



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 16, 2018 – 11:34 AM EST

PDB ID : 3H8E
Title : Low pH native structure of leucine aminopeptidase from *Pseudomonas putida*
Authors : Kale, A.; Dijkstra, B.W.; Sonke, T.; Thunnissen, A.M.W.H.
Deposited on : 2009-04-29
Resolution : 2.75 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

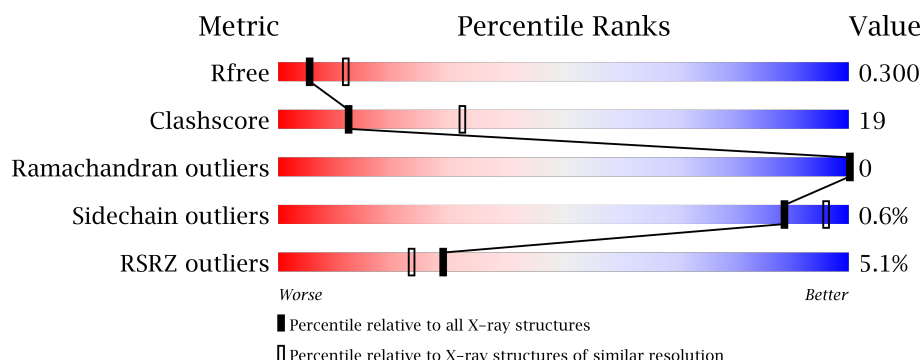
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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}	100719	3666 (2.80-2.72)
Clashscore	112137	4174 (2.80-2.72)
Ramachandran outliers	110173	4103 (2.80-2.72)
Sidechain outliers	110143	4106 (2.80-2.72)
RSRZ outliers	101464	3697 (2.80-2.72)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	497	<div> <div>5%</div> <div> <div></div> <div>74%</div> <div>18%</div> <div>• 5%</div> </div> </div>
1	B	497	<div> <div>5%</div> <div> <div></div> <div>71%</div> <div>21%</div> <div>• 5%</div> </div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7006 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.

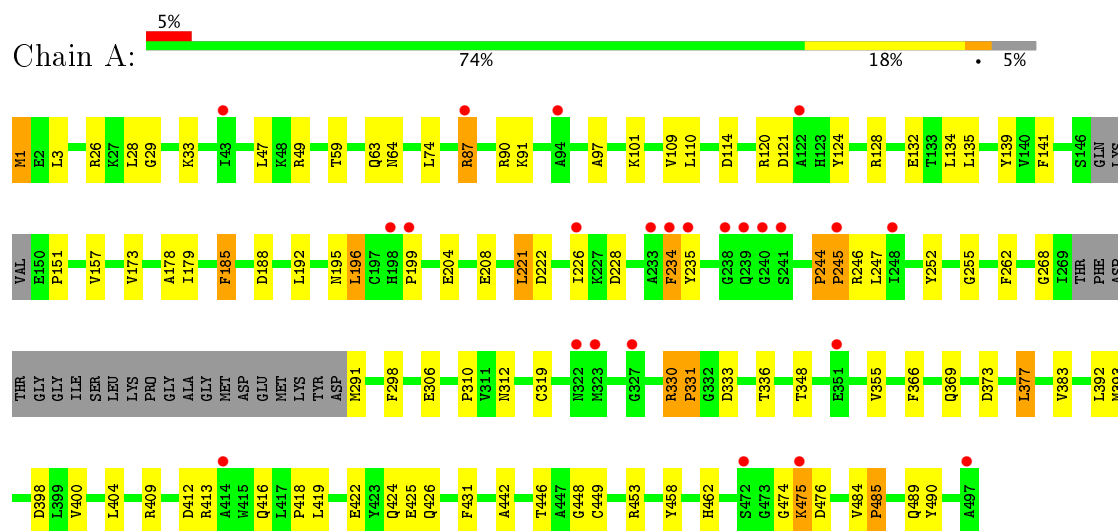
- Molecule 1 is a protein called Cytosol aminopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	473	Total	C	N	O	S	0	0	0
			3503	2212	616	659	16			
1	B	473	Total	C	N	O	S	0	0	0
			3503	2212	616	659	16			

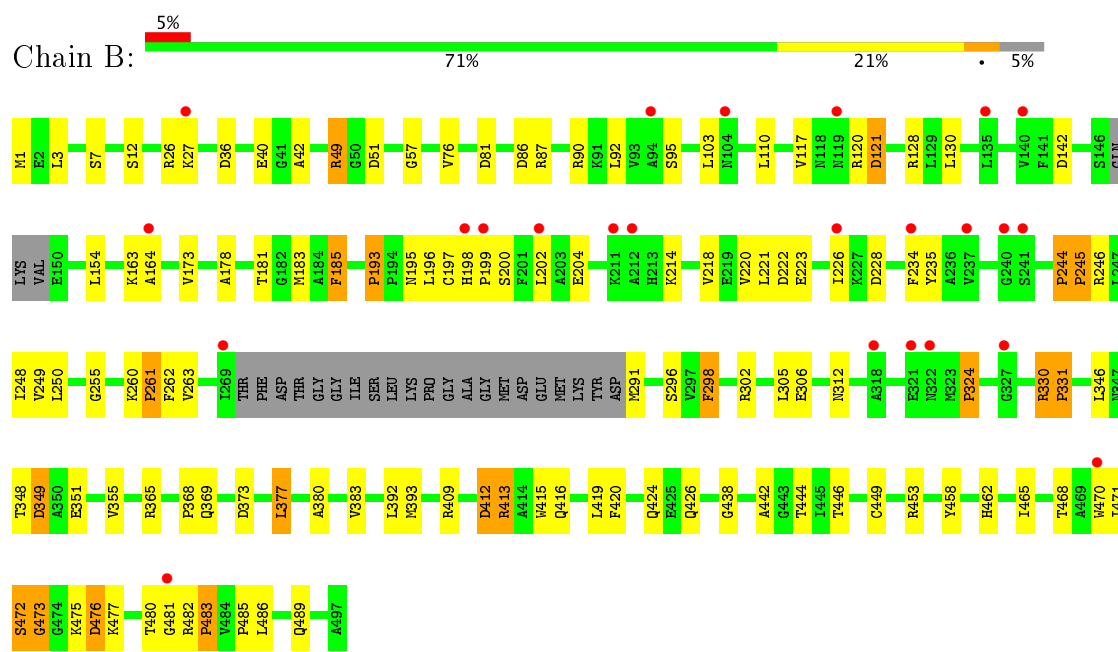
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Cytosol aminopeptidase



• Molecule 1: Cytosol aminopeptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	116.95Å 116.95Å 137.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	58.00 – 2.75 58.47 – 2.75	Depositor EDS
% Data completeness (in resolution range)	100.0 (58.00-2.75) 100.0 (58.47-2.75)	Depositor EDS
R_{merge}	0.35	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.11 (at 2.77Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.212 , 0.267 0.290 , 0.300	Depositor DCC
R_{free} test set	1399 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	41.2	Xtriage
Anisotropy	0.360	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.479 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.500 for h,-h-k,-l	Depositor
Outliers	0 of 27831 reflections	Xtriage
F_o, F_c correlation	0.81	EDS
Total number of atoms	7006	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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

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	1.38	9/3553 (0.3%)	1.34	39/4805 (0.8%)
1	B	1.35	16/3553 (0.5%)	1.31	40/4805 (0.8%)
All	All	1.37	25/7106 (0.4%)	1.32	79/9610 (0.8%)

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 (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	235	TYR	CD1-CE1	10.94	1.55	1.39
1	A	310	PRO	N-CD	-10.55	1.33	1.47
1	B	245	PRO	N-CD	-7.34	1.37	1.47
1	B	324	PRO	N-CD	-7.14	1.37	1.47
1	B	235	TYR	CD1-CE1	7.13	1.50	1.39
1	B	185	PHE	CD1-CE1	6.61	1.52	1.39
1	A	151	PRO	N-CD	-6.35	1.39	1.47
1	B	95	SER	CB-OG	6.17	1.50	1.42
1	B	12	SER	CB-OG	6.14	1.50	1.42
1	A	425	GLU	CB-CG	-5.73	1.41	1.52
1	B	204	GLU	CG-CD	5.70	1.60	1.51
1	B	235	TYR	CE2-CZ	-5.69	1.31	1.38
1	B	40	GLU	CD-OE2	-5.60	1.19	1.25
1	A	490	TYR	CD1-CE1	5.58	1.47	1.39
1	A	458	TYR	CD2-CE2	5.57	1.47	1.39
1	A	235	TYR	CE2-CZ	-5.56	1.31	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	235	TYR	CZ-OH	5.54	1.47	1.37
1	B	220	VAL	C-O	5.51	1.33	1.23
1	A	124	TYR	CE1-CZ	5.42	1.45	1.38
1	B	438	GLY	N-CA	5.38	1.54	1.46
1	B	305	LEU	C-O	5.38	1.33	1.23
1	B	42	ALA	C-O	5.35	1.33	1.23
1	A	431	PHE	CD1-CE1	5.10	1.49	1.39
1	B	380	ALA	CA-CB	5.09	1.63	1.52
1	B	193	PRO	N-CD	-5.05	1.40	1.47

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	246	ARG	NE-CZ-NH1	11.27	125.94	120.30
1	A	310	PRO	CA-N-CD	-9.63	98.02	111.50
1	A	235	TYR	CG-CD1-CE1	-9.49	113.71	121.30
1	B	185	PHE	CB-CG-CD1	9.33	127.33	120.80
1	B	413	ARG	NE-CZ-NH2	-9.23	115.68	120.30
1	A	246	ARG	NE-CZ-NH1	8.55	124.58	120.30
1	A	151	PRO	CA-N-CD	-8.48	99.62	111.50
1	A	235	TYR	CB-CG-CD2	-8.32	116.01	121.00
1	B	110	LEU	CB-CG-CD1	8.25	125.02	111.00
1	A	222	ASP	CB-CG-OD1	8.22	125.70	118.30
1	B	244	PRO	CA-N-CD	-8.17	100.06	111.50
1	B	261	PRO	CA-N-CD	-8.10	100.17	111.50
1	A	199	PRO	CA-N-CD	-8.01	100.29	111.50
1	B	193	PRO	CA-N-CD	-7.98	100.33	111.50
1	A	412	ASP	CB-CG-OD1	7.97	125.48	118.30
1	A	228	ASP	CB-CG-OD2	-7.97	111.13	118.30
1	B	483	PRO	CA-N-CD	-7.87	100.48	111.50
1	B	199	PRO	CA-N-CD	-7.80	100.59	111.50
1	A	245	PRO	CA-N-CD	-7.77	100.62	111.50
1	A	485	PRO	CA-N-CD	-7.75	100.64	111.50
1	B	349	ASP	CB-CG-OD1	7.73	125.26	118.30
1	A	90	ARG	NE-CZ-NH2	-7.70	116.45	120.30
1	B	331	PRO	CA-N-CD	-7.69	100.74	111.50
1	B	235	TYR	CB-CG-CD2	-7.64	116.42	121.00
1	A	185	PHE	CB-CG-CD1	7.62	126.13	120.80
1	B	185	PHE	CB-CG-CD2	-7.50	115.55	120.80
1	A	244	PRO	CA-N-CD	-7.47	101.04	111.50
1	B	245	PRO	CA-N-CD	-7.40	101.14	111.50
1	A	114	ASP	CB-CG-OD1	7.40	124.96	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	49	ARG	NE-CZ-NH2	7.35	123.97	120.30
1	B	453	ARG	NE-CZ-NH2	-7.33	116.64	120.30
1	A	185	PHE	CB-CG-CD2	-7.11	115.82	120.80
1	B	222	ASP	CB-CG-OD1	7.05	124.65	118.30
1	A	139	TYR	CB-CG-CD1	-6.99	116.81	121.00
1	A	331	PRO	CA-N-CD	-6.93	101.80	111.50
1	B	228	ASP	CB-CG-OD1	6.80	124.42	118.30
1	A	234	PHE	CB-CG-CD1	-6.78	116.06	120.80
1	A	409	ARG	NE-CZ-NH2	-6.65	116.98	120.30
1	B	324	PRO	CA-N-CD	-6.59	102.28	111.50
1	A	453	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	A	49	ARG	NE-CZ-NH2	6.40	123.50	120.30
1	B	121	ASP	CB-CG-OD1	-6.12	112.79	118.30
1	A	120	ARG	NE-CZ-NH2	-6.12	117.24	120.30
1	B	409	ARG	NE-CZ-NH1	6.11	123.36	120.30
1	B	458	TYR	CZ-CE2-CD2	-6.09	114.32	119.80
1	B	412	ASP	CB-CG-OD2	6.08	123.77	118.30
1	A	1	MET	CG-SD-CE	6.00	109.81	100.20
1	B	365	ARG	NE-CZ-NH2	6.00	123.30	120.30
1	A	431	PHE	CB-CG-CD1	-5.95	116.64	120.80
1	B	235	TYR	CG-CD1-CE1	-5.89	116.58	121.30
1	A	409	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	B	142	ASP	CB-CG-OD1	5.79	123.51	118.30
1	A	221	LEU	CB-CG-CD1	5.79	120.84	111.00
1	B	260	LYS	CD-CE-NZ	-5.68	98.64	111.70
1	A	413	ARG	NE-CZ-NH2	-5.63	117.48	120.30
1	B	90	ARG	NE-CZ-NH1	5.63	123.11	120.30
1	A	252	TYR	CZ-CE2-CD2	-5.51	114.84	119.80
1	B	86	ASP	CB-CG-OD1	5.50	123.25	118.30
1	A	366	PHE	CB-CG-CD2	5.49	124.64	120.80
1	B	228	ASP	CB-CG-OD2	-5.47	113.38	118.30
1	B	103	LEU	CB-CG-CD1	-5.46	101.72	111.00
1	A	453	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	B	222	ASP	CB-CG-OD2	-5.41	113.43	118.30
1	A	196	LEU	CB-CG-CD1	-5.37	101.87	111.00
1	B	87	ARG	NE-CZ-NH2	-5.35	117.63	120.30
1	B	36	ASP	CB-CG-OD2	-5.32	113.51	118.30
1	A	333	ASP	CB-CG-OD2	-5.32	113.52	118.30
1	B	346	LEU	CB-CG-CD1	-5.30	101.99	111.00
1	A	234	PHE	CB-CG-CD2	5.28	124.50	120.80
1	A	64	ASN	CB-CA-C	-5.23	99.94	110.40
1	A	398	ASP	CB-CG-OD2	-5.18	113.64	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	420	PHE	CB-CG-CD2	-5.13	117.21	120.80
1	A	252	TYR	CG-CD1-CE1	-5.13	117.19	121.30
1	B	349	ASP	CB-CG-OD2	-5.13	113.69	118.30
1	B	51	ASP	CB-CG-OD1	5.06	122.86	118.30
1	A	114	ASP	CB-CG-OD2	-5.06	113.75	118.30
1	B	298	PHE	CB-CG-CD1	-5.06	117.26	120.80
1	A	87	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	B	263	VAL	CG1-CB-CG2	-5.03	102.85	110.90

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	474	GLY	Peptide
1	A	475	LYS	Peptide
1	B	472	SER	Peptide
1	B	473	GLY	Peptide
1	B	476	ASP	Peptide

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	3503	0	3600	123	11
1	B	3503	0	3600	152	12
All	All	7006	0	7200	268	12

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 (268) 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:226:ILE:HD13	1:A:234:PHE:CE2	1.28	1.65
1:B:226:ILE:HD13	1:B:234:PHE:CE2	1.10	1.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:226:ILE:CD1	1:B:234:PHE:HE2	1.13	1.52
1:A:185:PHE:CE2	1:A:298:PHE:HB3	1.44	1.51
1:B:473:GLY:CA	1:B:477:LYS:HG3	1.38	1.49
1:A:226:ILE:CD1	1:A:234:PHE:HE2	1.28	1.45
1:B:185:PHE:CE2	1:B:298:PHE:HB3	1.54	1.40
1:A:185:PHE:HE2	1:A:298:PHE:CB	1.44	1.29
1:B:226:ILE:HG21	1:B:234:PHE:CD2	1.68	1.28
1:A:195:ASN:OD1	1:A:196:LEU:HG	1.34	1.25
1:A:1:MET:CE	1:A:134:LEU:HG	1.71	1.21
1:A:400:VAL:O	1:A:404:LEU:HD13	1.37	1.20
1:A:262:PHE:CZ	1:A:369:GLN:NE2	2.09	1.20
1:B:185:PHE:HE2	1:B:298:PHE:CB	1.54	1.19
1:A:188:ASP:O	1:A:192:LEU:HD23	1.37	1.18
1:B:473:GLY:CA	1:B:477:LYS:CG	2.21	1.16
1:B:202:LEU:HD21	1:B:291:MET:HE1	1.28	1.16
1:B:226:ILE:CG2	1:B:234:PHE:HD2	1.57	1.16
1:A:226:ILE:HG21	1:A:234:PHE:HD2	1.08	1.16
1:B:424:GLN:NE2	1:B:449:CYS:SG	2.19	1.15
1:B:202:LEU:HD11	1:B:291:MET:CE	1.76	1.14
1:B:226:ILE:CD1	1:B:234:PHE:CE2	1.98	1.13
1:B:296:SER:HB2	1:B:483:PRO:HB2	1.26	1.13
1:B:471:ILE:HG22	1:B:473:GLY:O	1.48	1.12
1:B:473:GLY:HA2	1:B:477:LYS:CG	1.79	1.11
1:B:473:GLY:HA2	1:B:477:LYS:HG3	1.18	1.11
1:B:3:LEU:HD23	1:B:173:VAL:HG13	1.15	1.11
1:B:468:THR:HB	1:B:482:ARG:HD3	1.35	1.08
1:B:262:PHE:CZ	1:B:369:GLN:NE2	2.23	1.06
1:A:226:ILE:HG21	1:A:234:PHE:CD2	1.89	1.05
1:B:473:GLY:HA3	1:B:477:LYS:HG3	1.11	1.04
1:A:226:ILE:CG2	1:A:234:PHE:HD2	1.71	1.04
1:B:473:GLY:HA3	1:B:477:LYS:CG	1.82	1.03
1:A:331:PRO:HD3	1:A:348:THR:HG23	1.37	1.03
1:A:1:MET:HE1	1:A:134:LEU:HG	1.06	1.02
1:B:331:PRO:HD3	1:B:348:THR:HG23	1.38	1.02
1:B:424:GLN:HE22	1:B:449:CYS:CB	1.72	1.02
1:B:226:ILE:HG21	1:B:234:PHE:HD2	0.89	1.02
1:A:226:ILE:CD1	1:A:234:PHE:CE2	2.15	1.01
1:A:3:LEU:HD22	1:A:173:VAL:CG1	1.91	1.00
1:A:392:LEU:HD23	1:A:404:LEU:HD11	1.42	0.99
1:A:26:ARG:HD3	1:A:47:LEU:O	1.63	0.99
1:A:1:MET:HE1	1:A:134:LEU:CG	1.93	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:183:MET:CE	1:B:481:GLY:HA3	1.94	0.97
1:B:202:LEU:CD2	1:B:291:MET:HE1	1.93	0.97
1:B:226:ILE:CG2	1:B:234:PHE:CD2	2.38	0.97
1:A:424:GLN:NE2	1:A:449:CYS:SG	2.38	0.96
1:A:373:ASP:OD1	1:A:462:HIS:HA	1.65	0.95
1:B:471:ILE:CG2	1:B:473:GLY:O	2.14	0.94
1:B:393:MET:SD	1:B:419:LEU:HD21	2.07	0.93
1:B:128:ARG:HH12	1:B:489:GLN:HE22	1.15	0.93
1:B:3:LEU:HD23	1:B:173:VAL:CG1	1.99	0.92
1:A:3:LEU:CD2	1:A:173:VAL:HG21	1.98	0.92
1:B:324:PRO:HD2	1:B:324:PRO:O	1.67	0.91
1:B:183:MET:HE2	1:B:481:GLY:HA3	1.49	0.91
1:A:28:LEU:O	1:A:33:LYS:HE2	1.70	0.91
1:B:373:ASP:OD1	1:B:462:HIS:HA	1.70	0.90
1:A:3:LEU:CD2	1:A:173:VAL:CG2	2.50	0.89
1:B:202:LEU:HD11	1:B:291:MET:HE1	1.54	0.89
1:A:377:LEU:O	1:A:377:LEU:HD12	1.72	0.89
1:B:202:LEU:HD11	1:B:291:MET:HE3	1.56	0.88
1:B:377:LEU:HD12	1:B:377:LEU:O	1.72	0.88
1:A:400:VAL:O	1:A:404:LEU:CD1	2.21	0.87
1:B:424:GLN:NE2	1:B:449:CYS:CB	2.36	0.87
1:A:393:MET:SD	1:A:419:LEU:HD21	2.16	0.85
1:A:392:LEU:CD2	1:A:404:LEU:HD11	2.05	0.85
1:A:128:ARG:HH22	1:A:489:GLN:HE22	1.19	0.85
1:A:392:LEU:CD2	1:A:404:LEU:CD1	2.55	0.85
1:B:261:PRO:HD2	1:B:368:PRO:HA	1.57	0.84
1:B:202:LEU:CD1	1:B:291:MET:CE	2.55	0.84
1:B:76:VAL:HG22	1:B:92:LEU:HD21	1.60	0.83
1:A:392:LEU:HD23	1:A:404:LEU:CD1	2.09	0.83
1:B:248:ILE:HG22	1:B:250:LEU:HD11	1.60	0.82
1:B:248:ILE:HG22	1:B:250:LEU:CD1	2.10	0.82
1:B:412:ASP:OD2	1:B:482:ARG:O	1.98	0.82
1:B:296:SER:CB	1:B:483:PRO:HB2	2.07	0.81
1:A:3:LEU:HD22	1:A:173:VAL:CG2	2.10	0.80
1:B:76:VAL:CG2	1:B:92:LEU:HD21	2.11	0.80
1:A:3:LEU:HD21	1:A:173:VAL:HG21	1.63	0.80
1:B:202:LEU:HD21	1:B:291:MET:CE	2.09	0.80
1:B:424:GLN:NE2	1:B:449:CYS:HB3	1.97	0.80
1:B:193:PRO:O	1:B:193:PRO:HD2	1.81	0.80
1:B:202:LEU:CD1	1:B:291:MET:HE1	2.10	0.80
1:B:178:ALA:HA	1:B:306:GLU:OE1	1.82	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:424:GLN:HE22	1:B:449:CYS:HB3	1.47	0.78
1:A:226:ILE:CG2	1:A:234:PHE:CD2	2.57	0.78
1:A:141:PHE:CZ	1:A:192:LEU:HD22	2.20	0.77
1:A:3:LEU:HD21	1:A:173:VAL:CG2	2.14	0.76
1:B:473:GLY:HA3	1:B:477:LYS:CD	2.14	0.76
1:A:1:MET:CE	1:A:134:LEU:CG	2.57	0.76
1:A:3:LEU:HD22	1:A:173:VAL:HG11	1.67	0.75
1:B:331:PRO:HD3	1:B:348:THR:CG2	2.16	0.75
1:A:195:ASN:OD1	1:A:196:LEU:N	2.20	0.75
1:B:296:SER:HB3	1:B:483:PRO:HG2	1.69	0.74
1:B:296:SER:HB2	1:B:483:PRO:CB	2.11	0.74
1:B:197:CYS:SG	1:B:291:MET:SD	2.85	0.74
1:A:3:LEU:HD22	1:A:173:VAL:HG13	1.70	0.73
1:A:110:LEU:HD12	1:A:110:LEU:N	2.03	0.73
1:A:244:PRO:HD2	1:A:244:PRO:O	1.88	0.73
1:B:244:PRO:O	1:B:244:PRO:HD2	1.89	0.72
1:B:195:ASN:OD1	1:B:196:LEU:HG	1.89	0.72
1:B:183:MET:HE3	1:B:481:GLY:HA3	1.73	0.71
1:A:268:GLY:HA2	1:A:291:MET:HG3	1.70	0.71
1:A:331:PRO:HD3	1:A:348:THR:CG2	2.17	0.70
1:B:245:PRO:O	1:B:245:PRO:HD2	1.92	0.69
1:B:468:THR:HB	1:B:482:ARG:CD	2.18	0.69
1:B:202:LEU:CG	1:B:291:MET:HE1	2.22	0.69
1:B:261:PRO:HD2	1:B:261:PRO:O	1.93	0.68
1:A:392:LEU:CD2	1:A:404:LEU:HD12	2.23	0.68
1:A:87:ARG:HG3	1:A:91:LYS:HE3	1.76	0.67
1:B:296:SER:CB	1:B:483:PRO:CB	2.70	0.67
1:B:249:VAL:C	1:B:250:LEU:HD12	2.15	0.67
1:A:110:LEU:HD13	1:A:157:VAL:HG13	1.76	0.67
1:A:178:ALA:HA	1:A:306:GLU:OE1	1.96	0.66
1:A:418:PRO:HD3	1:B:415:TRP:CE2	2.31	0.66
1:A:141:PHE:HZ	1:A:192:LEU:HD22	1.61	0.66
1:B:472:SER:N	1:B:473:GLY:O	2.30	0.65
1:A:393:MET:HE3	1:A:448:GLY:HA3	1.80	0.64
1:B:248:ILE:CG2	1:B:250:LEU:HD11	2.26	0.64
1:A:1:MET:HE3	1:A:134:LEU:HG	1.77	0.64
1:A:245:PRO:O	1:A:245:PRO:HD2	1.98	0.64
1:A:383:VAL:O	1:B:442:ALA:HA	1.97	0.63
1:B:185:PHE:HE2	1:B:298:PHE:HB3	0.63	0.63
1:B:202:LEU:CD1	1:B:291:MET:HE3	2.26	0.62
1:A:418:PRO:HD3	1:B:415:TRP:NE1	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:ASN:OD1	1:A:196:LEU:CG	2.28	0.62
1:A:110:LEU:N	1:A:110:LEU:CD1	2.62	0.61
1:B:473:GLY:HA2	1:B:477:LYS:HG2	1.76	0.61
1:B:473:GLY:CA	1:B:477:LYS:CD	2.75	0.61
1:B:324:PRO:O	1:B:324:PRO:CD	2.43	0.60
1:B:473:GLY:HA3	1:B:477:LYS:HD2	1.84	0.60
1:B:262:PHE:HZ	1:B:369:GLN:NE2	1.95	0.60
1:B:226:ILE:HD11	1:B:234:PHE:CE2	2.29	0.59
1:A:404:LEU:HD12	1:A:404:LEU:N	2.18	0.58
1:B:226:ILE:HG21	1:B:234:PHE:CE2	2.33	0.58
1:A:110:LEU:CD1	1:A:157:VAL:HG13	2.34	0.58
1:B:226:ILE:HG23	1:B:234:PHE:CD2	2.33	0.58
1:A:255:GLY:H	1:A:312:ASN:ND2	2.01	0.58
1:B:226:ILE:HD13	1:B:234:PHE:CD2	2.16	0.58
1:B:57:GLY:N	1:B:92:LEU:HD23	2.19	0.58
1:A:3:LEU:CD2	1:A:173:VAL:HG22	2.31	0.58
1:B:226:ILE:CG1	1:B:234:PHE:CE2	2.84	0.58
1:B:426:GLN:OE1	1:B:446:THR:HG21	2.05	0.56
1:A:1:MET:HE3	1:A:134:LEU:CD2	2.34	0.56
1:A:393:MET:SD	1:A:419:LEU:CD2	2.91	0.56
1:B:480:THR:CB	1:B:482:ARG:HG3	2.36	0.56
1:B:27:LYS:NZ	1:B:81:ASP:OD2	2.38	0.56
1:B:481:GLY:O	1:B:485:PRO:HD3	2.06	0.56
1:B:128:ARG:NH1	1:B:489:GLN:HE22	1.97	0.56
1:B:76:VAL:CG2	1:B:92:LEU:CD2	2.81	0.56
1:A:26:ARG:HD2	1:A:47:LEU:HB3	1.88	0.55
1:B:473:GLY:CA	1:B:477:LYS:HD2	2.35	0.55
1:B:480:THR:HB	1:B:482:ARG:HG3	1.88	0.55
1:B:470:TRP:CD1	1:B:472:SER:HB3	2.42	0.55
1:B:261:PRO:CD	1:B:368:PRO:HA	2.32	0.55
1:A:418:PRO:HB3	1:B:415:TRP:CH2	2.42	0.55
1:B:470:TRP:NE1	1:B:472:SER:HB3	2.21	0.55
1:A:110:LEU:HD13	1:A:157:VAL:CG1	2.37	0.54
1:A:185:PHE:CE2	1:A:298:PHE:CG	2.95	0.54
1:A:262:PHE:CE2	1:A:369:GLN:NE2	2.71	0.54
1:B:3:LEU:HD21	1:B:173:VAL:HG22	1.89	0.54
1:B:57:GLY:H	1:B:92:LEU:HD23	1.72	0.54
1:B:465:ILE:HD13	1:B:483:PRO:HG3	1.90	0.54
1:A:185:PHE:HE2	1:A:298:PHE:HB3	0.52	0.53
1:A:26:ARG:CD	1:A:47:LEU:O	2.47	0.53
1:A:392:LEU:HD21	1:A:404:LEU:CD1	2.35	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:422:GLU:CD	1:B:413:ARG:HH22	2.11	0.53
1:A:128:ARG:HH22	1:A:489:GLN:NE2	1.99	0.53
1:A:226:ILE:HD13	1:A:234:PHE:CD2	2.22	0.53
1:A:234:PHE:HD1	1:A:355:VAL:HB	1.74	0.53
1:B:426:GLN:OE1	1:B:446:THR:CG2	2.56	0.52
1:B:468:THR:CB	1:B:482:ARG:HD3	2.24	0.52
1:A:418:PRO:HB3	1:B:415:TRP:CZ3	2.43	0.52
1:B:255:GLY:H	1:B:312:ASN:ND2	2.07	0.52
1:B:475:LYS:O	1:B:476:ASP:OD1	2.26	0.52
1:A:128:ARG:NH2	1:A:489:GLN:HE22	2.00	0.52
1:B:468:THR:O	1:B:482:ARG:HD3	2.09	0.52
1:B:250:LEU:HD12	1:B:250:LEU:N	2.24	0.52
1:A:3:LEU:HD21	1:A:173:VAL:HG22	1.92	0.52
1:A:141:PHE:CE2	1:A:192:LEU:CD2	2.93	0.52
1:B:296:SER:CB	1:B:483:PRO:CG	2.88	0.52
1:B:193:PRO:CD	1:B:193:PRO:O	2.57	0.51
1:B:393:MET:SD	1:B:419:LEU:CD2	2.91	0.51
1:A:424:GLN:HE22	1:A:449:CYS:CB	2.23	0.51
1:A:404:LEU:CD1	1:A:404:LEU:N	2.74	0.51
1:A:234:PHE:CD1	1:A:355:VAL:HB	2.46	0.50
1:B:218:VAL:HG22	1:B:250:LEU:HG	1.91	0.50
1:A:262:PHE:HZ	1:A:369:GLN:NE2	1.95	0.50
1:B:76:VAL:HG21	1:B:92:LEU:CD2	2.42	0.50
1:B:76:VAL:HG21	1:B:92:LEU:HD21	1.89	0.50
1:A:185:PHE:HZ	1:A:298:PHE:CD2	2.29	0.50
1:A:185:PHE:CZ	1:A:298:PHE:CD2	3.00	0.50
1:B:471:ILE:HG23	1:B:473:GLY:O	2.08	0.50
1:A:226:ILE:HG23	1:A:234:PHE:CD2	2.46	0.49
1:B:185:PHE:CE2	1:B:298:PHE:CG	3.00	0.49
1:A:475:LYS:O	1:A:476:ASP:OD1	2.29	0.49
1:A:141:PHE:CE2	1:A:192:LEU:HD22	2.47	0.49
1:B:183:MET:HE3	1:B:481:GLY:CA	2.42	0.49
1:A:424:GLN:NE2	1:A:449:CYS:CB	2.75	0.49
1:A:3:LEU:CD2	1:A:173:VAL:HG11	2.40	0.49
1:A:185:PHE:CE2	1:A:298:PHE:CB	2.37	0.49
1:A:373:ASP:OD1	1:A:462:HIS:CA	2.52	0.48
1:A:268:GLY:CA	1:A:291:MET:HG3	2.40	0.48
1:B:185:PHE:CE2	1:B:298:PHE:CB	2.47	0.48
1:B:424:GLN:HE22	1:B:449:CYS:CA	2.24	0.48
1:A:377:LEU:C	1:A:377:LEU:HD12	2.33	0.48
1:B:296:SER:CB	1:B:483:PRO:HG2	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:426:GLN:OE1	1:A:446:THR:CG2	2.61	0.48
1:B:373:ASP:OD1	1:B:462:HIS:CA	2.53	0.48
1:A:404:LEU:CD1	1:A:404:LEU:H	2.28	0.47
1:A:426:GLN:OE1	1:A:446:THR:HG21	2.14	0.47
1:A:188:ASP:O	1:A:192:LEU:CD2	2.32	0.47
1:B:223:GLU:HB2	1:B:245:PRO:CD	2.43	0.47
1:A:226:ILE:HD13	1:A:234:PHE:HE2	0.40	0.47
1:A:244:PRO:CD	1:A:244:PRO:O	2.60	0.47
1:B:121:ASP:OD1	1:B:121:ASP:C	2.53	0.47
1:A:109:VAL:C	1:A:110:LEU:HD12	2.35	0.47
1:A:179:ILE:HG23	1:A:485:PRO:HD3	1.97	0.47
1:B:1:MET:HE2	1:B:154:LEU:CD2	2.44	0.47
1:B:475:LYS:C	1:B:476:ASP:OD1	2.53	0.47
1:B:198:HIS:NE2	1:B:200:SER:HB2	2.29	0.47
1:B:1:MET:HE2	1:B:154:LEU:HD23	1.96	0.46
1:B:76:VAL:HG22	1:B:92:LEU:CD2	2.40	0.46
1:B:26:ARG:HH11	1:B:26:ARG:HG3	1.81	0.46
1:B:486:LEU:HD23	1:B:486:LEU:C	2.36	0.46
1:B:244:PRO:CD	1:B:244:PRO:O	2.62	0.46
1:A:132:GLU:OE2	1:A:485:PRO:HG3	2.15	0.45
1:B:1:MET:CE	1:B:154:LEU:HD23	2.46	0.45
1:B:261:PRO:CD	1:B:261:PRO:O	2.64	0.45
1:B:202:LEU:CD2	1:B:291:MET:CE	2.80	0.44
1:B:331:PRO:CD	1:B:348:THR:HG23	2.27	0.44
1:B:393:MET:HE1	1:B:444:THR:O	2.17	0.44
1:A:26:ARG:CD	1:A:47:LEU:HB3	2.47	0.44
1:A:26:ARG:CD	1:A:47:LEU:C	2.87	0.44
1:A:484:VAL:HB	1:A:485:PRO:HD2	2.00	0.44
1:A:59:THR:HB	1:A:74:LEU:HD11	2.00	0.43
1:A:3:LEU:HD22	1:A:173:VAL:CB	2.41	0.43
1:B:250:LEU:CD1	1:B:250:LEU:N	2.81	0.43
1:A:392:LEU:O	1:A:416:GLN:HA	2.18	0.43
1:B:7:SER:OG	1:B:163:LYS:HG3	2.18	0.43
1:A:204:GLU:O	1:A:208:GLU:HG3	2.19	0.43
1:A:3:LEU:HD22	1:A:173:VAL:HG22	1.93	0.43
1:B:202:LEU:HD11	1:B:291:MET:SD	2.59	0.43
1:B:424:GLN:CD	1:B:449:CYS:HB3	2.38	0.43
1:A:26:ARG:HD3	1:A:47:LEU:C	2.36	0.42
1:A:221:LEU:HD22	1:A:247:LEU:HD23	2.02	0.42
1:B:121:ASP:OD1	1:B:121:ASP:O	2.38	0.42
1:B:185:PHE:CZ	1:B:298:PHE:CD2	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:ARG:O	1:A:331:PRO:C	2.57	0.42
1:A:331:PRO:CD	1:A:348:THR:HG23	2.28	0.42
1:B:130:LEU:HD23	1:B:130:LEU:C	2.39	0.42
1:B:181:THR:HG22	1:B:302:ARG:HD3	2.01	0.42
1:B:330:ARG:O	1:B:331:PRO:C	2.57	0.42
1:A:1:MET:CE	1:A:134:LEU:CD2	2.95	0.41
1:A:268:GLY:O	1:A:319:CYS:HA	2.21	0.41
1:B:226:ILE:CD1	1:B:234:PHE:CZ	2.88	0.41
1:B:349:ASP:O	1:B:351:GLU:OE1	2.38	0.41
1:B:392:LEU:O	1:B:416:GLN:HA	2.20	0.41
1:B:221:LEU:HD12	1:B:221:LEU:N	2.35	0.41
1:A:121:ASP:C	1:A:121:ASP:OD1	2.59	0.41
1:A:393:MET:HE3	1:A:448:GLY:CA	2.48	0.41
1:A:97:ALA:O	1:A:101:LYS:HG3	2.20	0.41
1:A:29:GLY:O	1:A:33:LYS:HG3	2.21	0.41
1:A:442:ALA:HA	1:B:383:VAL:O	2.21	0.40
1:B:234:PHE:HD1	1:B:355:VAL:HB	1.85	0.40
1:B:117:VAL:HG12	1:B:120:ARG:HG3	2.02	0.40
1:A:1:MET:HE2	1:A:135:LEU:HD23	2.03	0.40
1:B:185:PHE:HZ	1:B:298:PHE:CD2	2.39	0.40

All (12) 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:336:THR:CB	1:B:214:LYS:CE[4_444]	0.56	1.64
1:B:163:LYS:CE	1:B:164:ALA:O[2_445]	1.27	0.93
1:A:336:THR:CB	1:B:214:LYS:NZ[4_444]	1.56	0.64
1:A:336:THR:OG1	1:B:214:LYS:CE[4_444]	1.60	0.60
1:A:63:GLN:NE2	1:B:49:ARG:NH2[2_455]	1.64	0.56
1:A:336:THR:CG2	1:B:214:LYS:CE[4_444]	1.65	0.55
1:A:336:THR:OG1	1:B:214:LYS:CD[4_444]	1.69	0.51
1:A:336:THR:N	1:B:214:LYS:NZ[4_444]	1.81	0.39
1:A:336:THR:CB	1:B:214:LYS:CD[4_444]	1.89	0.31
1:A:336:THR:CA	1:B:214:LYS:NZ[4_444]	1.94	0.26
1:A:336:THR:OG1	1:B:214:LYS:NZ[4_444]	2.02	0.18
1:A:336:THR:CA	1:B:214:LYS:CE[4_444]	2.03	0.17

5.3 Torsion angles

5.3.1 Protein backbone

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	467/497 (94%)	455 (97%)	12 (3%)	0	100	100
1	B	467/497 (94%)	454 (97%)	13 (3%)	0	100	100
All	All	934/994 (94%)	909 (97%)	25 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	359/378 (95%)	357 (99%)	2 (1%)	89	96
1	B	359/378 (95%)	357 (99%)	2 (1%)	89	96
All	All	718/756 (95%)	714 (99%)	4 (1%)	89	96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	330	ARG
1	A	377	LEU
1	B	330	ARG
1	B	377	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	312	ASN
1	A	424	GLN
1	A	462	HIS
1	A	489	GLN
1	B	213	HIS
1	B	312	ASN
1	B	424	GLN
1	B	459	ASN
1	B	489	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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](#)

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	473/497 (95%)	0.45	24 (5%) 29 23	5, 10, 25, 45	0
1	B	473/497 (95%)	0.50	24 (5%) 29 23	6, 12, 28, 51	0
All	All	946/994 (95%)	0.47	48 (5%) 29 23	5, 11, 27, 51	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	269	ILE	4.2
1	A	239	GLN	4.0
1	A	241	SER	3.8
1	B	94	ALA	3.7
1	A	323	MET	3.7
1	B	198	HIS	3.5
1	B	240	GLY	3.4
1	A	327	GLY	3.4
1	B	119	ASN	3.3
1	A	122	ALA	3.1
1	B	321	GLU	3.1
1	A	234	PHE	3.1
1	B	470	TRP	3.1
1	B	322	ASN	3.0
1	B	327	GLY	2.8
1	B	104	ASN	2.8
1	A	43	ILE	2.7
1	A	226	ILE	2.7
1	B	199	PRO	2.7
1	B	234	PHE	2.6
1	A	198	HIS	2.6
1	A	322	ASN	2.6
1	A	240	GLY	2.6
1	A	87	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	135	LEU	2.5
1	A	475	LYS	2.4
1	B	202	LEU	2.4
1	A	233	ALA	2.4
1	B	212	ALA	2.4
1	B	318	ALA	2.3
1	A	351	GLU	2.3
1	A	245	PRO	2.3
1	B	226	ILE	2.3
1	B	27	LYS	2.2
1	B	241	SER	2.2
1	A	472	SER	2.2
1	A	94	ALA	2.2
1	B	237	VAL	2.2
1	B	140	VAL	2.1
1	B	164	ALA	2.1
1	B	211	LYS	2.1
1	A	199	PRO	2.1
1	A	248	ILE	2.1
1	A	414	ALA	2.0
1	B	481	GLY	2.0
1	A	235	TYR	2.0
1	A	238	GLY	2.0
1	A	497	ALA	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 carbohydrates 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.