



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 03:11 am BST

PDB ID : 6BUI
Title : Crystal structure of a membrane protein, crystal form III
Authors : Ma, D.; Wang, Z.; Xu, W.
Deposited on : 2017-12-10
Resolution : 3.27 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

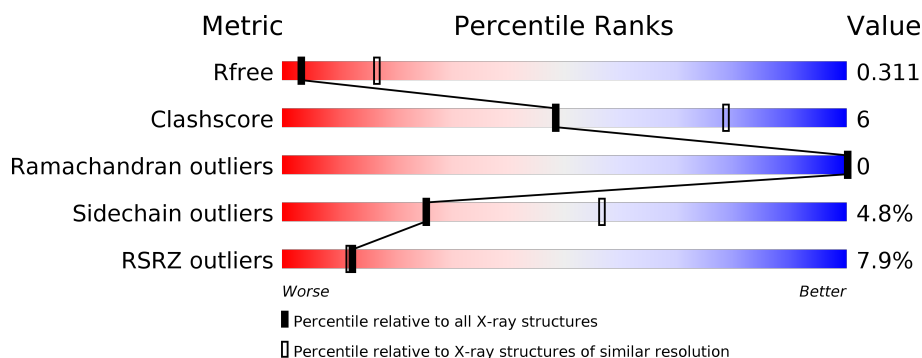
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.27 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}	130704	1177 (3.32-3.24)
Clashscore	141614	1044 (3.30-3.26)
Ramachandran outliers	138981	1026 (3.30-3.26)
Sidechain outliers	138945	1025 (3.30-3.26)
RSRZ outliers	127900	1141 (3.32-3.24)

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 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	425	
1	B	425	
1	C	425	
1	D	425	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 13792 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 Integral membrane protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	414	Total	C	N	O	S	0	0	0
			3448	2327	548	553	20			
1	A	414	Total	C	N	O	S	0	0	0
			3448	2327	548	553	20			
1	B	414	Total	C	N	O	S	0	0	0
			3448	2327	548	553	20			
1	D	414	Total	C	N	O	S	0	0	0
			3448	2327	548	553	20			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	416	LEU	-	expression tag	UNP Q5M4V4
C	417	GLU	-	expression tag	UNP Q5M4V4
C	418	HIS	-	expression tag	UNP Q5M4V4
C	419	HIS	-	expression tag	UNP Q5M4V4
C	420	HIS	-	expression tag	UNP Q5M4V4
C	421	HIS	-	expression tag	UNP Q5M4V4
C	422	HIS	-	expression tag	UNP Q5M4V4
C	423	HIS	-	expression tag	UNP Q5M4V4
C	424	HIS	-	expression tag	UNP Q5M4V4
C	425	HIS	-	expression tag	UNP Q5M4V4
A	416	LEU	-	expression tag	UNP Q5M4V4
A	417	GLU	-	expression tag	UNP Q5M4V4
A	418	HIS	-	expression tag	UNP Q5M4V4
A	419	HIS	-	expression tag	UNP Q5M4V4
A	420	HIS	-	expression tag	UNP Q5M4V4
A	421	HIS	-	expression tag	UNP Q5M4V4
A	422	HIS	-	expression tag	UNP Q5M4V4
A	423	HIS	-	expression tag	UNP Q5M4V4
A	424	HIS	-	expression tag	UNP Q5M4V4
A	425	HIS	-	expression tag	UNP Q5M4V4
B	416	LEU	-	expression tag	UNP Q5M4V4

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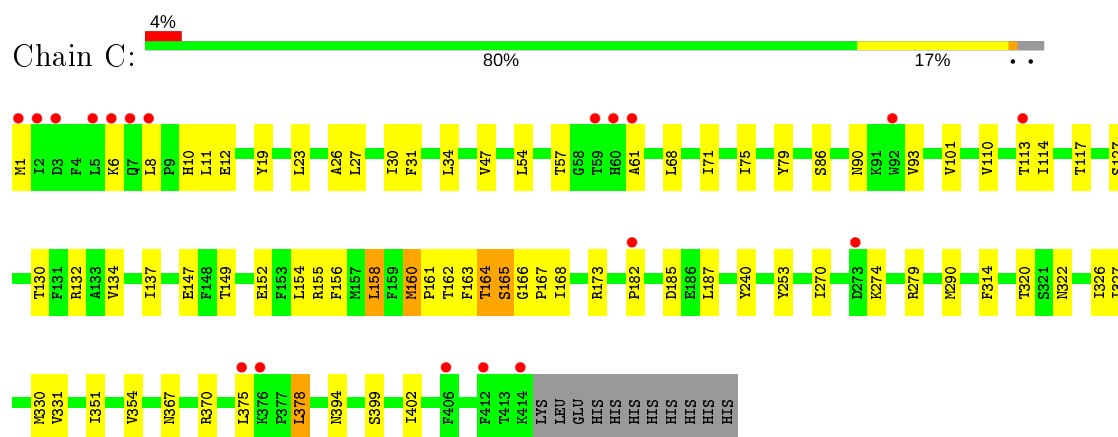
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Chain	Residue	Modelled	Actual	Comment	Reference
B	417	GLU	-	expression tag	UNP Q5M4V4
B	418	HIS	-	expression tag	UNP Q5M4V4
B	419	HIS	-	expression tag	UNP Q5M4V4
B	420	HIS	-	expression tag	UNP Q5M4V4
B	421	HIS	-	expression tag	UNP Q5M4V4
B	422	HIS	-	expression tag	UNP Q5M4V4
B	423	HIS	-	expression tag	UNP Q5M4V4
B	424	HIS	-	expression tag	UNP Q5M4V4
B	425	HIS	-	expression tag	UNP Q5M4V4
D	416	LEU	-	expression tag	UNP Q5M4V4
D	417	GLU	-	expression tag	UNP Q5M4V4
D	418	HIS	-	expression tag	UNP Q5M4V4
D	419	HIS	-	expression tag	UNP Q5M4V4
D	420	HIS	-	expression tag	UNP Q5M4V4
D	421	HIS	-	expression tag	UNP Q5M4V4
D	422	HIS	-	expression tag	UNP Q5M4V4
D	423	HIS	-	expression tag	UNP Q5M4V4
D	424	HIS	-	expression tag	UNP Q5M4V4
D	425	HIS	-	expression tag	UNP Q5M4V4

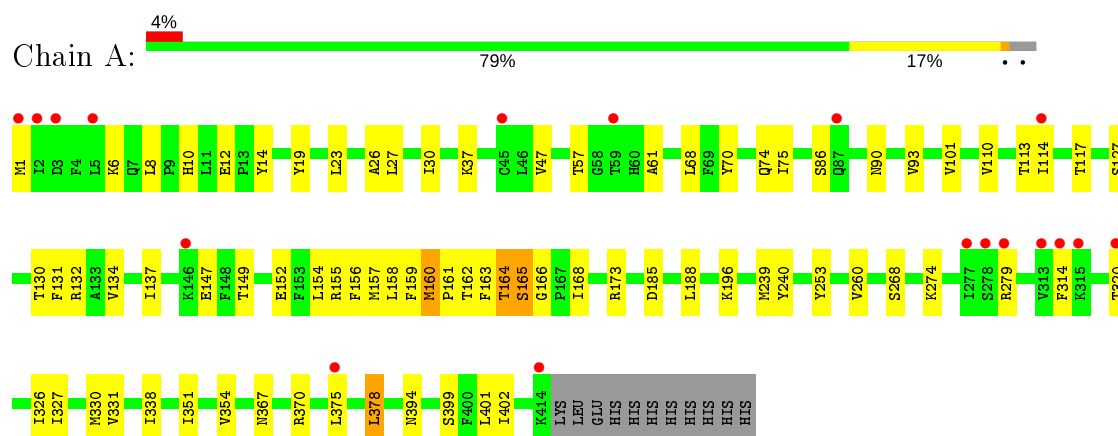
3 Residue-property plots [i](#)

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.

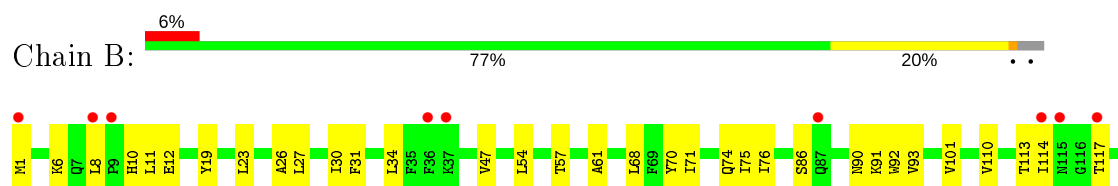
- Molecule 1: Integral membrane protein

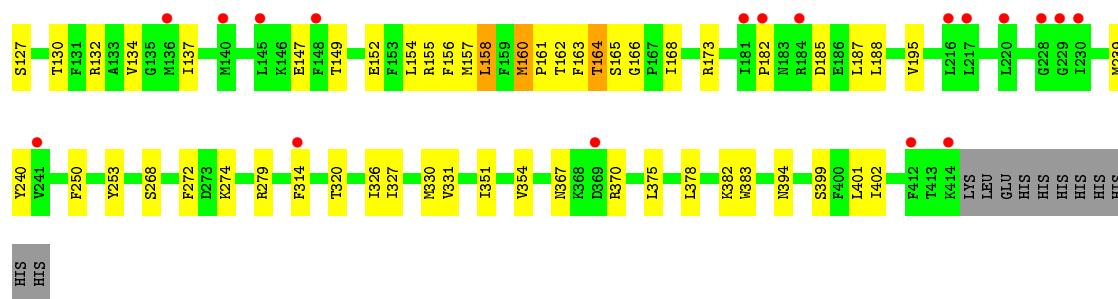


- Molecule 1: Integral membrane protein

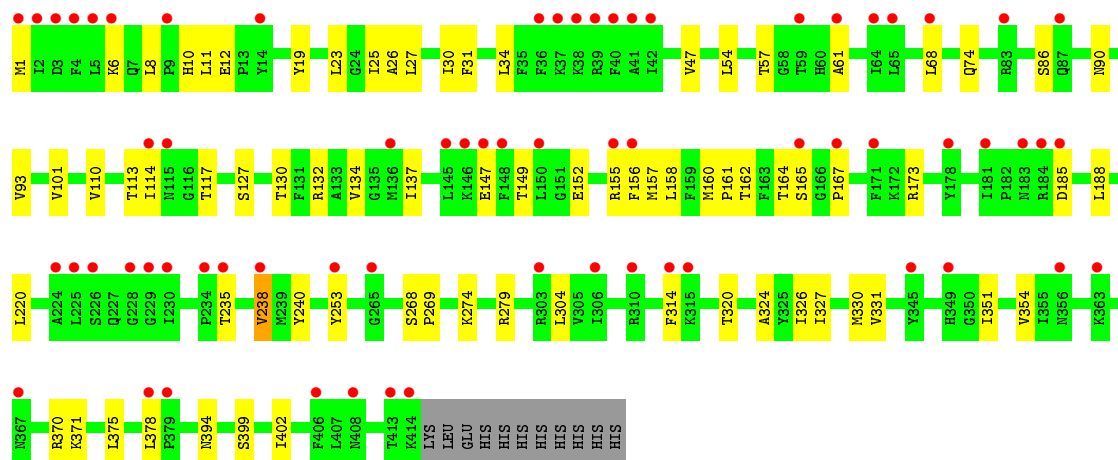
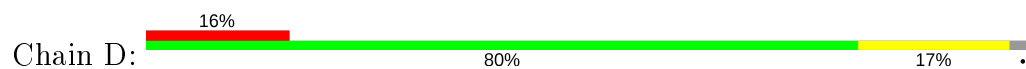


- Molecule 1: Integral membrane protein





- Molecule 1: Integral membrane protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	140.18 Å 242.06 Å 96.23 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	121.31 – 3.27 46.37 – 3.27	Depositor EDS
% Data completeness (in resolution range)	96.5 (121.31-3.27) 96.6 (46.37-3.27)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 3.25 Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.280 , 0.300 0.285 , 0.311	Depositor DCC
R_{free} test set	2434 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	117.2	Xtriage
Anisotropy	0.374	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 81.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	13792	wwPDB-VP
Average B, all atoms (Å ²)	151.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.53% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.49	0/3556	0.68	0/4811
1	B	0.48	0/3556	0.67	0/4811
1	C	0.48	0/3556	0.69	0/4811
1	D	0.46	0/3556	0.66	0/4811
All	All	0.48	0/14224	0.68	0/19244

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [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	3448	0	3527	38	0
1	B	3448	0	3527	54	0
1	C	3448	0	3527	38	0
1	D	3448	0	3527	44	0
All	All	13792	0	14108	166	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 6.

All (166) 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:160:MET:HG3	1:B:161:PRO:CD	2.01	0.90
1:C:160:MET:HG3	1:C:161:PRO:CD	2.03	0.88
1:D:235:THR:HA	1:D:238:VAL:HG22	1.58	0.86
1:B:76:ILE:HD13	1:D:25:ILE:HG12	1.60	0.82
1:B:76:ILE:HG12	1:D:25:ILE:CD1	2.09	0.81
1:C:160:MET:HG3	1:C:161:PRO:N	1.96	0.80
1:B:160:MET:HG3	1:B:161:PRO:HD3	1.63	0.80
1:B:76:ILE:HG12	1:D:25:ILE:HD11	1.64	0.79
1:D:165:SER:O	1:D:253:TYR:CE2	2.35	0.79
1:B:76:ILE:CD1	1:D:25:ILE:HG12	2.13	0.78
1:C:160:MET:HG3	1:C:161:PRO:HD3	1.65	0.77
1:B:160:MET:HG3	1:B:161:PRO:N	1.95	0.77
1:B:162:THR:HA	1:B:166:GLY:HA3	1.72	0.71
1:B:168:ILE:HD12	1:B:168:ILE:N	2.06	0.71
1:A:131:PHE:CD2	1:A:168:ILE:HD11	2.26	0.70
1:B:76:ILE:CG2	1:D:25:ILE:HD13	2.26	0.66
1:B:162:THR:CA	1:B:166:GLY:HA3	2.26	0.65
1:C:90:ASN:HD22	1:C:93:VAL:HG23	1.62	0.65
1:D:90:ASN:HD22	1:D:93:VAL:HG23	1.63	0.64
1:A:90:ASN:HD22	1:A:93:VAL:HG23	1.62	0.64
1:B:90:ASN:HD22	1:B:93:VAL:HG23	1.63	0.64
1:D:130:THR:O	1:D:134:VAL:HG23	1.99	0.63
1:D:370:ARG:HD2	1:D:378:LEU:HD12	1.81	0.63
1:A:130:THR:O	1:A:134:VAL:HG23	1.99	0.63
1:D:165:SER:O	1:D:253:TYR:HE2	1.82	0.63
1:C:130:THR:O	1:C:134:VAL:HG23	1.99	0.62
1:B:130:THR:O	1:B:134:VAL:HG23	1.99	0.62
1:B:76:ILE:HG21	1:D:25:ILE:HD13	1.80	0.62
1:B:168:ILE:HD12	1:B:168:ILE:H	1.62	0.62
1:D:110:VAL:HG12	1:D:114:ILE:HD12	1.81	0.61
1:D:235:THR:HA	1:D:238:VAL:CG2	2.29	0.61
1:A:164:THR:HG23	1:A:253:TYR:OH	2.00	0.61
1:C:113:THR:O	1:C:113:THR:HG22	2.01	0.61
1:C:160:MET:CG	1:C:161:PRO:HD3	2.30	0.61
1:B:160:MET:CG	1:B:161:PRO:HD3	2.29	0.61
1:A:314:PHE:HB2	1:A:320:THR:HG23	1.82	0.60
1:B:314:PHE:HB2	1:B:320:THR:HG23	1.81	0.60
1:D:314:PHE:HB2	1:D:320:THR:HG23	1.82	0.60
1:C:314:PHE:HB2	1:C:320:THR:HG23	1.81	0.60
1:B:164:THR:HG23	1:B:253:TYR:OH	2.02	0.59
1:A:165:SER:O	1:A:165:SER:OG	2.21	0.59
1:D:113:THR:HG22	1:D:113:THR:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:110:VAL:HG12	1:C:114:ILE:HD12	1.86	0.57
1:A:162:THR:O	1:A:162:THR:OG1	2.20	0.56
1:B:113:THR:O	1:B:113:THR:HG22	2.06	0.55
1:B:101:VAL:HG21	1:B:137:ILE:HD13	1.89	0.55
1:C:327:ILE:O	1:C:331:VAL:HG23	2.07	0.55
1:D:26:ALA:HB1	1:D:47:VAL:HG21	1.89	0.55
1:A:131:PHE:CD2	1:A:168:ILE:CD1	2.89	0.55
1:A:113:THR:O	1:A:113:THR:HG22	2.08	0.54
1:A:110:VAL:HG12	1:A:114:ILE:HD12	1.89	0.54
1:B:149:THR:HB	1:B:152:GLU:H	1.72	0.54
1:B:168:ILE:H	1:B:168:ILE:CD1	2.20	0.54
1:C:26:ALA:HB1	1:C:47:VAL:HG21	1.90	0.54
1:B:327:ILE:O	1:B:331:VAL:HG23	2.08	0.53
1:A:149:THR:HB	1:A:152:GLU:H	1.72	0.53
1:B:110:VAL:HG12	1:B:114:ILE:HD12	1.90	0.53
1:D:149:THR:HB	1:D:152:GLU:H	1.72	0.53
1:C:101:VAL:HG21	1:C:137:ILE:HD13	1.90	0.53
1:C:149:THR:HB	1:C:152:GLU:H	1.72	0.53
1:D:101:VAL:HG21	1:D:137:ILE:HD13	1.89	0.53
1:D:351:ILE:HA	1:D:354:VAL:HG22	1.91	0.53
1:A:26:ALA:HB1	1:A:47:VAL:HG21	1.91	0.53
1:A:327:ILE:O	1:A:331:VAL:HG23	2.07	0.53
1:B:382:LYS:HE3	1:B:383:TRP:CZ3	2.43	0.53
1:C:351:ILE:HA	1:C:354:VAL:HG22	1.91	0.52
1:A:101:VAL:HG21	1:A:137:ILE:HD13	1.90	0.52
1:D:327:ILE:O	1:D:331:VAL:HG23	2.08	0.52
1:B:76:ILE:HG12	1:D:25:ILE:HD13	1.89	0.52
1:B:168:ILE:N	1:B:168:ILE:CD1	2.73	0.52
1:D:10:HIS:HE1	1:D:12:GLU:HG2	1.75	0.52
1:A:10:HIS:HE1	1:A:12:GLU:HG2	1.75	0.51
1:B:26:ALA:HB1	1:B:47:VAL:HG21	1.91	0.51
1:B:351:ILE:HA	1:B:354:VAL:HG22	1.91	0.51
1:C:164:THR:HG23	1:C:253:TYR:OH	2.11	0.51
1:A:351:ILE:HA	1:A:354:VAL:HG22	1.92	0.51
1:B:71:ILE:HG12	1:B:158:LEU:HD21	1.92	0.51
1:A:240:TYR:OH	1:A:394:ASN:ND2	2.44	0.50
1:B:10:HIS:HE1	1:B:12:GLU:HG2	1.76	0.50
1:A:6:LYS:HG3	1:A:61:ALA:HB3	1.93	0.50
1:C:71:ILE:HG12	1:C:158:LEU:HD21	1.94	0.50
1:C:6:LYS:HG3	1:C:61:ALA:HB3	1.93	0.50
1:B:165:SER:OG	1:B:165:SER:O	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:10:HIS:HE1	1:C:12:GLU:HG2	1.75	0.49
1:D:268:SER:OG	1:D:269:PRO:HD2	2.12	0.49
1:A:74:GLN:HG3	1:A:157:MET:HE1	1.94	0.49
1:A:75:ILE:HD11	1:A:154:LEU:HD21	1.94	0.49
1:C:240:TYR:OH	1:C:394:ASN:ND2	2.47	0.48
1:D:6:LYS:HG3	1:D:61:ALA:HB3	1.94	0.48
1:B:8:LEU:HD23	1:B:57:THR:HG21	1.95	0.48
1:C:75:ILE:HD11	1:C:154:LEU:HD21	1.96	0.48
1:A:27:LEU:HA	1:A:30:ILE:HD12	1.97	0.47
1:D:74:GLN:HG3	1:D:157:MET:HE1	1.95	0.47
1:D:27:LEU:HA	1:D:30:ILE:HD12	1.96	0.47
1:B:74:GLN:HG3	1:B:157:MET:HE1	1.95	0.47
1:B:27:LEU:HA	1:B:30:ILE:HD12	1.97	0.47
1:D:240:TYR:OH	1:D:394:ASN:ND2	2.45	0.47
1:D:326:ILE:O	1:D:330:MET:HB2	2.15	0.47
1:B:75:ILE:HD11	1:B:154:LEU:HD21	1.96	0.47
1:C:162:THR:HG22	1:C:167:PRO:HD2	1.97	0.47
1:D:162:THR:HG22	1:D:167:PRO:HD2	1.97	0.47
1:B:6:LYS:HG3	1:B:61:ALA:HB3	1.96	0.46
1:A:166:GLY:HA2	1:A:253:TYR:HE2	1.80	0.46
1:A:326:ILE:O	1:A:330:MET:HB2	2.15	0.46
1:C:27:LEU:HA	1:C:30:ILE:HD12	1.97	0.46
1:B:326:ILE:O	1:B:330:MET:HB2	2.16	0.46
1:D:235:THR:CA	1:D:238:VAL:HG22	2.39	0.46
1:D:160:MET:HG3	1:D:161:PRO:HD3	1.98	0.46
1:C:79:TYR:CZ	1:A:1:MET:HG3	2.51	0.46
1:B:163:PHE:CD1	1:B:163:PHE:C	2.90	0.46
1:C:326:ILE:O	1:C:330:MET:HB2	2.16	0.46
1:B:240:TYR:OH	1:B:394:ASN:ND2	2.46	0.45
1:A:399:SER:HA	1:A:402:ILE:HD12	1.98	0.45
1:B:162:THR:HB	1:B:166:GLY:HA3	1.99	0.45
1:B:399:SER:HA	1:B:402:ILE:HD12	1.98	0.45
1:D:8:LEU:HD23	1:D:57:THR:HG21	1.98	0.45
1:C:182:PRO:HG2	1:C:187:LEU:HD13	1.99	0.45
1:D:110:VAL:CG1	1:D:114:ILE:HD12	2.47	0.45
1:A:8:LEU:HD23	1:A:57:THR:HG21	1.99	0.44
1:C:399:SER:HA	1:C:402:ILE:HD12	1.99	0.44
1:D:399:SER:HA	1:D:402:ILE:HD12	1.99	0.44
1:C:165:SER:O	1:C:165:SER:OG	2.35	0.44
1:A:159:PHE:CD2	1:A:161:PRO:HD2	2.53	0.44
1:A:163:PHE:C	1:A:163:PHE:CD1	2.91	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:163:PHE:C	1:C:163:PHE:CD1	2.91	0.43
1:A:131:PHE:HD2	1:A:168:ILE:HD11	1.79	0.43
1:B:182:PRO:HG2	1:B:187:LEU:HD13	2.00	0.43
1:B:70:TYR:HE2	1:B:157:MET:HE2	1.84	0.43
1:C:367:ASN:ND2	1:C:378:LEU:H	2.17	0.43
1:A:367:ASN:ND2	1:A:378:LEU:H	2.17	0.42
1:B:162:THR:CB	1:B:166:GLY:HA3	2.49	0.42
1:C:8:LEU:HD23	1:C:57:THR:HG21	2.00	0.42
1:B:367:ASN:ND2	1:B:378:LEU:H	2.17	0.42
1:C:132:ARG:HG2	1:C:156:PHE:CZ	2.54	0.42
1:A:160:MET:HE3	1:A:161:PRO:N	2.33	0.42
1:A:370:ARG:HG2	1:A:375:LEU:HD12	2.01	0.42
1:B:91:LYS:HG3	1:B:92:TRP:CD1	2.55	0.42
1:A:239:MET:HG3	1:A:401:LEU:HB2	2.02	0.42
1:D:160:MET:HG3	1:D:161:PRO:CD	2.50	0.42
1:D:110:VAL:HG12	1:D:114:ILE:CD1	2.48	0.42
1:D:132:ARG:HG2	1:D:156:PHE:CZ	2.55	0.42
1:C:19:TYR:HE2	1:C:23:LEU:HD22	1.85	0.41
1:A:159:PHE:CE2	1:A:161:PRO:HG2	2.55	0.41
1:A:132:ARG:HG2	1:A:156:PHE:CZ	2.54	0.41
1:B:370:ARG:HG2	1:B:375:LEU:HD12	2.03	0.41
1:A:70:TYR:HE2	1:A:157:MET:HE2	1.86	0.41
1:B:11:LEU:HD12	1:B:54:LEU:HD13	2.02	0.41
1:D:19:TYR:HE2	1:D:23:LEU:HD22	1.86	0.41
1:B:31:PHE:HA	1:B:34:LEU:HD12	2.02	0.41
1:C:110:VAL:CG1	1:C:114:ILE:HD12	2.50	0.41
1:D:370:ARG:HG2	1:D:375:LEU:HD12	2.03	0.41
1:B:19:TYR:HE1	1:B:23:LEU:HD22	1.85	0.41
1:C:370:ARG:HG2	1:C:375:LEU:HD12	2.02	0.41
1:C:11:LEU:HD12	1:C:54:LEU:HD13	2.02	0.41
1:C:270:ILE:HG23	1:C:290:MET:HE3	2.03	0.41
1:D:31:PHE:HA	1:D:34:LEU:HD12	2.02	0.41
1:A:14:TYR:HE1	1:A:260:VAL:HG21	1.86	0.41
1:C:31:PHE:HA	1:C:34:LEU:HD12	2.02	0.41
1:D:220:LEU:HB3	1:D:238:VAL:HG13	2.03	0.41
1:D:304:LEU:HD23	1:D:324:ALA:HA	2.03	0.41
1:B:132:ARG:HG2	1:B:156:PHE:CZ	2.55	0.40
1:D:11:LEU:HD12	1:D:54:LEU:HD13	2.02	0.40
1:B:239:MET:HG3	1:B:401:LEU:HB2	2.03	0.40
1:A:19:TYR:HE1	1:A:23:LEU:HD22	1.87	0.40
1:C:166:GLY:HA2	1:C:253:TYR:HE2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:250:PHE:HD2	1:B:272:PHE:CZ	2.40	0.40

There are no symmetry-related clashes.

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	412/425 (97%)	391 (95%)	21 (5%)	0	100	100
1	B	412/425 (97%)	392 (95%)	20 (5%)	0	100	100
1	C	412/425 (97%)	392 (95%)	20 (5%)	0	100	100
1	D	412/425 (97%)	391 (95%)	21 (5%)	0	100	100
All	All	1648/1700 (97%)	1566 (95%)	82 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	370/381 (97%)	350 (95%)	20 (5%)	22	53
1	B	370/381 (97%)	353 (95%)	17 (5%)	27	58
1	C	370/381 (97%)	352 (95%)	18 (5%)	25	56
1	D	370/381 (97%)	354 (96%)	16 (4%)	29	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1480/1524 (97%)	1409 (95%)	71 (5%)	25 56

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1	MET
1	C	68	LEU
1	C	86	SER
1	C	117	THR
1	C	127	SER
1	C	147	GLU
1	C	155	ARG
1	C	158	LEU
1	C	160	MET
1	C	164	THR
1	C	165	SER
1	C	168	ILE
1	C	173	ARG
1	C	185	ASP
1	C	274	LYS
1	C	279	ARG
1	C	322	ASN
1	C	378	LEU
1	A	37	LYS
1	A	68	LEU
1	A	86	SER
1	A	117	THR
1	A	127	SER
1	A	147	GLU
1	A	155	ARG
1	A	158	LEU
1	A	160	MET
1	A	164	THR
1	A	165	SER
1	A	173	ARG
1	A	185	ASP
1	A	188	LEU
1	A	196	LYS
1	A	268	SER
1	A	274	LYS
1	A	279	ARG
1	A	338	ILE

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Mol	Chain	Res	Type
1	A	378	LEU
1	B	1	MET
1	B	68	LEU
1	B	86	SER
1	B	117	THR
1	B	127	SER
1	B	147	GLU
1	B	155	ARG
1	B	158	LEU
1	B	160	MET
1	B	164	THR
1	B	173	ARG
1	B	185	ASP
1	B	188	LEU
1	B	195	VAL
1	B	268	SER
1	B	274	LYS
1	B	279	ARG
1	D	1	MET
1	D	68	LEU
1	D	86	SER
1	D	117	THR
1	D	127	SER
1	D	147	GLU
1	D	155	ARG
1	D	158	LEU
1	D	164	THR
1	D	173	ARG
1	D	185	ASP
1	D	188	LEU
1	D	238	VAL
1	D	274	LYS
1	D	279	ARG
1	D	371	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	10	HIS
1	C	63	GLN
1	C	90	ASN
1	C	183	ASN

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Mol	Chain	Res	Type
1	C	193	GLN
1	C	318	ASN
1	C	349	HIS
1	C	356	ASN
1	C	367	ASN
1	C	394	ASN
1	A	10	HIS
1	A	63	GLN
1	A	90	ASN
1	A	183	ASN
1	A	193	GLN
1	A	318	ASN
1	A	349	HIS
1	A	356	ASN
1	A	367	ASN
1	A	394	ASN
1	B	10	HIS
1	B	90	ASN
1	B	183	ASN
1	B	193	GLN
1	B	318	ASN
1	B	349	HIS
1	B	356	ASN
1	B	367	ASN
1	B	394	ASN
1	D	10	HIS
1	D	63	GLN
1	D	90	ASN
1	D	183	ASN
1	D	193	GLN
1	D	318	ASN
1	D	349	HIS
1	D	356	ASN
1	D	367	ASN
1	D	394	ASN

5.3.3 RNA ⓘ

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	414/425 (97%)	0.15	18 (4%) 35 33	86, 114, 163, 306	0
1	B	414/425 (97%)	0.22	27 (6%) 18 19	103, 138, 187, 236	0
1	C	414/425 (97%)	0.20	19 (4%) 32 30	86, 115, 171, 259	0
1	D	414/425 (97%)	0.74	67 (16%) 1 2	158, 217, 271, 289	0
All	All	1656/1700 (97%)	0.32	131 (7%) 12 12	86, 135, 249, 306	0

All (131) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	39	ARG	9.5
1	C	2	ILE	8.5
1	D	40	PHE	8.1
1	D	3	ASP	8.0
1	D	1	MET	7.9
1	A	2	ILE	7.7
1	A	1	MET	7.6
1	D	379	PRO	6.6
1	D	156	PHE	6.5
1	A	414	LYS	6.1
1	D	265	GLY	5.8
1	D	184	ARG	5.7
1	D	229	GLY	5.6
1	D	235	THR	5.5
1	C	6	LYS	5.5
1	D	2	ILE	5.3
1	C	5	LEU	5.2
1	B	414	LYS	5.1
1	B	114	ILE	5.0
1	D	115	ASN	5.0
1	C	414	LYS	5.0

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Mol	Chain	Res	Type	RSRZ
1	D	225	LEU	4.9
1	C	60	HIS	4.7
1	B	9	PRO	4.6
1	D	14	TYR	4.4
1	C	3	ASP	4.4
1	A	315	LYS	4.4
1	D	42	ILE	4.4
1	D	4	PHE	4.3
1	D	36	PHE	4.3
1	A	314	PHE	4.2
1	A	375	LEU	4.0
1	D	238	VAL	4.0
1	B	184	ARG	4.0
1	A	278	SER	4.0
1	D	9	PRO	3.9
1	D	406	PHE	3.9
1	A	146	LYS	3.9
1	D	224	ALA	3.8
1	D	136	MET	3.7
1	C	7	GLN	3.7
1	D	155	ARG	3.6
1	D	38	LYS	3.6
1	B	229	GLY	3.6
1	A	279	ARG	3.6
1	D	146	LYS	3.5
1	D	83	ARG	3.5
1	B	369	ASP	3.5
1	B	8	LEU	3.4
1	D	413	THR	3.4
1	B	36	PHE	3.4
1	D	145	LEU	3.3
1	C	59	THR	3.3
1	C	61	ALA	3.2
1	A	277	ILE	3.2
1	D	234	PRO	3.2
1	D	349	HIS	3.1
1	D	181	ILE	3.1
1	D	378	LEU	3.1
1	D	114	ILE	3.0
1	D	363	LYS	3.0
1	B	115	ASN	3.0
1	A	313	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	37	LYS	3.0
1	B	87	GLN	3.0
1	D	41	ALA	3.0
1	D	37	LYS	3.0
1	D	147	GLU	2.9
1	D	306	ILE	2.9
1	C	376	LYS	2.9
1	B	181	ILE	2.8
1	C	1	MET	2.8
1	B	230	ILE	2.8
1	C	92	TRP	2.8
1	D	356	ASN	2.7
1	B	220	LEU	2.7
1	D	314	PHE	2.7
1	D	167	PRO	2.7
1	A	3	ASP	2.7
1	C	406	PHE	2.7
1	D	178	TYR	2.7
1	B	217	LEU	2.7
1	A	320	THR	2.6
1	D	185	ASP	2.6
1	D	148	PHE	2.6
1	D	226	SER	2.6
1	C	273	ASP	2.6
1	D	59	THR	2.6
1	B	148	PHE	2.5
1	D	310	ARG	2.5
1	D	65	LEU	2.5
1	A	45	CYS	2.5
1	B	182	PRO	2.5
1	D	228	GLY	2.5
1	C	113	THR	2.5
1	D	367	ASN	2.5
1	B	216	LEU	2.4
1	D	6	LYS	2.4
1	C	375	LEU	2.4
1	A	59	THR	2.4
1	A	114	ILE	2.4
1	D	408	ASN	2.3
1	D	253	TYR	2.3
1	B	1	MET	2.3
1	D	183	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	8	LEU	2.2
1	B	314	PHE	2.2
1	D	165	SER	2.2
1	D	5	LEU	2.2
1	D	345	TYR	2.2
1	A	5	LEU	2.2
1	D	414	LYS	2.2
1	B	228	GLY	2.2
1	C	412	PHE	2.2
1	D	303	ARG	2.2
1	B	412	PHE	2.1
1	D	87	GLN	2.1
1	D	230	ILE	2.1
1	D	315	LYS	2.1
1	D	61	ALA	2.1
1	B	241	VAL	2.1
1	D	64	ILE	2.1
1	C	182	PRO	2.1
1	D	150	LEU	2.1
1	A	87	GLN	2.1
1	B	145	LEU	2.0
1	D	68	LEU	2.0
1	B	136	MET	2.0
1	B	140	MET	2.0
1	B	117	THR	2.0
1	D	171	PHE	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 [i](#)

There are no such residues in this entry.