



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:29 AM UTC

PDB ID : 3B77 / pdb_00003b77
Title : Crystal structure of a ph domain containing bacterial protein (exig_2160) from
exiguobacterium sibiricum 255-15 at 2.42 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2007-10-30
Resolution : 2.42 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:

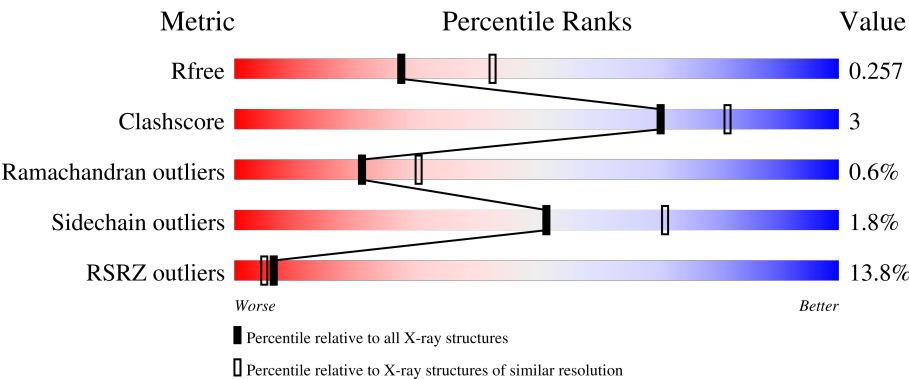
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.42 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	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	193	
1	B	193	
1	C	193	
1	D	193	
1	E	193	

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Mol	Chain	Length	Quality of chain
1	F	193	15% 84% 10% 5%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 9166 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	Se	0	0	0
			1525	983	247	291	1	3			
1	B	184	Total	C	N	O	S	Se	0	1	0
			1507	975	244	284	1	3			
1	C	184	Total	C	N	O	S	Se	0	0	0
			1490	965	239	282	1	3			
1	D	184	Total	C	N	O	S	Se	0	0	0
			1494	963	242	285	1	3			
1	E	183	Total	C	N	O	S	Se	0	0	1
			1468	953	234	277	1	3			
1	F	183	Total	C	N	O	S	Se	0	2	0
			1509	976	245	284	1	3			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	GLY	-	expression tag	UNP Q41E03
B	12	GLY	-	expression tag	UNP Q41E03
C	12	GLY	-	expression tag	UNP Q41E03
D	12	GLY	-	expression tag	UNP Q41E03
E	12	GLY	-	expression tag	UNP Q41E03
F	12	GLY	-	expression tag	UNP Q41E03

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	34	Total	O	0	0
			34	34		
2	B	43	Total	O	0	0
			43	43		
2	C	37	Total	O	0	0
			37	37		

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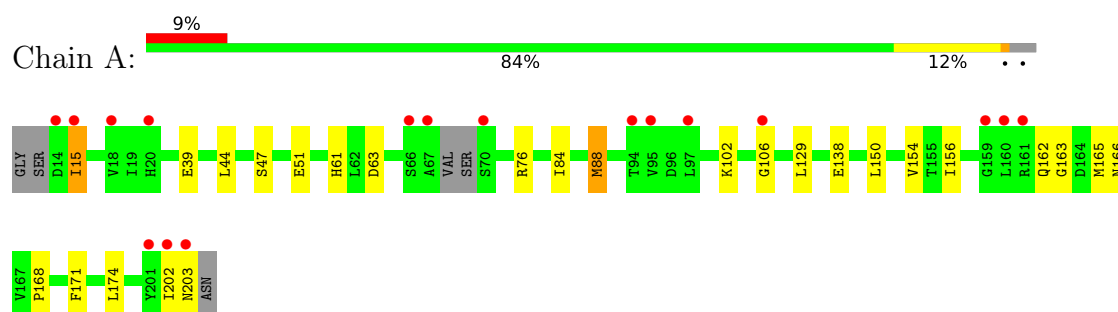
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	20	Total 20	O 20	0	0
2	E	17	Total 17	O 17	0	0
2	F	22	Total 22	O 22	0	0

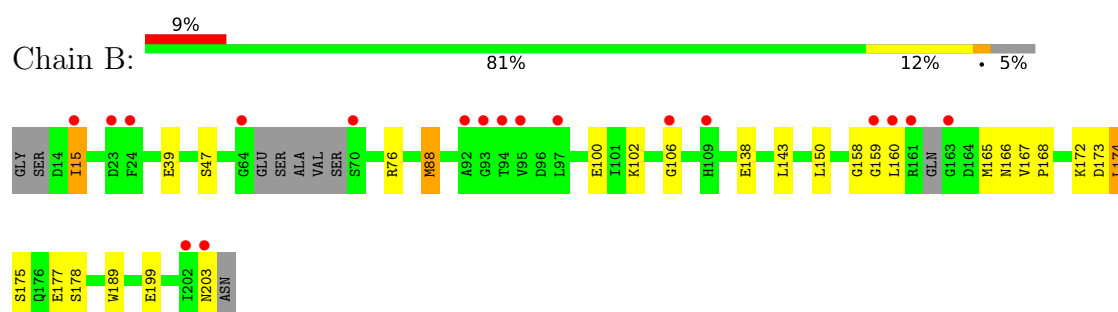
3 Residue-property plots [i](#)

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.

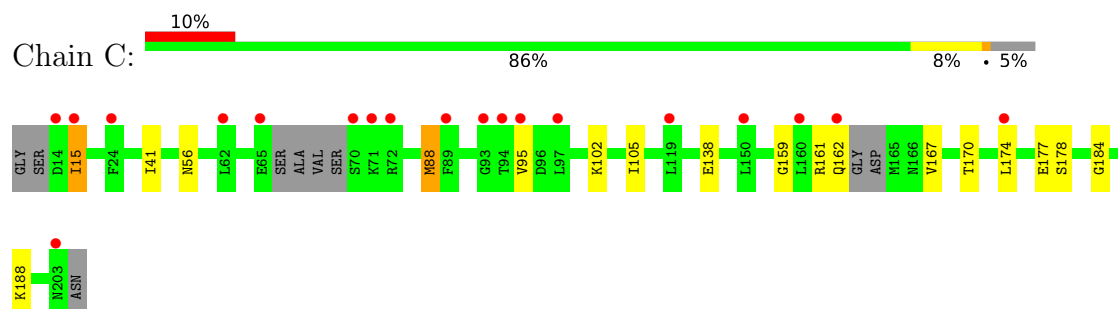
- Molecule 1: Uncharacterized protein



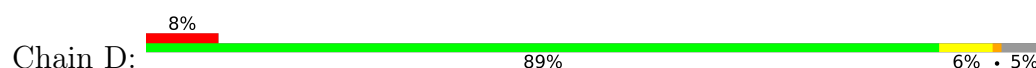
- Molecule 1: Uncharacterized protein



- Molecule 1: Uncharacterized protein

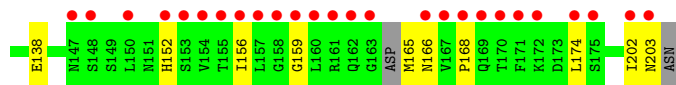
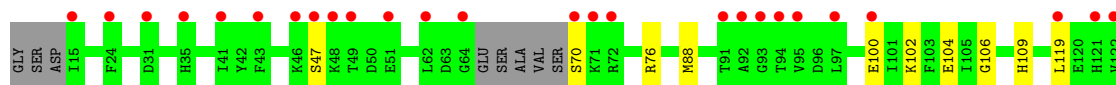
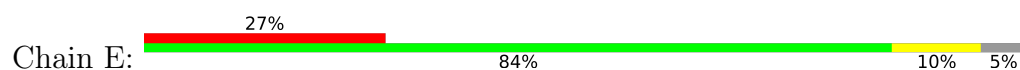


- Molecule 1: Uncharacterized protein

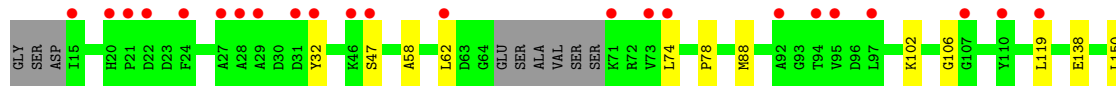
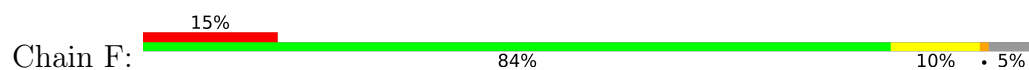




- Molecule 1: Uncharacterized protein



- Molecule 1: Uncharacterized protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, α , β , γ	150.99Å 150.99Å 76.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.73 – 2.42 47.73 – 2.42	Depositor EDS
% Data completeness (in resolution range)	99.7 (47.73-2.42) 99.7 (47.73-2.42)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.2.0019, PHENIX	Depositor
R, R_{free}	0.214 , 0.254 0.219 , 0.257	Depositor DCC
R_{free} test set	3326 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	46.5	Xtriage
Anisotropy	0.559	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.045 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9166	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.88% 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	0.89	3/1561 (0.2%)	0.90	2/2104 (0.1%)
1	B	1.10	6/1546 (0.4%)	1.05	4/2081 (0.2%)
1	C	0.89	2/1526 (0.1%)	0.95	1/2058 (0.0%)
1	D	0.80	1/1529 (0.1%)	0.86	1/2059 (0.0%)
1	E	0.85	0/1504	0.91	1/2027 (0.0%)
1	F	0.86	1/1551 (0.1%)	0.95	3/2088 (0.1%)
All	All	0.90	13/9217 (0.1%)	0.94	12/12417 (0.1%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	160	LEU	CA-C	8.74	1.56	1.52
1	B	88	MSE	SE-CE	8.38	2.20	1.95
1	B	175	SER	N-CA	7.30	1.55	1.46
1	B	150	LEU	C-O	7.27	1.32	1.24
1	A	88	MSE	SE-CE	7.27	2.17	1.95
1	F	153	SER	N-CA	7.17	1.55	1.46
1	B	172	LYS	C-O	7.03	1.32	1.24
1	C	167	VAL	C-O	-6.41	1.18	1.24
1	C	88	MSE	SE-CE	5.66	2.12	1.95
1	A	165	MSE	SE-CE	5.16	2.10	1.95
1	B	173	ASP	CG-OD2	5.12	1.35	1.25
1	A	171	PHE	C-O	-5.07	1.18	1.24
1	D	167	VAL	C-O	-5.03	1.20	1.24

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	106	GLY	N-CA-C	-6.90	98.16	110.86
1	F	106	GLY	N-CA-C	-6.73	98.51	111.02
1	E	106	GLY	N-CA-C	-6.59	98.76	111.02
1	A	106	GLY	N-CA-C	-6.28	99.31	110.86
1	B	172	LYS	CA-C-N	5.82	128.00	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	172	LYS	C-N-CA	5.82	128.00	120.44
1	D	106	GLY	N-CA-C	-5.70	100.42	111.02
1	B	172	LYS	O-C-N	5.48	127.73	122.03
1	F	151	ASN	N-CA-C	5.39	116.84	111.07
1	F	167	VAL	N-CA-CB	5.11	114.44	110.45
1	C	41	ILE	CB-CA-C	-5.07	104.56	111.15
1	A	165	MSE	N-CA-C	5.00	116.57	108.41

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	1525	0	1425	14	0
1	B	1507	0	1419	12	0
1	C	1490	0	1391	12	0
1	D	1494	0	1395	9	0
1	E	1468	0	1369	11	0
1	F	1509	0	1433	11	0
2	A	34	0	0	0	0
2	B	43	0	0	1	0
2	C	37	0	0	0	0
2	D	20	0	0	0	0
2	E	17	0	0	0	0
2	F	22	0	0	0	0
All	All	9166	0	8432	59	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 3.

All (59) 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:88:MSE:SE	1:B:88:MSE:CE	2.20	1.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:MSE:CE	1:A:88:MSE:SE	2.17	1.39
1:D:159:GLY:O	1:D:160:LEU:CB	2.43	0.66
1:B:100:GLU:OE1	1:B:102:LYS:HD2	1.95	0.66
1:C:15:ILE:N	1:C:15:ILE:HD12	2.15	0.61
1:D:130:LEU:HD21	1:E:76:ARG:HD2	1.85	0.59
1:C:188:LYS:HD3	1:D:95:VAL:HG12	1.85	0.57
1:C:15:ILE:N	1:C:15:ILE:CD1	2.69	0.56
1:A:150:LEU:C	1:A:150:LEU:HD23	2.31	0.55
1:A:166:ASN:OD1	1:A:168:PRO:HD2	2.06	0.55
1:C:188:LYS:CD	1:D:95:VAL:HG12	2.37	0.54
1:A:156:ILE:HD12	1:B:174:LEU:HD11	1.89	0.54
1:E:152:HIS:CD2	1:F:150:LEU:HD21	2.45	0.52
1:A:150:LEU:O	1:A:154:VAL:HG23	2.10	0.52
1:A:84:ILE:HD13	1:A:129:LEU:HD22	1.93	0.51
1:E:88:MSE:HB2	1:E:102:LYS:HB2	1.92	0.51
1:E:202:ILE:O	1:E:203:ASN:C	2.56	0.49
1:D:119:LEU:C	1:D:119:LEU:HD23	2.37	0.49
1:A:202:ILE:O	1:A:203:ASN:C	2.56	0.49
1:A:39:GLU:OE2	1:A:76:ARG:NH2	2.47	0.48
1:B:203:ASN:C	2:B:244:HOH:O	2.55	0.48
1:A:162:GLN:O	1:A:163:GLY:C	2.58	0.47
1:E:119:LEU:HD23	1:E:119:LEU:C	2.39	0.47
1:F:177:GLU:HA	1:F:177:GLU:OE1	2.14	0.47
1:B:199:GLU:O	1:B:203:ASN:HB2	2.15	0.47
1:F:88:MSE:HB2	1:F:102:LYS:HB2	1.97	0.46
1:C:95:VAL:HG12	1:C:95:VAL:O	2.15	0.46
1:D:100:GLU:OE1	1:D:102:LYS:HD2	2.16	0.46
1:C:184:GLY:C	1:D:95:VAL:HG21	2.40	0.46
1:E:156:ILE:HD12	1:F:174:LEU:HD11	1.98	0.46
1:F:32:TYR:HB3	1:F:74:LEU:HD21	1.97	0.46
1:B:165:MSE:HE3	1:C:162:GLN:HE22	1.81	0.44
1:D:156:ILE:HG21	1:E:174:LEU:HD21	2.00	0.44
1:E:166:ASN:OD1	1:E:168:PRO:HD2	2.17	0.44
1:F:62:LEU:HG	1:F:74:LEU:HD12	2.00	0.43
1:B:166:ASN:OD1	1:B:168:PRO:HD2	2.19	0.43
1:F:166:ASN:OD1	1:F:168:PRO:HD2	2.18	0.43
1:B:15:ILE:HD12	1:B:15:ILE:N	2.33	0.43
1:E:165:MSE:CE	1:F:162:GLN:HG3	2.49	0.42
1:B:143:LEU:HG	1:B:189:TRP:HB2	2.01	0.42
1:C:56:ASN:OD1	1:C:56:ASN:N	2.53	0.42
1:A:44:LEU:HD11	1:A:51:GLU:HG2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:100:GLU:OE1	1:E:102:LYS:HD2	2.20	0.42
1:B:177:GLU:O	1:B:178:SER:C	2.60	0.42
1:F:119:LEU:C	1:F:119:LEU:HD23	2.44	0.42
1:A:202:ILE:O	1:A:202:ILE:CG2	2.66	0.41
1:C:105:ILE:O	1:C:105:ILE:HG23	2.20	0.41
1:D:63:ASP:OD1	1:D:64:GLY:N	2.53	0.41
1:C:177:GLU:O	1:C:178:SER:C	2.63	0.41
1:A:88:MSE:HB2	1:A:102:LYS:HB2	2.02	0.41
1:B:166:ASN:O	1:B:167:VAL:C	2.63	0.41
1:C:88:MSE:HB2	1:C:102:LYS:HB2	2.03	0.41
1:F:58:ALA:HB2	1:F:78:PRO:HA	2.02	0.41
1:C:170:THR:O	1:C:174:LEU:HB2	2.21	0.40
1:A:61:HIS:CE1	1:A:63:ASP:HB2	2.56	0.40
1:B:39:GLU:OE2	1:B:76:ARG:NH2	2.54	0.40
1:E:104:GLU:OE2	1:E:109:HIS:NE2	2.54	0.40
1:A:15:ILE:CD1	1:A:15:ILE:N	2.85	0.40
1:F:202:ILE:O	1:F:202:ILE:CG2	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	184/193 (95%)	181 (98%)	3 (2%)	0	100	100
1	B	179/193 (93%)	174 (97%)	3 (2%)	2 (1%)	11	16
1	C	178/193 (92%)	173 (97%)	3 (2%)	2 (1%)	11	16
1	D	178/193 (92%)	173 (97%)	4 (2%)	1 (1%)	21	30
1	E	177/193 (92%)	172 (97%)	4 (2%)	1 (1%)	21	30
1	F	181/193 (94%)	177 (98%)	4 (2%)	0	100	100
All	All	1077/1158 (93%)	1050 (98%)	21 (2%)	6 (1%)	21	30

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	159	GLY
1	D	160	LEU
1	C	159	GLY
1	E	159	GLY
1	C	161	ARG
1	B	158	GLY

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	157/166 (95%)	153 (98%)	4 (2%)	42	62
1	B	157/166 (95%)	153 (98%)	4 (2%)	42	62
1	C	153/166 (92%)	151 (99%)	2 (1%)	61	78
1	D	155/166 (93%)	154 (99%)	1 (1%)	78	88
1	E	149/166 (90%)	146 (98%)	3 (2%)	48	68
1	F	158/166 (95%)	155 (98%)	3 (2%)	50	70
All	All	929/996 (93%)	912 (98%)	17 (2%)	51	71

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ILE
1	A	47	SER
1	A	138	GLU
1	A	174	LEU
1	B	15	ILE
1	B	47	SER
1	B	138	GLU
1	B	174	LEU
1	C	15	ILE
1	C	138	GLU
1	D	138	GLU

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Mol	Chain	Res	Type
1	E	47	SER
1	E	70	SER
1	E	138	GLU
1	F	47	SER
1	F	138	GLU
1	F	162	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	152	HIS
1	A	191	GLN
1	B	190	ASN
1	B	191	GLN
1	D	109	HIS
1	E	169	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 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 ⓘ

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	185/193 (95%)	0.90	17 (9%)	14 11	42, 65, 90, 103	0
1	B	181/193 (93%)	0.77	18 (9%)	13 9	42, 65, 88, 95	1 (0%)
1	C	181/193 (93%)	0.93	19 (10%)	11 8	42, 65, 88, 94	0
1	D	181/193 (93%)	0.71	15 (8%)	17 14	43, 65, 87, 95	0
1	E	180/193 (93%)	1.56	52 (28%)	1 1	43, 65, 87, 95	0
1	F	180/193 (93%)	1.15	29 (16%)	4 4	27, 65, 87, 94	2 (1%)
All	All	1088/1158 (93%)	1.00	150 (13%)	6 5	27, 65, 88, 103	3 (0%)

All (150) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	160	LEU	5.7
1	B	160	LEU	5.4
1	D	160	LEU	5.2
1	E	159	GLY	5.0
1	B	94	THR	4.9
1	E	163	GLY	4.9
1	C	94	THR	4.6
1	E	158	GLY	4.6
1	A	67	ALA	4.6
1	E	94	THR	4.2
1	F	94	THR	4.2
1	E	162	GLN	4.2
1	C	203	ASN	4.2
1	F	22	ASP	4.1
1	E	15	ILE	4.1
1	E	121	HIS	4.1
1	A	66	SER	4.0
1	E	161	ARG	4.0
1	D	14	ASP	3.8

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Mol	Chain	Res	Type	RSRZ
1	D	95	VAL	3.7
1	C	71	LYS	3.7
1	B	161	ARG	3.6
1	C	65	GLU	3.6
1	E	171	PHE	3.6
1	E	174	LEU	3.6
1	E	48	LYS	3.5
1	F	73	VAL	3.5
1	D	203	ASN	3.4
1	E	93	GLY	3.4
1	B	95	VAL	3.3
1	E	170	THR	3.3
1	E	97	LEU	3.3
1	E	95	VAL	3.3
1	E	150	LEU	3.2
1	C	97	LEU	3.2
1	C	70	SER	3.2
1	E	168	PRO	3.2
1	D	94	THR	3.2
1	E	43	PHE	3.1
1	B	109[A]	HIS	3.1
1	E	148	SER	3.1
1	E	71	LYS	3.1
1	A	94	THR	3.0
1	E	24	PHE	3.0
1	E	154	VAL	2.9
1	E	156	ILE	2.9
1	E	202	ILE	2.9
1	F	46	LYS	2.9
1	E	203	ASN	2.9
1	E	64	GLY	2.9
1	A	70	SER	2.8
1	E	70	SER	2.8
1	F	171	PHE	2.8
1	F	95	VAL	2.8
1	C	95	VAL	2.8
1	E	155	THR	2.8
1	F	160	LEU	2.8
1	C	24	PHE	2.8
1	B	106	GLY	2.8
1	F	203	ASN	2.8
1	E	167	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	F	21	PRO	2.8
1	D	159	GLY	2.7
1	F	24	PHE	2.8
1	E	175	SER	2.7
1	D	163	GLY	2.7
1	B	93	GLY	2.7
1	F	71	LYS	2.7
1	E	122	VAL	2.7
1	D	106	GLY	2.6
1	B	203	ASN	2.6
1	F	97	LEU	2.6
1	F	110	TYR	2.6
1	D	64	GLY	2.6
1	D	161	ARG	2.6
1	A	160	LEU	2.6
1	D	97	LEU	2.6
1	B	15	ILE	2.5
1	C	160	LEU	2.5
1	F	62	LEU	2.5
1	E	152	HIS	2.5
1	D	92	ALA	2.5
1	A	97	LEU	2.5
1	B	97	LEU	2.5
1	E	62	LEU	2.5
1	E	46	LYS	2.5
1	B	92	ALA	2.5
1	C	72	ARG	2.4
1	A	159	GLY	2.4
1	D	93	GLY	2.4
1	C	150	LEU	2.4
1	A	161	ARG	2.4
1	B	24	PHE	2.4
1	B	70	SER	2.4
1	A	15	ILE	2.4
1	E	119	LEU	2.4
1	F	74	LEU	2.4
1	F	107	GLY	2.4
1	E	157	LEU	2.4
1	E	92	ALA	2.4
1	D	70	SER	2.3
1	A	106	GLY	2.3
1	F	158	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	202	ILE	2.3
1	F	15	ILE	2.3
1	A	20	HIS	2.3
1	E	147	ASN	2.3
1	A	14	ASP	2.3
1	E	49	THR	2.3
1	C	14	ASP	2.3
1	F	159	GLY	2.3
1	F	119	LEU	2.3
1	F	29	ALA	2.2
1	B	159	GLY	2.2
1	E	47	SER	2.2
1	F	47	SER	2.2
1	F	27	ALA	2.2
1	F	32	TYR	2.2
1	B	64	GLY	2.2
1	A	95	VAL	2.2
1	A	203	ASN	2.2
1	E	91	THR	2.2
1	B	202	ILE	2.2
1	F	169	GLN	2.2
1	B	163	GLY	2.2
1	E	41	ILE	2.2
1	B	23	ASP	2.2
1	E	51	GLU	2.2
1	D	73	VAL	2.1
1	F	28	ALA	2.1
1	C	119	LEU	2.1
1	C	174	LEU	2.1
1	A	201	TYR	2.1
1	E	31	ASP	2.1
1	E	169	GLN	2.1
1	F	92	ALA	2.1
1	E	153	SER	2.1
1	A	18	VAL	2.1
1	E	166	ASN	2.1
1	E	100	GLU	2.1
1	C	89	PHE	2.0
1	C	62	LEU	2.0
1	C	15	ILE	2.0
1	E	172	LYS	2.0
1	F	20	HIS	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	162	GLN	2.0
1	E	72	ARG	2.0
1	C	93	GLY	2.0
1	F	31	ASP	2.0
1	E	35	HIS	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.