



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:59 PM UTC

PDB ID : 3D63 / pdb_00003d63
Title : Crystal structure of inorganic pyrophosphatase from Burkholderia pseudomallei
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2008-05-18
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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

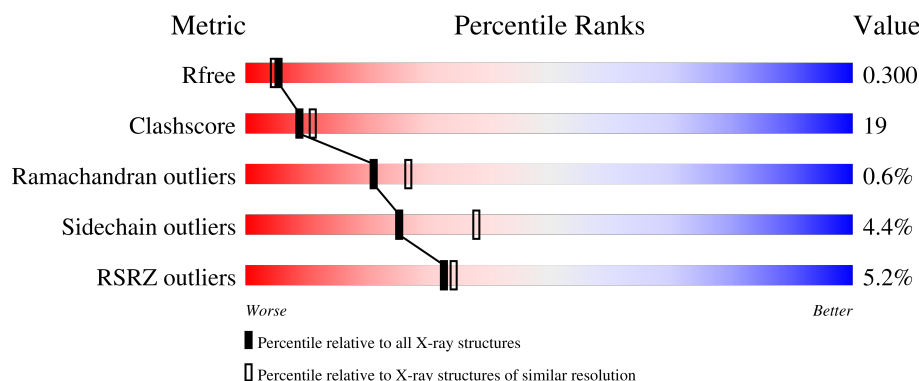
1 Overall quality at a glance

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))
R_{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 $\leq 5\%$. 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	196	5% 61% 23% • 12%
1	B	196	6% 63% 22% • • 12%
1	C	196	3% 51% 36% • • 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4255 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 Inorganic pyrophosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	173	Total	C	N	O	S	0	0	0
			1332	860	219	248	5			
1	B	173	Total	C	N	O	S	0	0	0
			1327	857	217	248	5			
1	C	178	Total	C	N	O	S	0	0	0
			1356	869	229	253	5			

There are 63 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP Q3JUV5
A	-19	ALA	-	expression tag	UNP Q3JUV5
A	-18	HIS	-	expression tag	UNP Q3JUV5
A	-17	HIS	-	expression tag	UNP Q3JUV5
A	-16	HIS	-	expression tag	UNP Q3JUV5
A	-15	HIS	-	expression tag	UNP Q3JUV5
A	-14	HIS	-	expression tag	UNP Q3JUV5
A	-13	HIS	-	expression tag	UNP Q3JUV5
A	-12	MET	-	expression tag	UNP Q3JUV5
A	-11	GLY	-	expression tag	UNP Q3JUV5
A	-10	THR	-	expression tag	UNP Q3JUV5
A	-9	LEU	-	expression tag	UNP Q3JUV5
A	-8	GLU	-	expression tag	UNP Q3JUV5
A	-7	ALA	-	expression tag	UNP Q3JUV5
A	-6	GLN	-	expression tag	UNP Q3JUV5
A	-5	THR	-	expression tag	UNP Q3JUV5
A	-4	GLN	-	expression tag	UNP Q3JUV5
A	-3	GLY	-	expression tag	UNP Q3JUV5
A	-2	PRO	-	expression tag	UNP Q3JUV5
A	-1	GLY	-	expression tag	UNP Q3JUV5
A	0	SER	-	expression tag	UNP Q3JUV5
B	-20	MET	-	expression tag	UNP Q3JUV5
B	-19	ALA	-	expression tag	UNP Q3JUV5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	HIS	-	expression tag	UNP Q3JUV5
B	-17	HIS	-	expression tag	UNP Q3JUV5
B	-16	HIS	-	expression tag	UNP Q3JUV5
B	-15	HIS	-	expression tag	UNP Q3JUV5
B	-14	HIS	-	expression tag	UNP Q3JUV5
B	-13	HIS	-	expression tag	UNP Q3JUV5
B	-12	MET	-	expression tag	UNP Q3JUV5
B	-11	GLY	-	expression tag	UNP Q3JUV5
B	-10	THR	-	expression tag	UNP Q3JUV5
B	-9	LEU	-	expression tag	UNP Q3JUV5
B	-8	GLU	-	expression tag	UNP Q3JUV5
B	-7	ALA	-	expression tag	UNP Q3JUV5
B	-6	GLN	-	expression tag	UNP Q3JUV5
B	-5	THR	-	expression tag	UNP Q3JUV5
B	-4	GLN	-	expression tag	UNP Q3JUV5
B	-3	GLY	-	expression tag	UNP Q3JUV5
B	-2	PRO	-	expression tag	UNP Q3JUV5
B	-1	GLY	-	expression tag	UNP Q3JUV5
B	0	SER	-	expression tag	UNP Q3JUV5
C	-20	MET	-	expression tag	UNP Q3JUV5
C	-19	ALA	-	expression tag	UNP Q3JUV5
C	-18	HIS	-	expression tag	UNP Q3JUV5
C	-17	HIS	-	expression tag	UNP Q3JUV5
C	-16	HIS	-	expression tag	UNP Q3JUV5
C	-15	HIS	-	expression tag	UNP Q3JUV5
C	-14	HIS	-	expression tag	UNP Q3JUV5
C	-13	HIS	-	expression tag	UNP Q3JUV5
C	-12	MET	-	expression tag	UNP Q3JUV5
C	-11	GLY	-	expression tag	UNP Q3JUV5
C	-10	THR	-	expression tag	UNP Q3JUV5
C	-9	LEU	-	expression tag	UNP Q3JUV5
C	-8	GLU	-	expression tag	UNP Q3JUV5
C	-7	ALA	-	expression tag	UNP Q3JUV5
C	-6	GLN	-	expression tag	UNP Q3JUV5
C	-5	THR	-	expression tag	UNP Q3JUV5
C	-4	GLN	-	expression tag	UNP Q3JUV5
C	-3	GLY	-	expression tag	UNP Q3JUV5
C	-2	PRO	-	expression tag	UNP Q3JUV5
C	-1	GLY	-	expression tag	UNP Q3JUV5
C	0	SER	-	expression tag	UNP Q3JUV5

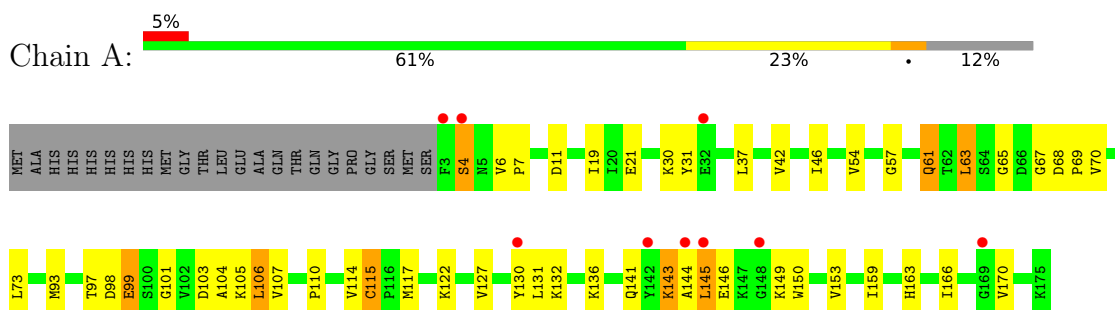
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	80	Total 80	O 80	0	0
2	B	82	Total 82	O 82	0	0
2	C	78	Total 78	O 78	0	0

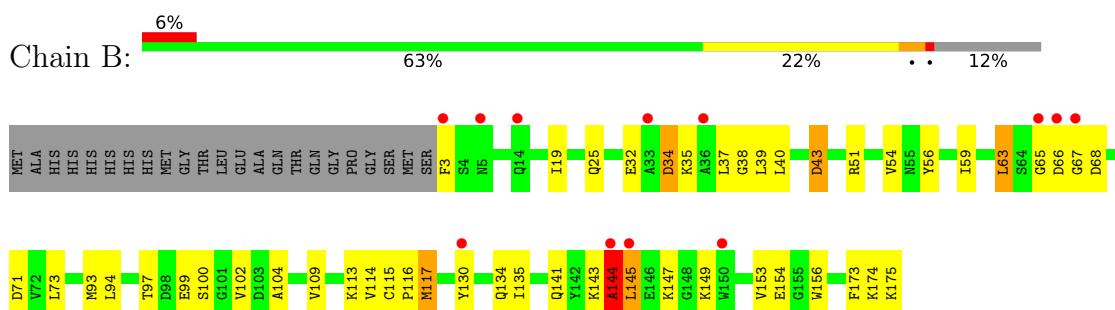
3 Residue-property plots [i](#)

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.

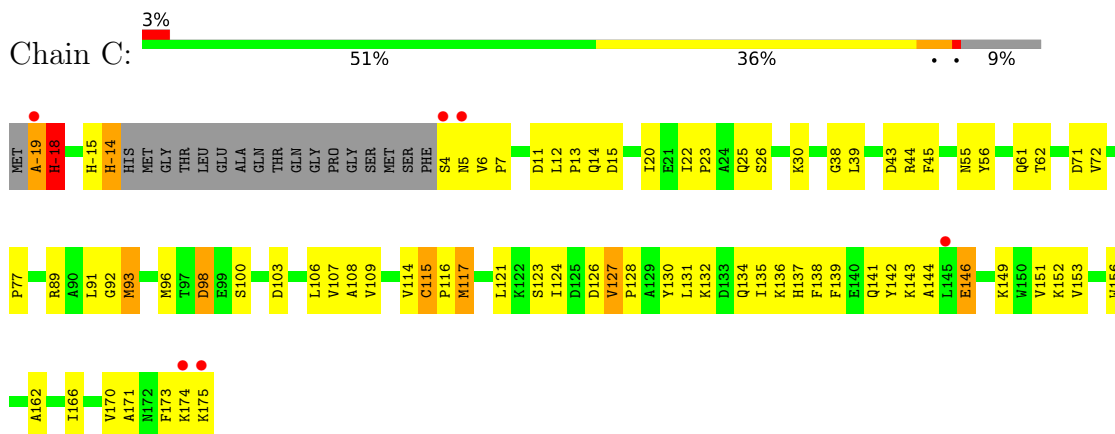
- Molecule 1: Inorganic pyrophosphatase



- Molecule 1: Inorganic pyrophosphatase



- Molecule 1: Inorganic pyrophosphatase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	83.89Å 122.02Å 71.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	61.90 – 2.30 61.90 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.4 (61.90-2.30) 99.3 (61.90-2.30)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.82 (at 2.29Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.231 , 0.300 0.233 , 0.300	Depositor DCC
R_{free} test set	1671 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	35.7	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4255	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.55% 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

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	0.88	0/1363	1.22	8/1850 (0.4%)
1	B	0.90	0/1358	1.20	9/1846 (0.5%)
1	C	0.91	1/1390 (0.1%)	1.29	13/1893 (0.7%)
All	All	0.90	1/4111 (0.0%)	1.24	30/5589 (0.5%)

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	B	0	1
1	C	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	55	ASN	N-CA	5.10	1.52	1.46

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	109	VAL	CA-C-N	-12.79	107.29	120.98
1	C	109	VAL	C-N-CA	-12.79	107.29	120.98
1	A	114	VAL	N-CA-C	-7.93	103.18	111.58
1	B	109	VAL	CA-C-N	-7.74	112.78	120.21
1	B	109	VAL	C-N-CA	-7.74	112.78	120.21
1	B	147	LYS	CB-CA-C	-7.03	108.46	116.54
1	B	65	GLY	N-CA-C	-6.99	105.59	115.30
1	C	72	VAL	N-CA-C	6.84	118.15	108.17
1	A	115	CYS	CA-C-N	6.80	126.43	119.56
1	A	115	CYS	C-N-CA	6.80	126.43	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	99	GLU	N-CA-C	-6.47	105.39	113.28
1	C	173	PHE	N-CA-C	-6.41	105.42	113.18
1	C	-18	HIS	N-CA-C	6.30	124.22	110.80
1	C	115	CYS	CA-C-N	5.87	125.54	119.56
1	C	115	CYS	C-N-CA	5.87	125.54	119.56
1	A	99	GLU	N-CA-C	-5.83	106.01	113.01
1	B	59	ILE	CA-C-N	-5.75	114.05	119.85
1	B	59	ILE	C-N-CA	-5.75	114.05	119.85
1	C	127	VAL	CA-C-N	-5.55	114.23	119.89
1	C	127	VAL	C-N-CA	-5.55	114.23	119.89
1	B	114	VAL	N-CA-C	-5.53	106.31	111.45
1	C	146	GLU	N-CA-C	5.47	117.44	108.52
1	A	70	VAL	CA-C-N	5.44	129.21	121.42
1	A	70	VAL	C-N-CA	5.44	129.21	121.42
1	A	143	LYS	N-CA-C	-5.41	106.68	113.28
1	B	173	PHE	N-CA-C	-5.34	106.02	112.54
1	C	93	MET	N-CA-C	5.23	117.20	108.99
1	C	131	LEU	N-CA-C	-5.23	105.66	111.36
1	C	114	VAL	N-CA-C	-5.10	106.17	111.58
1	A	61	GLN	N-CA-C	-5.09	106.37	112.58

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	144	ALA	Peptide
1	C	-19	ALA	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1332	0	1339	44	0
1	B	1327	0	1326	40	0
1	C	1356	0	1317	68	0
2	A	80	0	0	0	0
2	B	82	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	78	0	0	2	0
All	All	4255	0	3982	149	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

All (149) 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:C:130:TYR:CE2	1:C:134:GLN:OE1	2.06	1.07
1:B:116:PRO:HD2	1:B:117:MET:HE3	1.32	1.04
1:C:38:GLY:O	1:C:39:LEU:HD12	1.60	1.01
1:A:99:GLU:OE2	1:A:143:LYS:NZ	2.04	0.91
1:B:93:MET:CE	1:B:104:ALA:HB1	2.03	0.89
1:B:116:PRO:CD	1:B:117:MET:HE3	2.07	0.85
1:B:93:MET:HE2	1:B:104:ALA:HB1	1.59	0.83
1:A:110:PRO:HG2	1:A:115:CYS:HB3	1.59	0.82
1:B:144:ALA:HB3	1:B:145:LEU:HB2	1.62	0.82
1:A:30:LYS:HB2	1:A:46:ILE:HD11	1.62	0.81
1:C:116:PRO:HD2	1:C:117:MET:HE3	1.62	0.79
1:A:141:GLN:O	1:A:144:ALA:HB3	1.88	0.74
1:C:174:LYS:O	1:C:175:LYS:C	2.32	0.73
1:C:130:TYR:CZ	1:C:134:GLN:OE1	2.42	0.72
1:B:35:LYS:C	1:B:37:LEU:H	1.97	0.71
1:B:3:PHE:HA	1:B:19:ILE:HD13	1.73	0.70
1:B:66:ASP:C	1:B:68:ASP:H	1.96	0.70
1:C:38:GLY:O	1:C:39:LEU:CD1	2.39	0.70
1:B:38:GLY:O	1:B:39:LEU:HD12	1.92	0.69
1:C:162:ALA:O	1:C:166:ILE:HG13	1.92	0.69
1:A:144:ALA:O	1:A:145:LEU:CB	2.43	0.66
1:A:110:PRO:HG2	1:A:115:CYS:CB	2.27	0.65
1:C:-14:HIS:N	1:C:-14:HIS:ND1	2.45	0.64
1:A:63:LEU:HD11	1:A:67:GLY:HA2	1.80	0.64
1:C:92:GLY:O	1:C:93:MET:HG2	1.98	0.63
1:C:98:ASP:HB3	1:C:100:SER:H	1.63	0.63
1:A:99:GLU:HA	1:A:150:TRP:CZ2	2.35	0.62
1:C:-15:HIS:C	1:C:-14:HIS:ND1	2.57	0.62
1:B:25:GLN:O	1:B:51:ARG:HD3	2.00	0.62
1:B:144:ALA:CB	1:B:145:LEU:HB2	2.30	0.62
1:C:-19:ALA:CB	1:C:100:SER:O	2.48	0.61
1:C:106:LEU:HD23	1:C:107:VAL:N	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:TYR:CG	1:A:131:LEU:N	2.70	0.60
1:C:25:GLN:HA	1:C:25:GLN:OE1	2.01	0.60
1:A:159:ILE:HG22	1:A:163:HIS:CE1	2.37	0.59
1:B:174:LYS:O	1:B:175:LYS:CB	2.50	0.59
1:C:-18:HIS:ND1	1:C:103:ASP:OD1	2.35	0.59
1:B:116:PRO:HD2	1:B:117:MET:CE	2.22	0.59
1:C:-19:ALA:HB2	1:C:100:SER:C	2.29	0.58
1:C:130:TYR:HE2	1:C:134:GLN:OE1	1.78	0.58
1:A:127:VAL:O	1:A:132:LYS:HE2	2.03	0.58
1:A:97:THR:HG22	1:A:98:ASP:N	2.19	0.58
1:A:93:MET:HE3	1:A:104:ALA:HB1	1.86	0.57
1:A:103:ASP:OD2	1:A:105:LYS:NZ	2.38	0.57
1:A:159:ILE:CG2	1:A:163:HIS:CE1	2.88	0.56
1:B:34:ASP:HB3	1:B:37:LEU:HB3	1.86	0.56
1:C:98:ASP:OD1	1:C:143:LYS:HE2	2.05	0.56
1:C:4:SER:O	1:C:61:GLN:NE2	2.39	0.56
1:B:3:PHE:HA	1:B:19:ILE:CD1	2.34	0.56
1:B:93:MET:CE	1:B:104:ALA:CB	2.81	0.56
1:C:174:LYS:O	1:C:175:LYS:O	2.24	0.55
1:B:66:ASP:C	1:B:68:ASP:N	2.65	0.55
1:B:141:GLN:O	1:B:144:ALA:HB2	2.06	0.55
1:C:13:PRO:HD2	1:C:14:GLN:OE1	2.06	0.55
1:C:143:LYS:HD3	1:C:151:VAL:HG23	1.88	0.55
1:A:99:GLU:OE1	1:A:149:LYS:HD3	2.06	0.55
1:C:166:ILE:O	1:C:170:VAL:HG23	2.06	0.55
1:C:11:ASP:HB3	1:C:15:ASP:HB3	1.88	0.54
1:B:35:LYS:C	1:B:37:LEU:N	2.65	0.54
1:A:98:ASP:N	1:A:101:GLY:O	2.37	0.54
1:C:124:ILE:O	1:C:132:LYS:HD3	2.08	0.54
1:C:-19:ALA:HB2	1:C:100:SER:O	2.08	0.54
1:A:63:LEU:HD11	1:A:67:GLY:CA	2.38	0.53
1:C:136:LYS:HB2	1:C:153:VAL:HG11	1.89	0.52
1:C:98:ASP:C	1:C:100:SER:H	2.16	0.52
1:B:56:TYR:OH	1:B:71:ASP:OD1	2.23	0.52
1:A:106:LEU:HD23	1:A:107:VAL:H	1.74	0.52
1:C:151:VAL:CG1	1:C:152:LYS:N	2.72	0.52
1:B:32:GLU:HB2	1:B:43:ASP:OD2	2.10	0.51
1:B:130:TYR:O	1:B:134:GLN:HG3	2.11	0.51
1:B:38:GLY:C	1:B:39:LEU:HD12	2.37	0.50
1:C:23:PRO:HD2	1:C:26:SER:OG	2.11	0.50
1:C:106:LEU:HD11	1:C:166:ILE:HD11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:44:ARG:HG2	1:C:45:PHE:N	2.26	0.49
1:C:134:GLN:NE2	2:C:227:HOH:O	2.32	0.49
1:C:137:HIS:O	1:C:138:PHE:C	2.55	0.49
1:C:107:VAL:HG12	1:C:108:ALA:N	2.28	0.49
1:B:63:LEU:HD11	1:B:67:GLY:HA2	1.94	0.49
1:A:122:LYS:O	1:A:159:ILE:HD11	2.12	0.48
1:C:38:GLY:C	1:C:39:LEU:HD12	2.36	0.48
1:A:103:ASP:OD1	1:A:105:LYS:NZ	2.46	0.48
1:C:135:ILE:O	1:C:139:PHE:HD2	1.96	0.47
1:A:11:ASP:OD1	1:C:14:GLN:NE2	2.47	0.47
1:C:30:LYS:O	1:C:43:ASP:CB	2.61	0.47
1:C:130:TYR:O	1:C:134:GLN:HG3	2.14	0.47
1:C:6:VAL:HA	1:C:7:PRO:HD3	1.73	0.47
1:C:151:VAL:HG12	1:C:152:LYS:N	2.29	0.47
1:C:56:TYR:OH	1:C:71:ASP:OD1	2.33	0.47
1:A:136:LYS:HB2	1:A:153:VAL:HG21	1.97	0.46
1:A:30:LYS:HE3	1:A:31:TYR:O	2.16	0.46
1:A:97:THR:CG2	1:A:98:ASP:N	2.78	0.46
1:A:65:GLY:O	1:B:102:VAL:CG2	2.63	0.46
1:A:106:LEU:HD23	1:A:107:VAL:N	2.30	0.46
1:A:146:GLU:HB3	1:A:149:LYS:HG3	1.98	0.46
1:A:65:GLY:O	1:B:102:VAL:HG21	2.15	0.46
1:C:171:ALA:O	1:C:174:LYS:CB	2.64	0.46
1:C:38:GLY:C	1:C:39:LEU:CD1	2.88	0.45
1:B:115:CYS:SG	1:B:117:MET:HG2	2.57	0.45
1:C:20:ILE:N	1:C:20:ILE:HD13	2.31	0.45
1:B:143:LYS:CD	1:B:149:LYS:HB3	2.46	0.45
1:A:146:GLU:HB2	1:A:149:LYS:HB2	1.99	0.45
1:B:97:THR:CG2	1:B:154:GLU:OE2	2.64	0.45
1:A:166:ILE:O	1:A:170:VAL:HG23	2.16	0.45
1:B:134:GLN:NE2	2:B:261:HOH:O	2.44	0.45
1:C:89:ARG:NH1	1:C:121:LEU:O	2.44	0.45
1:C:96:MET:HE3	1:C:96:MET:HB2	1.47	0.45
1:A:68:ASP:HB3	1:A:69:PRO:HD2	1.99	0.44
1:C:92:GLY:C	1:C:93:MET:HG2	2.43	0.44
1:B:54:VAL:HG11	1:B:135:ILE:HD11	2.00	0.44
1:C:141:GLN:O	1:C:144:ALA:HB2	2.18	0.44
1:C:123:SER:O	1:C:126:ASP:HB2	2.18	0.43
1:A:63:LEU:HD11	1:A:67:GLY:C	2.43	0.43
1:C:22:ILE:HB	1:C:56:TYR:HB3	2.00	0.43
1:C:146:GLU:OE1	1:C:149:LYS:HD3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:LEU:HD23	1:A:37:LEU:HA	1.69	0.43
1:B:34:ASP:HB3	1:B:37:LEU:CB	2.48	0.43
1:A:21:GLU:HG3	1:A:57:GLY:HA2	2.00	0.43
1:B:94:LEU:HD13	1:B:156:TRP:CH2	2.54	0.42
1:A:63:LEU:CD1	1:A:67:GLY:C	2.92	0.42
1:A:103:ASP:CG	1:A:105:LYS:NZ	2.78	0.42
1:C:62:THR:HG22	1:C:170:VAL:HG22	2.01	0.42
1:B:94:LEU:HD11	1:B:153:VAL:HG11	2.01	0.42
1:B:32:GLU:CB	1:B:43:ASP:OD2	2.68	0.42
1:B:143:LYS:HD2	1:B:149:LYS:HB3	2.00	0.42
1:C:127:VAL:O	1:C:128:PRO:C	2.61	0.42
1:A:31:TYR:CE1	1:A:42:VAL:HG22	2.55	0.41
1:C:-18:HIS:CE1	1:C:103:ASP:OD1	2.73	0.41
1:C:77:PRO:HG3	1:C:117:MET:HG3	2.02	0.41
1:C:98:ASP:C	1:C:100:SER:N	2.78	0.41
1:B:40:LEU:HD23	1:B:40:LEU:HA	1.78	0.41
1:C:156:TRP:NE1	2:C:181:HOH:O	2.52	0.41
1:B:35:LYS:O	1:B:37:LEU:N	2.54	0.41
1:C:-18:HIS:CE1	1:C:71:ASP:HB2	2.56	0.41
1:A:19:ILE:O	1:A:57:GLY:HA3	2.20	0.41
1:A:106:LEU:CD2	1:A:107:VAL:N	2.84	0.41
1:A:127:VAL:HG12	1:A:132:LYS:HG3	2.02	0.41
1:C:146:GLU:HB2	1:C:149:LYS:HD2	2.03	0.41
1:A:6:VAL:HA	1:A:7:PRO:HD3	1.97	0.41
1:A:99:GLU:HA	1:A:150:TRP:CE2	2.56	0.41
1:B:113:LYS:HA	1:B:113:LYS:HD2	1.83	0.41
1:C:107:VAL:CG1	1:C:108:ALA:N	2.84	0.40
1:C:115:CYS:SG	1:C:117:MET:HG2	2.61	0.40
1:C:106:LEU:HD23	1:C:107:VAL:O	2.21	0.40
1:A:4:SER:O	1:A:61:GLN:NE2	2.54	0.40
1:C:30:LYS:O	1:C:43:ASP:HB3	2.20	0.40
1:C:91:LEU:O	1:C:124:ILE:HG12	2.22	0.40
1:B:93:MET:HE2	1:B:93:MET:HB3	1.92	0.40
1:C:12:LEU:HD13	1:C:170:VAL:HG21	2.03	0.40
1:C:146:GLU:OE1	1:C:149:LYS:CD	2.69	0.40

There are no symmetry-related clashes.

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	171/196 (87%)	166 (97%)	4 (2%)	1 (1%)	21	27
1	B	171/196 (87%)	158 (92%)	12 (7%)	1 (1%)	21	27
1	C	174/196 (89%)	168 (97%)	5 (3%)	1 (1%)	21	27
All	All	516/588 (88%)	492 (95%)	21 (4%)	3 (1%)	21	27

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	144	ALA
1	A	145	LEU
1	C	-18	HIS

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	143/162 (88%)	137 (96%)	6 (4%)	26	40
1	B	142/162 (88%)	135 (95%)	7 (5%)	22	34
1	C	142/162 (88%)	136 (96%)	6 (4%)	26	40
All	All	427/486 (88%)	408 (96%)	19 (4%)	25	38

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	SER
1	A	54	VAL
1	A	63	LEU
1	A	73	LEU
1	A	106	LEU
1	A	117	MET
1	B	34	ASP
1	B	43	ASP
1	B	63	LEU
1	B	73	LEU
1	B	100	SER
1	B	117	MET
1	B	145	LEU
1	C	-18	HIS
1	C	-14	HIS
1	C	5	ASN
1	C	98	ASP
1	C	117	MET
1	C	142	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	137	HIS
1	C	5	ASN
1	C	134	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides 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	173/196 (88%)	0.35	9 (5%) 33 34	22, 32, 52, 58	0
1	B	173/196 (88%)	0.39	12 (6%) 23 25	22, 32, 51, 58	0
1	C	178/196 (90%)	0.53	6 (3%) 48 50	23, 33, 51, 55	0
All	All	524/588 (89%)	0.43	27 (5%) 33 34	22, 33, 51, 58	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	144	ALA	4.3
1	B	3	PHE	4.2
1	A	3	PHE	3.4
1	A	145	LEU	3.2
1	C	174	LYS	3.1
1	A	148	GLY	2.8
1	B	145	LEU	2.7
1	C	4	SER	2.7
1	B	36	ALA	2.7
1	B	144	ALA	2.7
1	B	150	TRP	2.6
1	A	130	TYR	2.5
1	C	175	LYS	2.5
1	B	67	GLY	2.5
1	B	66	ASP	2.5
1	B	33	ALA	2.3
1	A	142	TYR	2.3
1	C	145	LEU	2.3
1	B	14	GLN	2.3
1	C	5	ASN	2.2
1	B	65	GLY	2.2
1	A	4	SER	2.2
1	A	169	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	130	TYR	2.2
1	A	32	GLU	2.1
1	C	-19	ALA	2.0
1	B	5	ASN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.