



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 01:13 AM UTC

PDB ID : 5DH1 / pdb_00005dh1
Title : Structure of the siderophore periplasmic binding protein from the fuscachelin gene cluster of *Thermobifida fusca* in P21
Authors : Li, K.; Bruner, S.D.
Deposited on : 2015-08-29
Resolution : 2.84 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

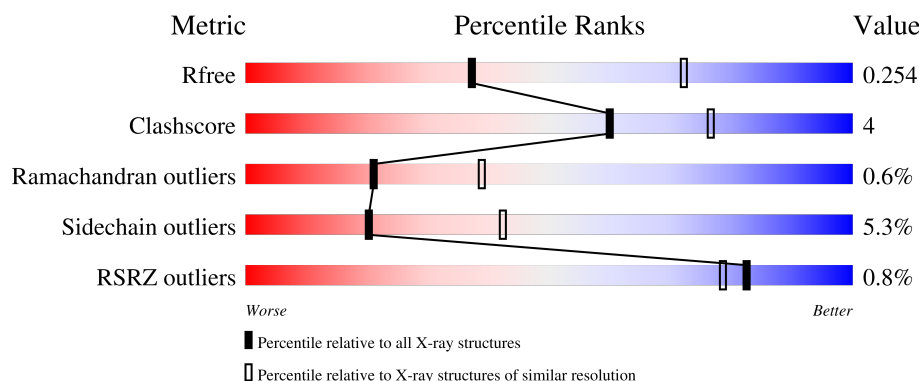
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.84 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	1520 (2.86-2.82)
Clashscore	190562	1559 (2.86-2.82)
Ramachandran outliers	187476	1517 (2.86-2.82)
Sidechain outliers	187428	1518 (2.86-2.82)
RSRZ outliers	180081	1521 (2.86-2.82)

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	309	
1	B	309	
1	C	309	
1	D	309	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8547 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 siderophore periplasmic binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	277	Total	C	N	O	S	0	0	0
			2141	1353	350	436	2			
1	B	276	Total	C	N	O	S	0	0	0
			2134	1349	350	433	2			
1	C	274	Total	C	N	O	S	0	0	0
			2121	1340	344	435	2			
1	D	276	Total	C	N	O	S	0	0	0
			2128	1347	347	432	2			

There are 136 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	53	MET	-	initiating methionine	UNP Q47NS2
A	54	GLY	-	expression tag	UNP Q47NS2
A	55	SER	-	expression tag	UNP Q47NS2
A	56	SER	-	expression tag	UNP Q47NS2
A	57	HIS	-	expression tag	UNP Q47NS2
A	58	HIS	-	expression tag	UNP Q47NS2
A	59	HIS	-	expression tag	UNP Q47NS2
A	60	HIS	-	expression tag	UNP Q47NS2
A	61	HIS	-	expression tag	UNP Q47NS2
A	62	HIS	-	expression tag	UNP Q47NS2
A	63	SER	-	expression tag	UNP Q47NS2
A	64	SER	-	expression tag	UNP Q47NS2
A	65	GLY	-	expression tag	UNP Q47NS2
A	66	LEU	-	expression tag	UNP Q47NS2
A	67	VAL	-	expression tag	UNP Q47NS2
A	68	PRO	-	expression tag	UNP Q47NS2
A	69	ARG	-	expression tag	UNP Q47NS2
A	70	GLY	-	expression tag	UNP Q47NS2
A	71	SER	-	expression tag	UNP Q47NS2
A	72	HIS	-	expression tag	UNP Q47NS2
A	73	MET	-	expression tag	UNP Q47NS2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	74	ALA	-	expression tag	UNP Q47NS2
A	75	SER	-	expression tag	UNP Q47NS2
A	76	MET	-	expression tag	UNP Q47NS2
A	77	THR	-	expression tag	UNP Q47NS2
A	78	GLY	-	expression tag	UNP Q47NS2
A	79	GLY	-	expression tag	UNP Q47NS2
A	80	GLN	-	expression tag	UNP Q47NS2
A	81	GLN	-	expression tag	UNP Q47NS2
A	82	MET	-	expression tag	UNP Q47NS2
A	83	GLY	-	expression tag	UNP Q47NS2
A	84	ARG	-	expression tag	UNP Q47NS2
A	85	GLY	-	expression tag	UNP Q47NS2
A	86	SER	-	expression tag	UNP Q47NS2
B	53	MET	-	initiating methionine	UNP Q47NS2
B	54	GLY	-	expression tag	UNP Q47NS2
B	55	SER	-	expression tag	UNP Q47NS2
B	56	SER	-	expression tag	UNP Q47NS2
B	57	HIS	-	expression tag	UNP Q47NS2
B	58	HIS	-	expression tag	UNP Q47NS2
B	59	HIS	-	expression tag	UNP Q47NS2
B	60	HIS	-	expression tag	UNP Q47NS2
B	61	HIS	-	expression tag	UNP Q47NS2
B	62	HIS	-	expression tag	UNP Q47NS2
B	63	SER	-	expression tag	UNP Q47NS2
B	64	SER	-	expression tag	UNP Q47NS2
B	65	GLY	-	expression tag	UNP Q47NS2
B	66	LEU	-	expression tag	UNP Q47NS2
B	67	VAL	-	expression tag	UNP Q47NS2
B	68	PRO	-	expression tag	UNP Q47NS2
B	69	ARG	-	expression tag	UNP Q47NS2
B	70	GLY	-	expression tag	UNP Q47NS2
B	71	SER	-	expression tag	UNP Q47NS2
B	72	HIS	-	expression tag	UNP Q47NS2
B	73	MET	-	expression tag	UNP Q47NS2
B	74	ALA	-	expression tag	UNP Q47NS2
B	75	SER	-	expression tag	UNP Q47NS2
B	76	MET	-	expression tag	UNP Q47NS2
B	77	THR	-	expression tag	UNP Q47NS2
B	78	GLY	-	expression tag	UNP Q47NS2
B	79	GLY	-	expression tag	UNP Q47NS2
B	80	GLN	-	expression tag	UNP Q47NS2
B	81	GLN	-	expression tag	UNP Q47NS2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	82	MET	-	expression tag	UNP Q47NS2
B	83	GLY	-	expression tag	UNP Q47NS2
B	84	ARG	-	expression tag	UNP Q47NS2
B	85	GLY	-	expression tag	UNP Q47NS2
B	86	SER	-	expression tag	UNP Q47NS2
C	53	MET	-	initiating methionine	UNP Q47NS2
C	54	GLY	-	expression tag	UNP Q47NS2
C	55	SER	-	expression tag	UNP Q47NS2
C	56	SER	-	expression tag	UNP Q47NS2
C	57	HIS	-	expression tag	UNP Q47NS2
C	58	HIS	-	expression tag	UNP Q47NS2
C	59	HIS	-	expression tag	UNP Q47NS2
C	60	HIS	-	expression tag	UNP Q47NS2
C	61	HIS	-	expression tag	UNP Q47NS2
C	62	HIS	-	expression tag	UNP Q47NS2
C	63	SER	-	expression tag	UNP Q47NS2
C	64	SER	-	expression tag	UNP Q47NS2
C	65	GLY	-	expression tag	UNP Q47NS2
C	66	LEU	-	expression tag	UNP Q47NS2
C	67	VAL	-	expression tag	UNP Q47NS2
C	68	PRO	-	expression tag	UNP Q47NS2
C	69	ARG	-	expression tag	UNP Q47NS2
C	70	GLY	-	expression tag	UNP Q47NS2
C	71	SER	-	expression tag	UNP Q47NS2
C	72	HIS	-	expression tag	UNP Q47NS2
C	73	MET	-	expression tag	UNP Q47NS2
C	74	ALA	-	expression tag	UNP Q47NS2
C	75	SER	-	expression tag	UNP Q47NS2
C	76	MET	-	expression tag	UNP Q47NS2
C	77	THR	-	expression tag	UNP Q47NS2
C	78	GLY	-	expression tag	UNP Q47NS2
C	79	GLY	-	expression tag	UNP Q47NS2
C	80	GLN	-	expression tag	UNP Q47NS2
C	81	GLN	-	expression tag	UNP Q47NS2
C	82	MET	-	expression tag	UNP Q47NS2
C	83	GLY	-	expression tag	UNP Q47NS2
C	84	ARG	-	expression tag	UNP Q47NS2
C	85	GLY	-	expression tag	UNP Q47NS2
C	86	SER	-	expression tag	UNP Q47NS2
D	53	MET	-	initiating methionine	UNP Q47NS2
D	54	GLY	-	expression tag	UNP Q47NS2
D	55	SER	-	expression tag	UNP Q47NS2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	56	SER	-	expression tag	UNP Q47NS2
D	57	HIS	-	expression tag	UNP Q47NS2
D	58	HIS	-	expression tag	UNP Q47NS2
D	59	HIS	-	expression tag	UNP Q47NS2
D	60	HIS	-	expression tag	UNP Q47NS2
D	61	HIS	-	expression tag	UNP Q47NS2
D	62	HIS	-	expression tag	UNP Q47NS2
D	63	SER	-	expression tag	UNP Q47NS2
D	64	SER	-	expression tag	UNP Q47NS2
D	65	GLY	-	expression tag	UNP Q47NS2
D	66	LEU	-	expression tag	UNP Q47NS2
D	67	VAL	-	expression tag	UNP Q47NS2
D	68	PRO	-	expression tag	UNP Q47NS2
D	69	ARG	-	expression tag	UNP Q47NS2
D	70	GLY	-	expression tag	UNP Q47NS2
D	71	SER	-	expression tag	UNP Q47NS2
D	72	HIS	-	expression tag	UNP Q47NS2
D	73	MET	-	expression tag	UNP Q47NS2
D	74	ALA	-	expression tag	UNP Q47NS2
D	75	SER	-	expression tag	UNP Q47NS2
D	76	MET	-	expression tag	UNP Q47NS2
D	77	THR	-	expression tag	UNP Q47NS2
D	78	GLY	-	expression tag	UNP Q47NS2
D	79	GLY	-	expression tag	UNP Q47NS2
D	80	GLN	-	expression tag	UNP Q47NS2
D	81	GLN	-	expression tag	UNP Q47NS2
D	82	MET	-	expression tag	UNP Q47NS2
D	83	GLY	-	expression tag	UNP Q47NS2
D	84	ARG	-	expression tag	UNP Q47NS2
D	85	GLY	-	expression tag	UNP Q47NS2
D	86	SER	-	expression tag	UNP Q47NS2

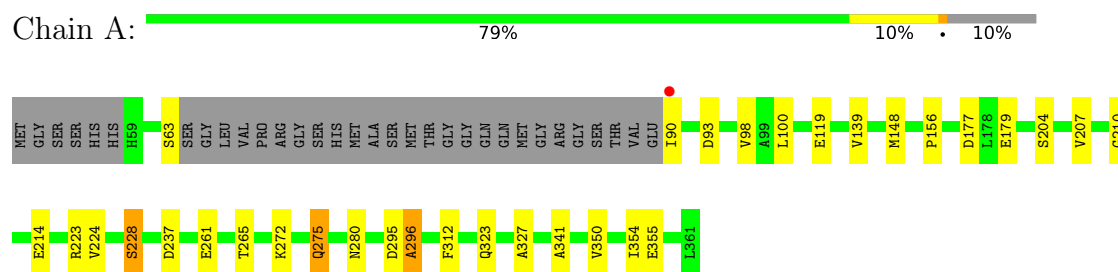
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	5	Total O 5 5	0	0
2	B	5	Total O 5 5	0	0
2	C	4	Total O 4 4	0	0
2	D	9	Total O 9 9	0	0

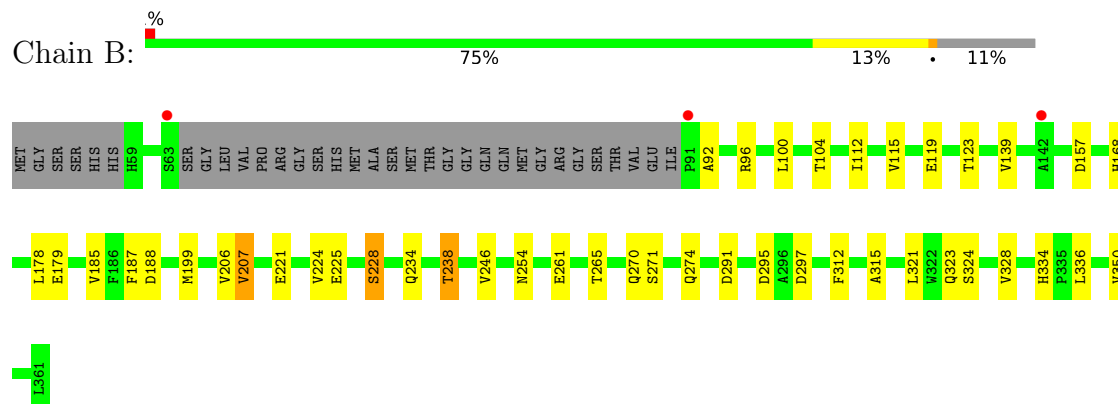
3 Residue-property plots [i](#)

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.

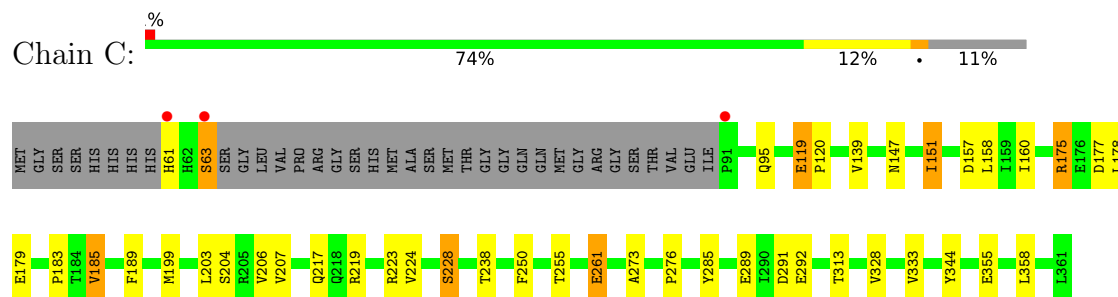
- Molecule 1: siderophore periplasmic binding protein



- Molecule 1: siderophore periplasmic binding protein

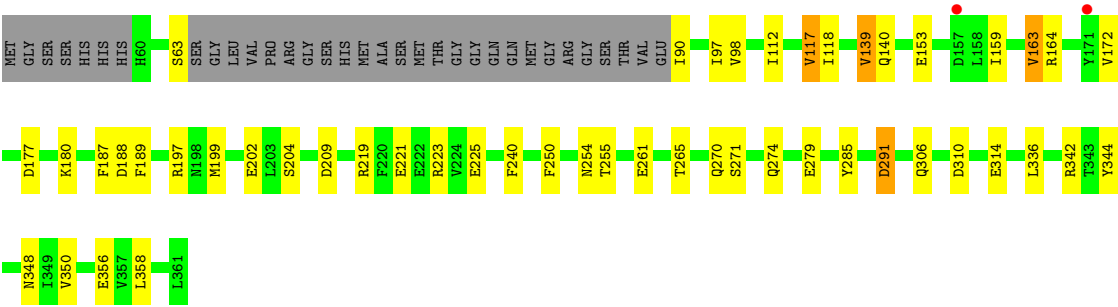


- Molecule 1: siderophore periplasmic binding protein



- Molecule 1: siderophore periplasmic binding protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.41Å 135.56Å 80.94Å 90.00° 91.98° 90.00°	Depositor
Resolution (Å)	46.53 – 2.84 46.53 – 2.84	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.53-2.84) 99.7 (46.53-2.84)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.183 , 0.247 0.193 , 0.254	Depositor DCC
R_{free} test set	1624 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	45.9	Xtriage
Anisotropy	0.621	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.035 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8547	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.32% 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	0.77	1/2184 (0.0%)	1.03	10/2976 (0.3%)
1	B	0.72	0/2177	0.98	4/2964 (0.1%)
1	C	0.73	0/2162	0.96	2/2943 (0.1%)
1	D	0.75	0/2170	1.00	2/2956 (0.1%)
All	All	0.74	1/8693 (0.0%)	0.99	18/11839 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	93	ASP	N-CA	5.15	1.50	1.46

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	313	THR	N-CA-C	-6.35	103.66	111.40
1	B	238	THR	N-CA-C	6.18	119.58	109.76
1	A	119	GLU	CA-C-N	6.08	126.43	119.93
1	A	119	GLU	C-N-CA	6.08	126.43	119.93
1	A	93	ASP	CB-CA-C	-6.04	106.91	111.20
1	A	275	GLN	CA-C-N	-6.03	113.53	120.04
1	A	275	GLN	C-N-CA	-6.03	113.53	120.04
1	D	209	ASP	N-CA-C	-5.71	105.62	112.59
1	B	92	ALA	N-CA-C	5.58	117.82	111.02
1	C	185	VAL	N-CA-C	5.34	114.44	106.85
1	A	296	ALA	N-CA-C	5.30	118.25	109.46
1	D	139	VAL	N-CA-C	-5.23	108.74	113.71
1	B	334	HIS	CA-C-N	-5.16	115.25	120.31
1	B	334	HIS	C-N-CA	-5.16	115.25	120.31
1	A	90	ILE	CA-C-N	-5.14	114.51	119.90
1	A	90	ILE	C-N-CA	-5.14	114.51	119.90
1	A	93	ASP	CA-C-N	5.01	125.24	119.83
1	A	93	ASP	C-N-CA	5.01	125.24	119.83

There are no chirality outliers.

There are no planarity outliers.

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	2141	0	2023	13	0
1	B	2134	0	2022	19	0
1	C	2121	0	2014	22	0
1	D	2128	0	2019	20	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	4	0	0	0	0
2	D	9	0	0	0	0
All	All	8547	0	8078	71	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 4.

All (71) 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:D:189:PHE:CD1	1:D:199:MET:HE2	2.35	0.62
1:A:223:ARG:NH2	1:A:355:GLU:OE1	2.31	0.62
1:A:280:ASN:HB3	1:C:63:SER:HB3	1.83	0.61
1:B:185:VAL:HG11	1:B:206:VAL:HG21	1.83	0.61
1:B:323:GLN:HA	1:B:328:VAL:HG11	1.85	0.58
1:B:224:VAL:O	1:B:228:SER:HB3	2.04	0.58
1:D:97:ILE:HD12	1:D:112:ILE:HG21	1.85	0.58
1:A:350:VAL:O	1:A:354:ILE:HG13	2.06	0.56
1:C:189:PHE:CD2	1:C:199:MET:HE2	2.40	0.56
1:D:291:ASP:N	1:D:291:ASP:OD1	2.38	0.55
1:D:164:ARG:HH11	1:D:164:ARG:HG3	1.70	0.55
1:D:117:VAL:HG13	1:D:118:ILE:O	2.06	0.55
1:C:223:ARG:NH2	1:C:355:GLU:OE2	2.36	0.54
1:D:98:VAL:HG23	1:D:159:ILE:HG23	1.89	0.53
1:D:219:ARG:O	1:D:223:ARG:HG3	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:147:ASN:O	1:C:151:ILE:HG13	2.10	0.52
1:C:224:VAL:O	1:C:228:SER:HB3	2.10	0.51
1:B:321:LEU:HD12	1:B:321:LEU:H	1.75	0.50
1:C:217:GLN:HA	1:C:344:TYR:CD1	2.47	0.50
1:C:95:GLN:N	1:C:157:ASP:OD2	2.34	0.49
1:B:246:VAL:HB	1:D:221:GLU:OE2	2.13	0.49
1:B:221:GLU:O	1:B:225:GLU:HG3	2.12	0.49
1:B:187:PHE:HB3	1:B:199:MET:HG2	1.94	0.49
1:D:255:THR:O	1:D:261:GLU:HA	2.12	0.49
1:C:158:LEU:HD12	1:C:183:PRO:O	2.15	0.47
1:C:160:ILE:HB	1:C:203:LEU:HD22	1.97	0.47
1:D:358:LEU:HD23	1:D:358:LEU:HA	1.81	0.47
1:D:197:ARG:HD2	1:D:344:TYR:CE1	2.50	0.47
1:A:312:PHE:CZ	1:C:224:VAL:HG21	2.50	0.46
1:B:254:ASN:HA	1:B:274:GLN:HE21	1.80	0.46
1:A:98:VAL:HG23	1:A:156:PRO:HB3	1.97	0.46
1:B:96:ARG:HB3	1:B:115:VAL:HG11	1.99	0.45
1:D:187:PHE:CE1	1:D:202:GLU:HG3	2.51	0.45
1:D:310:ASP:OD1	1:D:310:ASP:C	2.60	0.45
1:A:148:MET:SD	1:A:177:ASP:OD2	2.75	0.45
1:A:272:LYS:HG2	1:A:295:ASP:OD2	2.18	0.44
1:C:204:SER:HA	1:C:207:VAL:HG22	1.99	0.44
1:C:328:VAL:HG22	1:C:333:VAL:HG21	1.98	0.44
1:A:224:VAL:O	1:A:228:SER:HB3	2.18	0.44
1:B:157:ASP:OD1	1:B:157:ASP:N	2.51	0.44
1:C:250:PHE:CE1	1:C:285:TYR:HB2	2.53	0.44
1:C:273:ALA:O	1:C:276:PRO:HD2	2.18	0.43
1:C:157:ASP:O	1:C:183:PRO:HD2	2.19	0.43
1:A:296:ALA:O	1:A:327:ALA:HB2	2.18	0.43
1:C:289:GLU:O	1:C:292:GLU:HB2	2.19	0.43
1:D:240:PHE:O	1:D:270:GLN:HA	2.18	0.43
1:B:168:HIS:ND1	1:B:188:ASP:OD2	2.52	0.43
1:B:238:THR:HG23	1:B:297:ASP:HB2	2.00	0.42
1:A:210:GLY:O	1:A:214:GLU:HG3	2.19	0.42
1:A:261:GLU:OE2	1:A:265:THR:OG1	2.36	0.42
1:B:336:LEU:HD11	1:B:350:VAL:HG13	2.00	0.42
1:C:175:ARG:O	1:C:179:GLU:HB2	2.19	0.42
1:D:118:ILE:HG13	1:D:140:GLN:HB3	2.02	0.42
1:D:336:LEU:HD11	1:D:350:VAL:HG13	2.00	0.42
1:B:291:ASP:OD1	1:B:291:ASP:N	2.50	0.42
1:D:163:VAL:O	1:D:188:ASP:HA	2.18	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:250:PHE:CE1	1:D:285:TYR:HB2	2.55	0.42
1:B:234:GLN:OE1	1:B:234:GLN:N	2.43	0.41
1:C:255:THR:O	1:C:261:GLU:HA	2.20	0.41
1:D:164:ARG:HG3	1:D:164:ARG:NH1	2.35	0.41
1:B:312:PHE:O	1:B:315:ALA:HB3	2.20	0.41
1:A:323:GLN:H	1:A:323:GLN:HG2	1.73	0.41
1:C:119:GLU:HA	1:C:120:PRO:HD3	1.95	0.41
1:B:261:GLU:OE2	1:B:265:THR:OG1	2.32	0.41
1:B:270:GLN:HB2	1:B:274:GLN:OE1	2.20	0.41
1:C:185:VAL:HG11	1:C:206:VAL:HG21	2.02	0.41
1:A:223:ARG:HH11	1:A:223:ARG:HD3	1.71	0.40
1:C:219:ARG:O	1:C:223:ARG:HG3	2.21	0.40
1:D:254:ASN:HA	1:D:274:GLN:HG2	2.02	0.40
1:B:112:ILE:HD12	1:B:207:VAL:HG13	2.03	0.40
1:C:358:LEU:HD23	1:C:358:LEU:HA	1.97	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	273/309 (88%)	259 (95%)	12 (4%)	2 (1%)	18	35
1	B	272/309 (88%)	255 (94%)	14 (5%)	3 (1%)	11	23
1	C	270/309 (87%)	255 (94%)	15 (6%)	0	100	100
1	D	272/309 (88%)	246 (90%)	24 (9%)	2 (1%)	18	35
All	All	1087/1236 (88%)	1015 (93%)	65 (6%)	7 (1%)	21	39

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	265	THR
1	B	271	SER
1	B	295	ASP
1	D	271	SER
1	B	100	LEU
1	A	100	LEU
1	A	341	ALA

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	222/249 (89%)	214 (96%)	8 (4%)	31	56
1	B	221/249 (89%)	212 (96%)	9 (4%)	27	52
1	C	221/249 (89%)	209 (95%)	12 (5%)	20	42
1	D	220/249 (88%)	202 (92%)	18 (8%)	10	23
All	All	884/996 (89%)	837 (95%)	47 (5%)	20	42

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	SER
1	A	139	VAL
1	A	179	GLU
1	A	204	SER
1	A	207	VAL
1	A	228	SER
1	A	237	ASP
1	A	275	GLN
1	B	104	THR
1	B	119	GLU
1	B	123	THR
1	B	139	VAL
1	B	178	LEU
1	B	179	GLU
1	B	207	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	228	SER
1	B	324	SER
1	C	61	HIS
1	C	63	SER
1	C	119	GLU
1	C	139	VAL
1	C	151	ILE
1	C	175	ARG
1	C	177	ASP
1	C	178	LEU
1	C	228	SER
1	C	238	THR
1	C	261	GLU
1	C	291	ASP
1	D	63	SER
1	D	90	ILE
1	D	117	VAL
1	D	139	VAL
1	D	153	GLU
1	D	163	VAL
1	D	172	VAL
1	D	177	ASP
1	D	180	LYS
1	D	204	SER
1	D	225	GLU
1	D	279	GLU
1	D	291	ASP
1	D	306	GLN
1	D	314	GLU
1	D	342	ARG
1	D	348	ASN
1	D	356	GLU

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

Mol	Chain	Res	Type
1	A	95	GLN
1	A	217	GLN
1	B	132	GLN
1	B	198	ASN
1	B	217	GLN
1	B	270	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	61	HIS
1	C	62	HIS
1	D	264	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	277/309 (89%)	-0.44	1 (0%) 88 87	21, 35, 55, 68	0
1	B	276/309 (89%)	-0.27	3 (1%) 78 73	23, 42, 69, 79	0
1	C	274/309 (88%)	-0.28	3 (1%) 78 73	20, 38, 67, 77	0
1	D	276/309 (89%)	-0.32	2 (0%) 84 80	19, 35, 67, 92	0
All	All	1103/1236 (89%)	-0.33	9 (0%) 82 78	19, 37, 66, 92	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	171	TYR	3.3
1	B	91	PRO	3.0
1	A	90	ILE	2.6
1	C	63	SER	2.6
1	C	61	HIS	2.5
1	C	91	PRO	2.4
1	D	157	ASP	2.1
1	B	63	SER	2.0
1	B	142	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 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.