	TRP	CG-CD1-NE1	-5.40	104.70	110.10
1	A	85	TRP	CB-CG-CD1	-5.40	119.98	127.00
1	B	331	ASP	CB-CG-OD1	5.39	123.15	118.30
1	A	111	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	B	27	ILE	CA-CB-CG1	-5.34	100.86	111.00
1	A	252	TRP	CG-CD1-NE1	-5.32	104.78	110.10
1	B	85	TRP	CB-CG-CD1	-5.29	120.12	127.00
1	B	27	ILE	CA-CB-CG2	5.28	121.46	110.90
1	B	206	ILE	N-CA-CB	-5.27	98.68	110.80
1	A	21	VAL	CA-CB-CG2	-5.23	103.06	110.90
1	B	89	MET	CG-SD-CE	-5.15	91.96	100.20
1	B	363	LYS	CB-CG-CD	-5.15	98.22	111.60
1	A	220	THR	N-CA-CB	-5.14	100.54	110.30
1	A	17	TRP	CG-CD1-NE1	-5.08	105.02	110.10
1	A	85	TRP	CA-CB-CG	5.08	123.35	113.70
1	A	300	SER	CA-CB-OG	5.04	124.80	111.20
1	A	338	TRP	CG-CD1-NE1	-5.00	105.10	110.10

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	333	SER	Peptide,Mainchain
1	B	333	SER	Peptide,Mainchain
1	B	71	ARG	Sidechain

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	3501	0	3334	32	2
1	B	3501	0	3334	39	2
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	397	0	0	7	1
3	B	308	0	0	1	2
All	All	7709	0	6668	66	4

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 5.

All (66) 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:165:THR:HG21	1:B:169:VAL:HG23	1.57	0.85
1:B:395:LEU:HD22	1:B:422:VAL:HG11	1.63	0.78
1:A:443:LEU:H	1:B:48:ASN:HD21	1.32	0.77
1:A:111:ARG:HH21	1:B:408:ILE:HG23	1.56	0.70
1:B:399:LYS:HD3	1:B:443:LEU:HD13	1.74	0.68
1:B:84:SER:O	1:B:88:THR:HG23	1.95	0.67
1:B:199:VAL:H	1:B:223:HIS:HD2	1.44	0.64
1:A:84:SER:O	1:A:88:THR:HG23	1.99	0.62
1:A:242:LEU:HD22	1:A:242:LEU:H	1.70	0.56
1:B:232:LYS:HD3	1:B:233:GLU:HG3	1.88	0.56
1:A:147:HIS:CD2	1:A:171:ARG:HG2	2.42	0.55
1:B:171:ARG:HD3	1:B:198:PHE:CD2	2.42	0.55
1:B:412:LEU:HD12	1:B:439:ARG:HD2	1.89	0.55
1:B:147:HIS:CD2	1:B:171:ARG:HG2	2.42	0.55
1:A:360:PHE:CZ	1:A:399:LYS:HE2	2.42	0.54
1:A:199:VAL:H	1:A:223:HIS:HD2	1.57	0.52
1:A:48:ASN:HD21	1:B:443:LEU:H	1.58	0.52
1:A:79:ASP:HA	3:A:1097:HOH:O	2.09	0.52
1:B:71:ARG:HD2	1:B:99:VAL:HG21	1.93	0.51
1:A:223:HIS:HA	1:A:321:VAL:HA	1.93	0.51
1:B:128:VAL:O	1:B:132:VAL:HG13	2.10	0.51
1:B:422:VAL:HG13	1:B:430:PHE:HB2	1.93	0.51
1:B:89:MET:HE3	1:B:149:ILE:HD13	1.93	0.50
1:A:234:MET:H	1:A:262:ASN:ND2	2.10	0.50
1:A:316:GLY:HA3	3:A:1306:HOH:O	2.12	0.49
1:A:27:ILE:HG13	1:A:119:GLN:HG3	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:TRP:CZ3	1:A:122:ARG:HD3	2.49	0.48
1:A:88:THR:HG22	3:A:1038:HOH:O	2.15	0.47
1:B:203:HIS:HB3	1:B:206:ILE:CD1	2.45	0.47
1:A:341:ARG:HH11	1:A:341:ARG:HG3	1.80	0.47
1:B:223:HIS:HA	1:B:321:VAL:HA	1.96	0.47
1:B:359:LEU:HG	1:B:395:LEU:HD21	1.96	0.46
1:B:17:TRP:CZ3	1:B:122:ARG:HD3	2.51	0.46
1:A:220:THR:HG23	3:A:1083:HOH:O	2.17	0.45
1:B:118:SER:O	1:B:121:VAL:HG22	2.16	0.45
1:A:358:SER:OG	1:A:399:LYS:HB2	2.17	0.45
1:B:411:THR:HG22	1:B:412:LEU:HD22	1.99	0.45
1:B:403:TYR:HA	1:B:440:GLU:HG3	1.98	0.44
1:A:33:LYS:HE3	3:A:1032:HOH:O	2.17	0.44
1:A:443:LEU:H	1:B:48:ASN:ND2	2.08	0.44
1:B:414:LYS:HB3	1:B:437:THR:HB	1.99	0.44
1:B:352:THR:O	1:B:406:ASN:HB2	2.17	0.44
1:A:181:CYS:SG	3:A:968:HOH:O	2.62	0.44
1:A:48:ASN:HD21	1:B:443:LEU:N	2.16	0.44
1:B:165:THR:HG22	1:B:168:ALA:HB3	2.00	0.43
1:B:377:LYS:HD2	3:B:1119:HOH:O	2.17	0.43
1:B:412:LEU:HD12	1:B:439:ARG:CD	2.47	0.43
1:B:316:GLY:HA2	1:B:319:LYS:HG2	2.01	0.42
1:B:34:VAL:O	1:B:108:SER:HB2	2.19	0.42
1:A:171:ARG:HD2	1:A:200:ASP:OD1	2.19	0.42
1:B:105:ASP:OD2	1:B:107:LYS:HE3	2.19	0.42
1:B:401:ILE:HB	1:B:443:LEU:HD23	2.02	0.42
1:A:344:VAL:O	1:A:381:THR:HA	2.20	0.41
1:A:398:VAL:HG11	1:A:420:ILE:HG21	2.02	0.41
1:B:171:ARG:HA	1:B:198:PHE:O	2.19	0.41
1:A:351:VAL:HG11	1:A:402:TRP:CZ3	2.55	0.41
1:A:83:GLU:H	1:A:83:GLU:CD	2.23	0.41
1:A:171:ARG:HD3	1:A:198:PHE:CD2	2.55	0.41
1:B:351:VAL:HG22	1:B:352:THR:N	2.36	0.41
1:B:424:ARG:HH11	1:B:424:ARG:HD2	1.74	0.41
1:A:338:TRP:CD1	1:A:391:GLU:HG3	2.56	0.40
1:B:148:ILE:O	1:B:172:ILE:HA	2.21	0.40
1:B:56:PRO:O	1:B:60:GLN:HB2	2.21	0.40
1:A:238:GLN:H	1:A:238:GLN:CD	2.24	0.40
1:A:343:ASP:O	1:A:420:ILE:HA	2.22	0.40
1:A:433:CYS:HB3	3:A:1124:HOH:O	2.21	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1:ASN:OD1	3:A:1307:HOH:O[2_565]	1.68	0.52
1:A:302:GLU:OE2	3:B:1043:HOH:O[2_564]	1.97	0.23
1:B:256:ARG:NH2	1:B:396:GLU:OE2[3_655]	2.12	0.08
1:A:302:GLU:CD	3:B:1043:HOH:O[2_564]	2.18	0.02

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	447/449 (100%)	431 (96%)	16 (4%)	0	100	100
1	B	447/449 (100%)	430 (96%)	15 (3%)	2 (0%)	30	39
All	All	894/898 (100%)	861 (96%)	31 (4%)	2 (0%)	44	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	410	LEU
1	B	411	THR

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	385/385 (100%)	364 (94%)	21 (6%)	18	26
1	B	385/385 (100%)	360 (94%)	25 (6%)	14	20

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	770/770 (100%)	724 (94%)	46 (6%)	16	23

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	32	GLU
1	A	39	LEU
1	A	53	VAL
1	A	83	GLU
1	A	88	THR
1	A	211	PRO
1	A	215	PHE
1	A	220	THR
1	A	242	LEU
1	A	257	ASP
1	A	284	SER
1	A	302	GLU
1	A	351	VAL
1	A	391	GLU
1	A	397	LYS
1	A	404	ASN
1	A	406	ASN
1	A	436	GLU
1	A	444	LEU
1	A	447	THR
1	B	3	VAL
1	B	15	SER
1	B	27	ILE
1	B	32	GLU
1	B	53	VAL
1	B	68	ARG
1	B	80	LYS
1	B	111	ARG
1	B	112	THR
1	B	140	ASP
1	B	206	ILE
1	B	211	PRO
1	B	215	PHE
1	B	242	LEU
1	B	244	GLN
1	B	327	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	355	VAL
1	B	356	LEU
1	B	359	LEU
1	B	365	ASN
1	B	406	ASN
1	B	411	THR
1	B	412	LEU
1	B	437	THR
1	B	444	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	ASN
1	A	223	HIS
1	A	262	ASN
1	A	328	ASN
1	A	404	ASN
1	B	48	ASN
1	B	223	HIS
1	B	328	ASN

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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 ⓘ

Warning: The R factor obtained from EDS is 0.331, which does not match the depositor's R factor of 0.159. Please interpret the results in this section carefully.

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	449/449 (100%)	1.11	62 (13%) 8 8	3, 16, 38, 49	0
1	B	449/449 (100%)	1.79	166 (36%) 1 1	3, 16, 38, 57	0
All	All	898/898 (100%)	1.45	228 (25%) 2 2	3, 16, 38, 57	0

All (228) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	378	PRO	5.5
1	B	411	THR	5.2
1	A	412	LEU	4.9
1	B	409	ASN	4.8
1	B	351	VAL	4.6
1	B	408	ILE	4.5
1	B	416	GLY	4.5
1	B	379	ASP	4.5
1	B	402	TRP	4.4
1	A	411	THR	4.4
1	A	30	TRP	4.1
1	A	410	LEU	4.1
1	B	192	ASP	4.0
1	A	257	ASP	4.0
1	B	14	ASP	3.9
1	B	15	SER	3.9
1	B	207	ALA	3.7
1	B	126	ALA	3.6
1	B	143	PRO	3.6
1	A	408	ILE	3.6
1	B	314	PHE	3.6
1	B	415	VAL	3.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	372	PHE	3.5
1	A	373	GLN	3.5
1	A	407	VAL	3.5
1	A	365	ASN	3.4
1	B	404	ASN	3.4
1	B	20	ILE	3.4
1	B	220	THR	3.4
1	B	320	GLY	3.4
1	B	142	SER	3.3
1	A	25	LEU	3.3
1	B	294	ASN	3.3
1	B	373	GLN	3.2
1	A	3	VAL	3.2
1	B	400	PHE	3.2
1	B	154	GLY	3.2
1	B	187	GLU	3.1
1	A	254	GLY	3.1
1	B	429	VAL	3.1
1	B	261	CYS	3.1
1	B	427	GLY	3.1
1	B	194	SER	3.1
1	B	380	ASN	3.1
1	B	321	VAL	3.1
1	B	369	TYR	3.1
1	B	322	GLY	3.0
1	B	410	LEU	3.0
1	B	417	ALA	3.0
1	B	245	ILE	3.0
1	B	285	CYS	3.0
1	B	348	GLY	3.0
1	A	57	SER	3.0
1	B	325	PHE	3.0
1	B	350	LYS	3.0
1	B	345	THR	2.9
1	B	166	ASN	2.9
1	B	347	SER	2.9
1	A	442	VAL	2.9
1	B	343	ASP	2.9
1	B	246	VAL	2.9
1	B	232	LYS	2.9
1	B	242	LEU	2.9
1	A	30(A)	SER	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	244	GLN	2.9
1	B	407	VAL	2.9
1	B	435	GLU	2.9
1	A	364	GLY	2.8
1	A	245	ILE	2.8
1	A	137	SER	2.8
1	A	352	THR	2.8
1	B	9	GLY	2.8
1	A	55	ASP	2.8
1	B	3	VAL	2.8
1	B	221	ALA	2.8
1	B	449	CYS	2.8
1	B	354	HIS	2.8
1	A	333	SER	2.8
1	B	113	ALA	2.7
1	B	332	ALA	2.7
1	B	243	SER	2.7
1	B	344	VAL	2.7
1	B	157	ALA	2.7
1	B	165	THR	2.7
1	B	132	VAL	2.7
1	B	377	LYS	2.7
1	B	289	SER	2.7
1	B	46	PRO	2.7
1	B	231	GLY	2.6
1	A	255	THR	2.6
1	B	106	TRP	2.6
1	B	252	TRP	2.6
1	B	299	CYS	2.6
1	B	304	CYS	2.6
1	B	383	SER	2.6
1	B	442	VAL	2.6
1	A	42	THR	2.6
1	B	284	SER	2.6
1	B	323	GLN	2.6
1	A	351	VAL	2.6
1	B	101	CYS	2.6
1	B	193	PRO	2.6
1	A	441	ASP	2.6
1	B	140	ASP	2.6
1	A	111	ARG	2.6
1	B	164	ARG	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	1	ASN	2.6
1	A	52	ILE	2.6
1	B	413	PRO	2.6
1	B	296	CYS	2.6
1	B	133	GLY	2.5
1	A	403	TYR	2.5
1	A	244	GLN	2.5
1	B	333	SER	2.5
1	A	249	ASP	2.5
1	A	242	LEU	2.5
1	B	421	THR	2.5
1	B	414	LYS	2.5
1	B	115	SER	2.5
1	B	300	SER	2.5
1	A	379	ASP	2.5
1	A	17	TRP	2.5
1	A	109	GLY	2.5
1	B	293	ALA	2.5
1	B	432	PHE	2.5
1	B	185	THR	2.5
1	B	282	GLY	2.5
1	B	316	GLY	2.5
1	B	201	VAL	2.5
1	B	206	ILE	2.4
1	B	358	SER	2.4
1	B	21	VAL	2.4
1	B	88	THR	2.4
1	B	173	THR	2.4
1	B	381	THR	2.4
1	B	16	PRO	2.4
1	B	27	ILE	2.4
1	B	130	TYR	2.4
1	B	76	GLY	2.4
1	B	222	GLY	2.4
1	B	230	GLY	2.4
1	A	448	ALA	2.4
1	A	409	ASN	2.4
1	A	88	THR	2.4
1	B	428	SER	2.4
1	A	250	GLY	2.4
1	B	279	GLY	2.4
1	B	168	ALA	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	226	PHE	2.4
1	A	159	GLY	2.4
1	B	156	HIS	2.4
1	B	303	GLY	2.4
1	B	258	PHE	2.3
1	B	177	PRO	2.3
1	B	262	ASN	2.3
1	B	181	CYS	2.3
1	A	375	THR	2.3
1	B	70	THR	2.3
1	B	318	THR	2.3
1	B	390	VAL	2.3
1	B	30(A)	SER	2.3
1	A	113	ALA	2.3
1	B	161	ALA	2.3
1	B	239	LYS	2.3
1	B	10	CYS	2.3
1	B	445	THR	2.3
1	B	312	ASP	2.3
1	B	269	TYR	2.3
1	A	212	ASN	2.3
1	B	62	SER	2.3
1	B	110	SER	2.3
1	B	159	GLY	2.3
1	B	198	PHE	2.2
1	A	237	CYS	2.2
1	B	17	TRP	2.2
1	B	266	SER	2.2
1	B	212	ASN	2.2
1	B	382	TYR	2.2
1	A	354	HIS	2.2
1	A	285	CYS	2.2
1	B	4	CYS	2.2
1	A	133	GLY	2.2
1	B	346	LEU	2.2
1	B	362	ASN	2.2
1	A	79	ASP	2.2
1	B	237	CYS	2.2
1	A	84	SER	2.2
1	A	243	SER	2.2
1	A	32	GLU	2.2
1	A	106	TRP	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	404	ASN	2.2
1	A	406	ASN	2.2
1	B	406	ASN	2.2
1	B	412	LEU	2.2
1	B	298	PRO	2.2
1	B	315	PRO	2.2
1	B	257	ASP	2.2
1	A	449	CYS	2.1
1	B	155	SER	2.1
1	A	47	ASP	2.1
1	B	79	ASP	2.1
1	B	170	GLY	2.1
1	B	361	GLY	2.1
1	A	56	PRO	2.1
1	B	129	ALA	2.1
1	B	2	GLU	2.1
1	B	200	ASP	2.1
1	B	172	ILE	2.1
1	B	295	LYS	2.1
1	A	157	ALA	2.1
1	A	21	VAL	2.1
1	B	23	ARG	2.1
1	B	139	PHE	2.1
1	B	364	GLY	2.1
1	B	388	SER	2.1
1	B	251	ILE	2.1
1	B	228	PRO	2.1
1	A	87	SER	2.0
1	B	287	SER	2.0
1	B	274	ILE	2.0
1	B	319	LYS	2.0
1	A	4	CYS	2.0
1	A	24	PRO	2.0
1	A	378	PRO	2.0
1	B	186	PRO	2.0
1	B	188	LEU	2.0
1	B	211	PRO	2.0
1	B	103	CYS	2.0

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

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	CA	B	970	1/1	0.66	0.12	21,21,21,21	0
2	CA	A	960	1/1	0.67	0.08	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.