



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 02:33 PM GMT

PDB ID : 2CXI
Title : Crystal Structure Of An N-terminal Fragment Of The Phenylalanyl-tRNA Synthetase Beta-Subunit From Pyrococcus Horikoshii
Authors : Sasaki, H.; Sekine, S.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2005-06-29
Resolution : 1.94 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

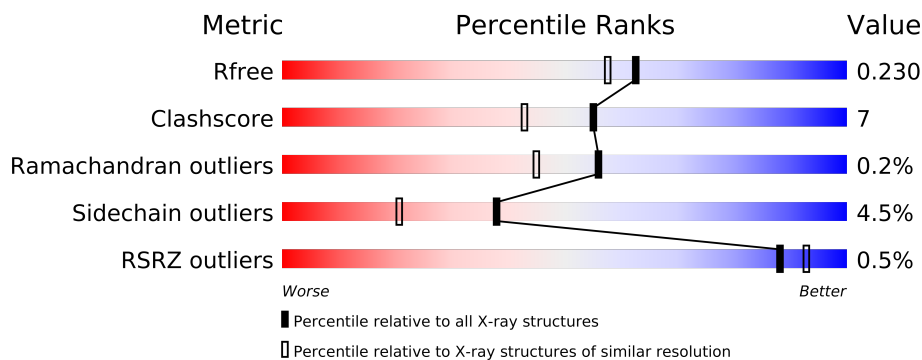
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.94 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}	66092	2024 (1.96-1.92)
Clashscore	79885	2281 (1.96-1.92)
Ramachandran outliers	78287	2255 (1.96-1.92)
Sidechain outliers	78261	2255 (1.96-1.92)
RSRZ outliers	66119	2024 (1.96-1.92)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	348	
1	B	348	
1	C	348	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9228 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Phenylalanyl-tRNA synthetase beta chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	347	Total	C	N	O	S	Se	0	2	0
			2848	1833	466	538	1	10			
1	B	347	Total	C	N	O	S	Se	0	2	0
			2848	1833	466	538	1	10			
1	C	347	Total	C	N	O	S	Se	0	2	0
			2848	1833	466	538	1	10			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP O73984
A	122	MSE	MET	MODIFIED RESIDUE	UNP O73984
A	174	MSE	MET	MODIFIED RESIDUE	UNP O73984
A	212	MSE	MET	MODIFIED RESIDUE	UNP O73984
A	244	MSE	MET	MODIFIED RESIDUE	UNP O73984
A	250	MSE	MET	MODIFIED RESIDUE	UNP O73984
A	310	MSE	MET	MODIFIED RESIDUE	UNP O73984
A	311	MSE	MET	MODIFIED RESIDUE	UNP O73984
A	333	MSE	MET	MODIFIED RESIDUE	UNP O73984
B	1	MSE	MET	MODIFIED RESIDUE	UNP O73984
B	122	MSE	MET	MODIFIED RESIDUE	UNP O73984
B	174	MSE	MET	MODIFIED RESIDUE	UNP O73984
B	212	MSE	MET	MODIFIED RESIDUE	UNP O73984
B	244	MSE	MET	MODIFIED RESIDUE	UNP O73984
B	250	MSE	MET	MODIFIED RESIDUE	UNP O73984
B	310	MSE	MET	MODIFIED RESIDUE	UNP O73984
B	311	MSE	MET	MODIFIED RESIDUE	UNP O73984
B	333	MSE	MET	MODIFIED RESIDUE	UNP O73984
C	1	MSE	MET	MODIFIED RESIDUE	UNP O73984
C	122	MSE	MET	MODIFIED RESIDUE	UNP O73984
C	174	MSE	MET	MODIFIED RESIDUE	UNP O73984
C	212	MSE	MET	MODIFIED RESIDUE	UNP O73984
C	244	MSE	MET	MODIFIED RESIDUE	UNP O73984

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Chain	Residue	Modelled	Actual	Comment	Reference
C	250	MSE	MET	MODIFIED RESIDUE	UNP O73984
C	310	MSE	MET	MODIFIED RESIDUE	UNP O73984
C	311	MSE	MET	MODIFIED RESIDUE	UNP O73984
C	333	MSE	MET	MODIFIED RESIDUE	UNP O73984

- Molecule 2 is water.

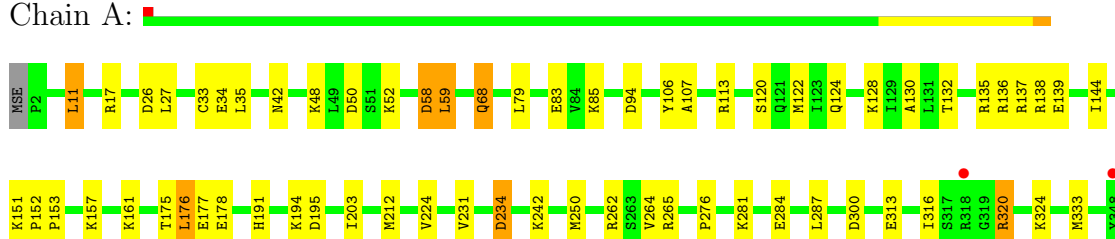
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	249	Total O 249 249	0	0
2	B	208	Total O 208 208	0	0
2	C	227	Total O 227 227	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

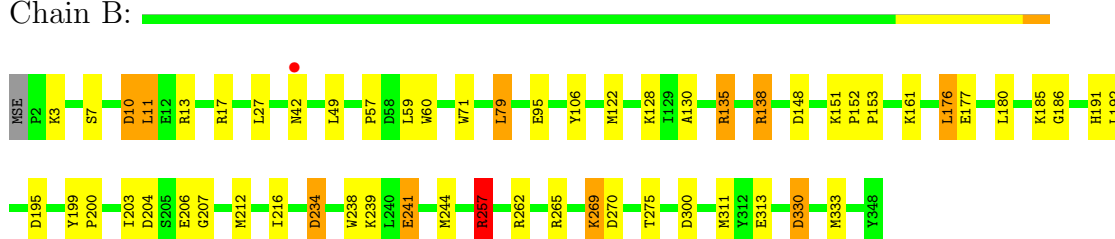
- Molecule 1: Phenylalanyl-tRNA synthetase beta chain

Chain A:



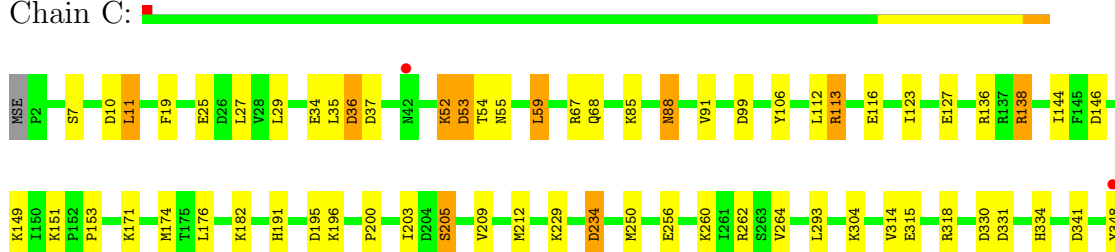
- Molecule 1: Phenylalanyl-tRNA synthetase beta chain

Chain B:



- Molecule 1: Phenylalanyl-tRNA synthetase beta chain

Chain C:



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	142.78Å 81.97Å 139.10Å 90.00° 116.79° 90.00°	Depositor
Resolution (Å)	41.52 – 1.94 41.39 – 1.94	Depositor EDS
% Data completeness (in resolution range)	99.2 (41.52-1.94) 99.2 (41.39-1.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.1.9999	Depositor
R, R_{free}	0.188 , 0.231 0.188 , 0.230	Depositor DCC
R_{free} test set	5267 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 35.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 104803 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9228	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.81	0/2905	0.90	7/3895 (0.2%)
1	B	0.79	0/2905	0.92	13/3895 (0.3%)
1	C	0.76	0/2905	0.89	11/3895 (0.3%)
All	All	0.79	0/8715	0.90	31/11685 (0.3%)

There are no bond length outliers.

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	257	ARG	NE-CZ-NH2	-8.82	115.89	120.30
1	B	257	ARG	NE-CZ-NH1	7.77	124.18	120.30
1	C	341	ASP	CB-CG-OD2	7.42	124.98	118.30
1	B	195	ASP	CB-CG-OD2	7.33	124.89	118.30
1	B	265	ARG	NE-CZ-NH2	-7.07	116.76	120.30
1	C	195	ASP	CB-CG-OD2	7.01	124.61	118.30
1	A	11	LEU	CB-CG-CD1	6.84	122.64	111.00
1	B	138	ARG	NE-CZ-NH1	-6.77	116.91	120.30
1	B	265	ARG	NE-CZ-NH1	6.73	123.67	120.30
1	A	195	ASP	CB-CG-OD2	6.40	124.06	118.30
1	B	79	LEU	CA-CB-CG	6.05	129.22	115.30
1	A	265	ARG	NE-CZ-NH2	-6.03	117.29	120.30
1	B	11	LEU	CA-CB-CG	5.96	129.00	115.30
1	C	331	ASP	CB-CG-OD2	5.90	123.61	118.30
1	B	262	ARG	NE-CZ-NH2	-5.89	117.35	120.30
1	B	10	ASP	CB-CG-OD2	5.87	123.58	118.30
1	C	53	ASP	CB-CG-OD2	5.86	123.58	118.30
1	A	79	LEU	CA-CB-CG	5.81	128.67	115.30
1	C	11	LEU	CB-CG-CD1	5.65	120.61	111.00
1	B	300	ASP	CB-CG-OD2	5.64	123.37	118.30
1	C	36	ASP	CB-CG-OD2	5.62	123.36	118.30
1	C	330	ASP	CB-CG-OD2	5.61	123.35	118.30
1	A	58	ASP	CB-CG-OD2	5.59	123.33	118.30
1	C	10	ASP	CB-CG-OD2	5.48	123.23	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	136	ARG	NE-CZ-NH1	5.39	123.00	120.30
1	A	26	ASP	CB-CG-OD2	5.30	123.07	118.30
1	C	138	ARG	CG-CD-NE	-5.26	100.75	111.80
1	A	265	ARG	NE-CZ-NH1	5.25	122.93	120.30
1	B	330	ASP	CB-CG-OD2	5.24	123.01	118.30
1	C	67	ARG	NE-CZ-NH2	-5.21	117.69	120.30
1	B	262	ARG	NE-CZ-NH1	5.20	122.90	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2848	0	2887	48	1
1	B	2848	0	2887	33	1
1	C	2848	0	2887	39	0
2	A	249	0	0	8	0
2	B	208	0	0	5	2
2	C	227	0	0	11	2
All	All	9228	0	8661	115	3

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

All (115) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:250:MSE:HE3	2:A:490:HOH:O	1.56	1.02
1:B:135:ARG:HH21	1:C:36:ASP:HA	1.41	0.84
1:A:34:GLU:HG3	1:A:52:LYS:NZ	1.97	0.78
1:A:59:LEU:HD11	1:A:68:GLN:NE2	1.98	0.78
1:A:59:LEU:CD1	1:A:68:GLN:HE22	1.98	0.76
1:A:59:LEU:CD1	1:A:68:GLN:NE2	2.47	0.76
1:B:138:ARG:HG3	1:B:192:LEU:HD22	1.68	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:138:ARG:NH1	1:C:25:GLU:OE2	2.23	0.72
1:B:3:LYS:O	1:B:128:LYS:HE2	1.89	0.72
1:C:59:LEU:HD11	1:C:68:GLN:HE21	1.54	0.71
1:C:348:TYR:O	2:C:541:HOH:O	2.09	0.69
1:A:144:ILE:HG23	1:A:231:VAL:CG2	2.23	0.69
1:A:113:ARG:HG2	2:A:585:HOH:O	1.91	0.68
1:C:334:HIS:ND1	2:C:415:HOH:O	2.25	0.68
1:A:250:MSE:CE	2:A:490:HOH:O	2.23	0.68
1:B:135:ARG:NH2	1:C:36:ASP:HA	2.08	0.67
1:B:95:GLU:OE1	1:B:269:LYS:HE2	1.96	0.66
1:A:135:ARG:HG3	1:A:139:GLU:OE1	1.95	0.65
1:C:256:GLU:OE2	2:C:477:HOH:O	2.14	0.65
1:A:59:LEU:HD12	1:A:68:GLN:HE22	1.59	0.65
1:B:130:ALA:HB2	2:B:534:HOH:O	1.96	0.65
1:C:52:LYS:CD	1:C:52:LYS:H	2.14	0.61
1:B:313:GLU:OE1	2:B:537:HOH:O	2.15	0.61
1:A:313:GLU:OE1	2:A:580:HOH:O	2.17	0.61
1:B:161:LYS:HB3	1:B:177:GLU:HG2	1.83	0.60
1:A:130:ALA:HB2	2:A:592:HOH:O	2.02	0.58
1:A:59:LEU:HD12	1:A:68:GLN:NE2	2.17	0.58
1:C:203:ILE:HB	2:C:487:HOH:O	2.03	0.58
1:B:191:HIS:HE1	1:C:37:ASP:OD1	1.87	0.57
1:A:284:GLU:OE1	1:A:320:ARG:NH1	2.37	0.57
1:B:269:LYS:HD2	1:B:270:ASP:OD1	2.04	0.56
1:B:151:LYS:HD3	1:B:206:GLU:HG2	1.87	0.56
1:C:151:LYS:O	1:C:205:SER:HB2	2.05	0.55
1:A:34:GLU:HG3	1:A:52:LYS:HZ1	1.70	0.55
1:C:138:ARG:HD3	2:C:378:HOH:O	2.06	0.55
1:B:191:HIS:HD2	2:B:519:HOH:O	1.90	0.54
1:A:144:ILE:HG23	1:A:231:VAL:HG23	1.88	0.54
1:A:138:ARG:HD3	2:A:351:HOH:O	2.09	0.53
1:B:330:ASP:O	1:B:333[B]:MSE:HE2	2.09	0.53
1:A:106:TYR:CE1	1:A:234:ASP:HB2	2.43	0.52
1:A:144:ILE:HG23	1:A:231:VAL:HG21	1.91	0.52
1:B:152:PRO:HA	1:B:153:PRO:C	2.31	0.52
1:C:203:ILE:CG2	2:C:487:HOH:O	2.58	0.51
1:A:161:LYS:HB3	1:A:177:GLU:HG2	1.91	0.51
1:A:58:ASP:OD1	1:A:59:LEU:HD13	2.10	0.51
1:B:176:LEU:HG	1:B:212:MSE:SE	2.61	0.50
1:B:106:TYR:CE1	1:B:234:ASP:HB2	2.47	0.49
1:B:244[B]:MSE:HE3	1:B:275:THR:HG22	1.94	0.49
1:C:19:PHE:CG	1:C:27:LEU:HD11	2.47	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:85:LYS:O	1:C:262:ARG:HA	2.13	0.49
1:A:59:LEU:HD11	1:A:68:GLN:CD	2.34	0.48
1:A:191:HIS:HA	1:A:194:LYS:HG2	1.96	0.48
1:C:144:ILE:HD11	1:C:250:MSE:HE2	1.95	0.48
1:A:34:GLU:HG3	1:A:52:LYS:CE	2.44	0.48
1:A:157:LYS:HE2	1:A:203:ILE:HG21	1.94	0.48
1:A:136:ARG:O	1:A:137:ARG:HB2	2.13	0.48
1:A:132:THR:OG1	2:A:538:HOH:O	2.01	0.47
1:C:106:TYR:CE1	1:C:234:ASP:HB2	2.49	0.47
1:C:304:LYS:HG3	1:C:314:VAL:HB	1.96	0.47
1:C:99:ASP:O	1:C:196:LYS:HE2	2.15	0.47
1:C:113:ARG:NH2	2:C:537:HOH:O	2.48	0.46
1:B:10:ASP:OD1	1:B:257:ARG:NH2	2.40	0.46
1:B:151:LYS:O	1:B:204:ASP:HB2	2.15	0.46
1:B:176:LEU:HB3	1:B:199:TYR:HD2	1.80	0.46
1:C:123:ILE:O	1:C:127:GLU:HG3	2.16	0.46
1:C:19:PHE:CD1	1:C:27:LEU:HD11	2.51	0.46
1:B:241:GLU:HG3	2:B:509:HOH:O	2.16	0.45
1:B:203:ILE:HD11	1:B:207:GLY:HA2	1.98	0.45
1:C:191:HIS:HD2	2:C:420:HOH:O	1.99	0.45
1:C:55:ASN:HB2	2:C:491:HOH:O	2.16	0.45
1:A:242:LYS:HB3	1:A:242:LYS:HE3	1.82	0.45
1:A:144:ILE:HG22	1:A:224:VAL:HG21	1.99	0.44
1:C:153:PRO:HD2	1:C:205:SER:OG	2.16	0.44
1:A:135:ARG:HG3	1:A:139:GLU:CD	2.38	0.44
1:A:83:GLU:OE2	1:A:85:LYS:HE2	2.16	0.44
1:A:313:GLU:HB3	1:A:324:LYS:HB2	2.00	0.44
1:C:34:GLU:HG2	1:C:52:LYS:HE3	2.00	0.43
1:C:250:MSE:HE3	2:C:413:HOH:O	2.18	0.43
1:C:88:ASN:ND2	1:C:88:ASN:C	2.70	0.43
1:B:3:LYS:HA	1:B:49:LEU:O	2.18	0.43
1:A:122:MSE:HG2	1:A:144:ILE:HD13	1.99	0.43
1:A:175:THR:OG1	1:A:178:GLU:HG3	2.19	0.43
1:A:33:CYS:HB2	1:A:50:ASP:O	2.19	0.43
1:B:10:ASP:O	1:B:13:ARG:HG2	2.18	0.43
1:A:124:GLN:O	1:A:128:LYS:HG2	2.19	0.43
1:A:85:LYS:O	1:A:262:ARG:HA	2.19	0.43
1:B:185:LYS:HG3	1:B:216:ILE:HD13	2.01	0.43
1:A:152:PRO:HA	1:A:153:PRO:C	2.39	0.43
1:A:287:LEU:HD11	1:A:316:ILE:HG12	2.01	0.43
1:B:180:LEU:HA	1:B:186:GLY:HA3	2.02	0.42
1:B:135:ARG:NH2	1:C:36:ASP:OD1	2.52	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:203:ILE:HG22	1:C:209:VAL:HG22	2.00	0.42
1:A:300:ASP:HB3	1:A:316:ILE:HD13	2.02	0.42
1:C:116:GLU:N	1:C:116:GLU:OE2	2.49	0.42
1:A:94:ASP:HB2	1:A:157:LYS:HA	2.02	0.42
1:A:191:HIS:HD2	2:A:420:HOH:O	2.02	0.42
1:C:146:ASP:OD2	1:C:149:LYS:HE3	2.20	0.42
1:C:174:MSE:HE2	1:C:182:LYS:HD2	2.02	0.42
1:A:107:ALA:HB2	1:A:276:PRO:HD3	2.01	0.42
1:B:57:PRO:HA	1:B:60:TRP:CD2	2.55	0.41
1:A:48:LYS:HE2	1:A:48:LYS:HB2	1.87	0.41
1:C:29:LEU:CD2	1:C:34:GLU:OE2	2.69	0.41
1:C:203:ILE:HG21	2:C:487:HOH:O	2.20	0.41
1:A:151:LYS:HA	1:A:152:PRO:HD2	1.92	0.41
1:B:238:TRP:O	1:B:239:LYS:HD2	2.20	0.41
1:B:128:LYS:NZ	2:B:525:HOH:O	2.53	0.41
1:C:112:LEU:O	1:C:229:LYS:HD2	2.20	0.41
1:C:88:ASN:C	1:C:88:ASN:HD22	2.24	0.41
1:C:200:PRO:O	1:C:212:MSE:HG3	2.21	0.41
1:A:281:LYS:O	1:A:324:LYS:HA	2.20	0.41
1:B:71:TRP:CD1	1:B:311:MSE:HG2	2.56	0.41
1:A:176:LEU:HG	1:A:212:MSE:SE	2.72	0.40
1:A:68:GLN:HB2	1:A:68:GLN:HE21	1.35	0.40
1:B:200:PRO:O	1:B:212:MSE:HG3	2.21	0.40
1:C:91:VAL:HG23	1:C:264:VAL:CG1	2.52	0.40

All (3) 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	Distance(Å)	Clash(Å)
2:B:552:HOH:O	2:C:575:HOH:O[2_655]	1.59	0.61
2:B:552:HOH:O	2:C:480:HOH:O[2_655]	2.01	0.19
1:A:113:ARG:NH2	1:B:148:ASP:O[3_455]	2.16	0.04

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	347/348 (100%)	337 (97%)	10 (3%)	0	100	100
1	B	347/348 (100%)	336 (97%)	10 (3%)	1 (0%)	50	37
1	C	347/348 (100%)	339 (98%)	7 (2%)	1 (0%)	50	37
All	All	1041/1044 (100%)	1012 (97%)	27 (3%)	2 (0%)	56	45

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	42	ASN
1	C	53	ASP

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	311/301 (103%)	297 (96%)	14 (4%)	38	21
1	B	311/301 (103%)	298 (96%)	13 (4%)	40	23
1	C	311/301 (103%)	295 (95%)	16 (5%)	33	16
All	All	933/903 (103%)	890 (95%)	43 (5%)	38	20

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LEU
1	A	17	ARG
1	A	27	LEU
1	A	35	LEU
1	A	42	ASN
1	A	59	LEU
1	A	68	GLN
1	A	120	SER
1	A	176	LEU
1	A	234	ASP
1	A	264	VAL
1	A	320	ARG
1	A	333[A]	MSE

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Mol	Chain	Res	Type
1	A	333[B]	MSE
1	B	7	SER
1	B	11	LEU
1	B	17	ARG
1	B	27	LEU
1	B	59	LEU
1	B	79	LEU
1	B	122	MSE
1	B	135	ARG
1	B	176	LEU
1	B	234	ASP
1	B	241	GLU
1	B	257	ARG
1	B	269	LYS
1	C	7	SER
1	C	11	LEU
1	C	35	LEU
1	C	52	LYS
1	C	54	THR
1	C	59	LEU
1	C	88	ASN
1	C	113	ARG
1	C	171	LYS
1	C	176	LEU
1	C	205	SER
1	C	234	ASP
1	C	260	LYS
1	C	293	LEU
1	C	315	GLU
1	C	318	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	ASN
1	A	68	GLN
1	A	126	GLN
1	A	191	HIS
1	A	248	ASN
1	B	88	ASN
1	B	191	HIS
1	B	208	ASN

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Mol	Chain	Res	Type
1	B	248	ASN
1	C	68	GLN
1	C	88	ASN
1	C	126	GLN
1	C	191	HIS
1	C	248	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	347/348 (99%)	-0.28	2 (0%) 86 91	13, 23, 34, 50	0
1	B	347/348 (99%)	-0.32	1 (0%) 91 95	13, 25, 36, 44	0
1	C	347/348 (99%)	-0.20	2 (0%) 86 91	15, 26, 39, 52	0
All	All	1041/1044 (99%)	-0.27	5 (0%) 88 93	13, 25, 37, 52	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	42	ASN	3.3
1	C	348	TYR	3.3
1	A	318	ARG	2.9
1	A	348	TYR	2.4
1	B	42	ASN	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.