



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 11:29 PM UTC

PDB ID : 4CBV / pdb_00004cbv
Title : X-ray structure of full-length ComE from *Streptococcus pneumoniae*.
Authors : Boudes, M.; Durand, D.; Graille, M.; van Tilbeurgh, H.; Quevillon-Cheruel, S.
Deposited on : 2013-10-16
Resolution : 3.39 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

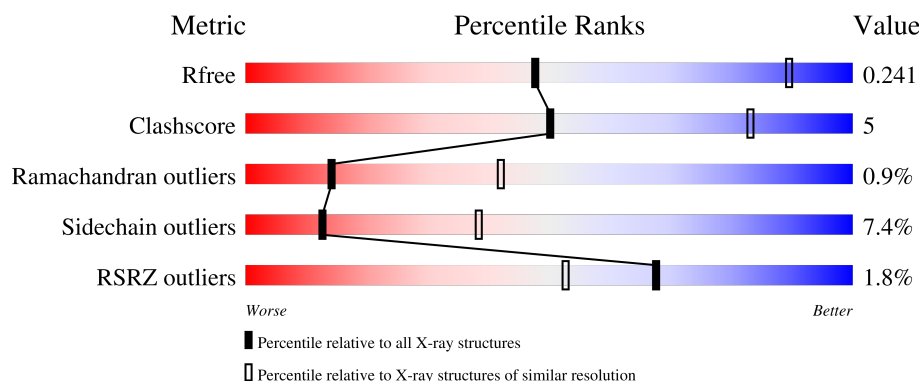
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.39 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	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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	256	72% 23%
1	B	256	73% 22%
1	C	256	75% 21%
1	D	256	82% 14%
1	E	256	79% 17%

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Mol	Chain	Length	Quality of chain
1	F	256	% 84% 15% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12732 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 COME.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	Se	0	0	0
			2123	1368	355	395	1	4			
1	B	251	Total	C	N	O	S	Se	0	0	0
			2123	1368	355	395	1	4			
1	C	249	Total	C	N	O	S	Se	0	0	0
			2104	1356	350	393	1	4			
1	D	250	Total	C	N	O	S	Se	0	0	0
			2113	1362	352	394	1	4			
1	E	248	Total	C	N	O	S	Se	0	0	0
			2096	1351	349	392	1	3			
1	F	256	Total	C	N	O	S	Se	0	0	0
			2173	1398	370	400	1	4			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	251	HIS	-	expression tag	UNP Q79CK7
A	252	HIS	-	expression tag	UNP Q79CK7
A	253	HIS	-	expression tag	UNP Q79CK7
A	254	HIS	-	expression tag	UNP Q79CK7
A	255	HIS	-	expression tag	UNP Q79CK7
A	256	HIS	-	expression tag	UNP Q79CK7
A	58	ALA	ASP	engineered mutation	UNP Q79CK7
B	251	HIS	-	expression tag	UNP Q79CK7
B	252	HIS	-	expression tag	UNP Q79CK7
B	253	HIS	-	expression tag	UNP Q79CK7
B	254	HIS	-	expression tag	UNP Q79CK7
B	255	HIS	-	expression tag	UNP Q79CK7
B	256	HIS	-	expression tag	UNP Q79CK7
B	58	ALA	ASP	engineered mutation	UNP Q79CK7
C	251	HIS	-	expression tag	UNP Q79CK7
C	252	HIS	-	expression tag	UNP Q79CK7
C	253	HIS	-	expression tag	UNP Q79CK7

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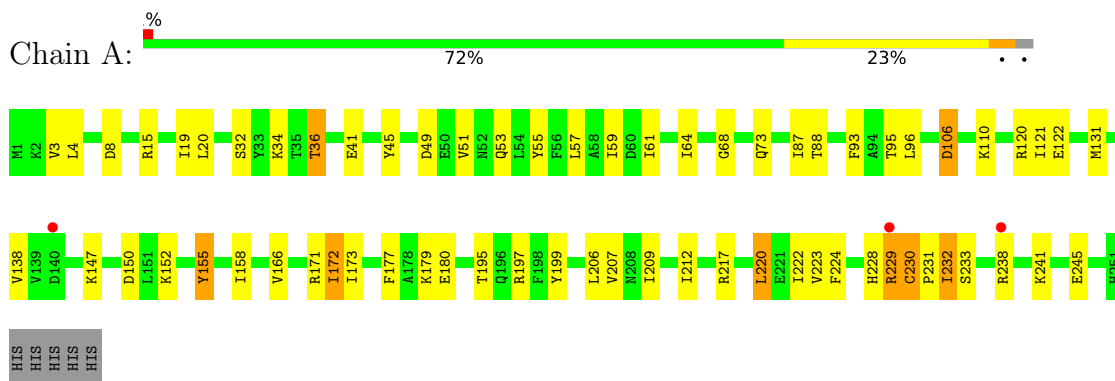
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Chain	Residue	Modelled	Actual	Comment	Reference
C	254	HIS	-	expression tag	UNP Q79CK7
C	255	HIS	-	expression tag	UNP Q79CK7
C	256	HIS	-	expression tag	UNP Q79CK7
C	58	ALA	ASP	engineered mutation	UNP Q79CK7
D	251	HIS	-	expression tag	UNP Q79CK7
D	252	HIS	-	expression tag	UNP Q79CK7
D	253	HIS	-	expression tag	UNP Q79CK7
D	254	HIS	-	expression tag	UNP Q79CK7
D	255	HIS	-	expression tag	UNP Q79CK7
D	256	HIS	-	expression tag	UNP Q79CK7
D	58	ALA	ASP	engineered mutation	UNP Q79CK7
E	251	HIS	-	expression tag	UNP Q79CK7
E	252	HIS	-	expression tag	UNP Q79CK7
E	253	HIS	-	expression tag	UNP Q79CK7
E	254	HIS	-	expression tag	UNP Q79CK7
E	255	HIS	-	expression tag	UNP Q79CK7
E	256	HIS	-	expression tag	UNP Q79CK7
E	58	ALA	ASP	engineered mutation	UNP Q79CK7
F	251	HIS	-	expression tag	UNP Q79CK7
F	252	HIS	-	expression tag	UNP Q79CK7
F	253	HIS	-	expression tag	UNP Q79CK7
F	254	HIS	-	expression tag	UNP Q79CK7
F	255	HIS	-	expression tag	UNP Q79CK7
F	256	HIS	-	expression tag	UNP Q79CK7
F	58	ALA	ASP	engineered mutation	UNP Q79CK7

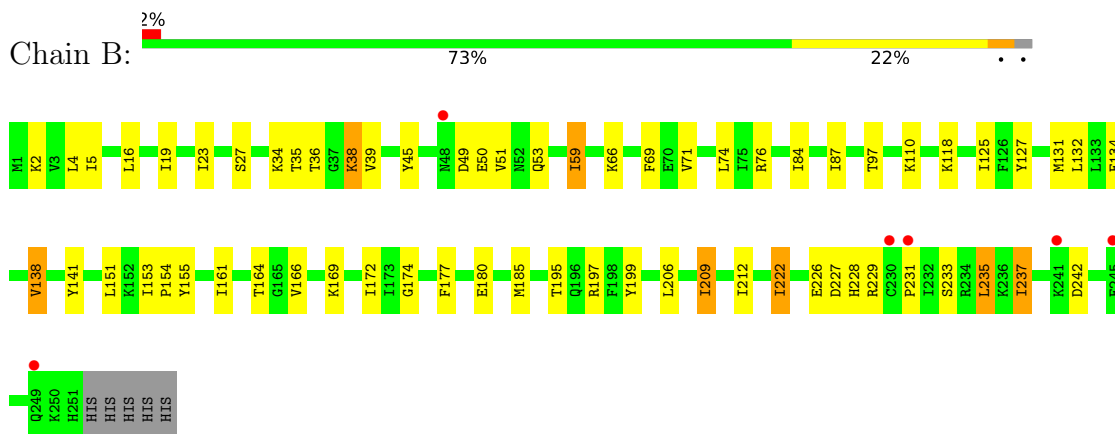
3 Residue-property plots

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.

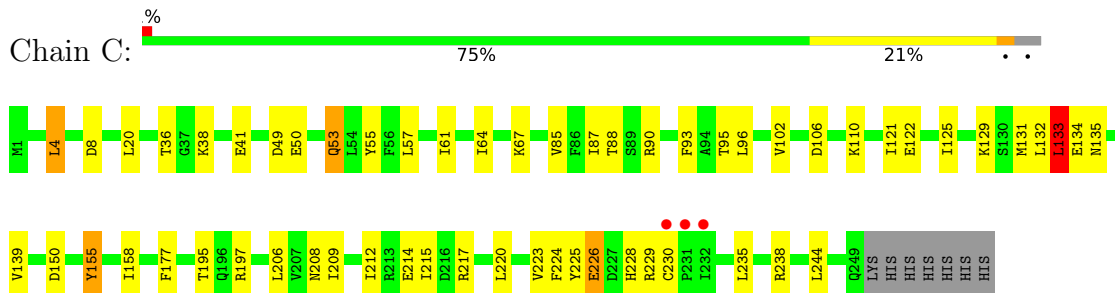
- Molecule 1: COME



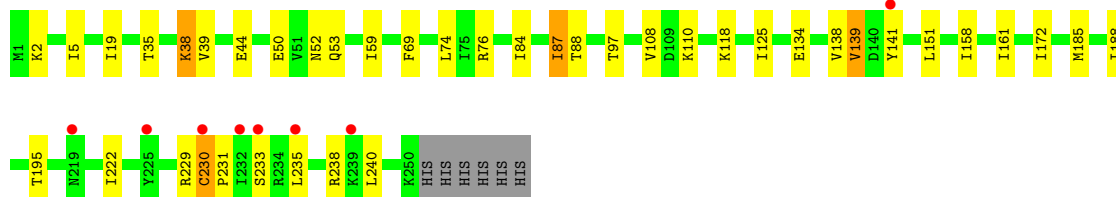
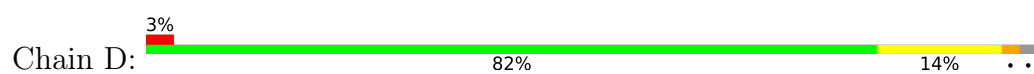
- Molecule 1: COME



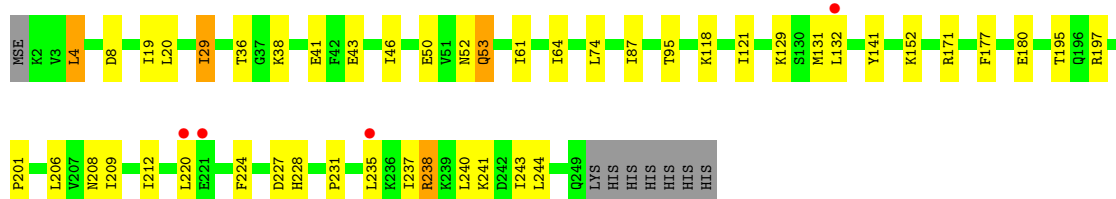
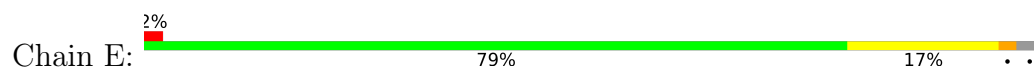
- Molecule 1: COME



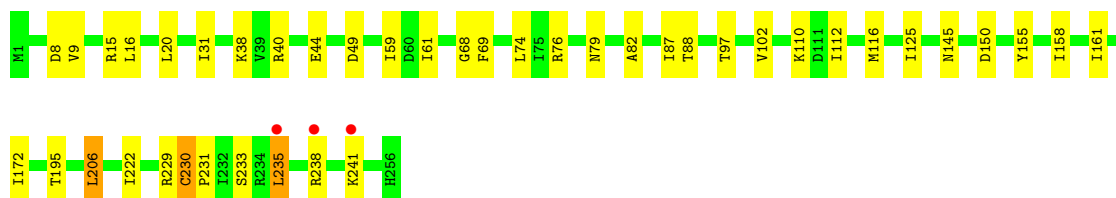
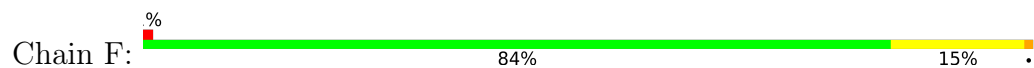
- Molecule 1: COME



• Molecule 1: COME



• Molecule 1: COME



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	88.89Å 135.00Å 461.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.95 – 3.39 37.95 – 3.39	Depositor EDS
% Data completeness (in resolution range)	96.3 (37.95-3.39) 96.2 (37.95-3.39)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.74 (at 3.40Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.196 , 0.223 0.211 , 0.241	Depositor DCC
R_{free} test set	1898 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	79.7	Xtriage
Anisotropy	0.336	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 115.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	12732	wwPDB-VP
Average B, all atoms (Å ²)	114.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.90% 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	0.77	0/2163	1.31	7/2903 (0.2%)
1	B	0.73	0/2163	1.28	7/2903 (0.2%)
1	C	0.75	0/2143	1.27	10/2877 (0.3%)
1	D	0.76	0/2152	1.26	4/2888 (0.1%)
1	E	0.78	0/2135	1.23	2/2867 (0.1%)
1	F	0.74	0/2218	1.26	2/2978 (0.1%)
All	All	0.76	0/12974	1.27	32/17416 (0.2%)

There are no bond length outliers.

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	50	GLU	CA-C-N	6.78	134.17	121.97
1	B	50	GLU	C-N-CA	6.78	134.17	121.97
1	A	122	GLU	CA-C-N	6.19	128.86	120.38
1	A	122	GLU	C-N-CA	6.19	128.86	120.38
1	B	235	LEU	CA-C-N	5.96	129.09	120.38
1	B	235	LEU	C-N-CA	5.96	129.09	120.38
1	B	237	ILE	N-CA-CB	-5.92	105.29	112.33
1	C	90	ARG	CA-C-N	5.76	128.58	120.28
1	C	90	ARG	C-N-CA	5.76	128.58	120.28
1	D	50	GLU	CA-C-N	5.68	129.10	120.13
1	D	50	GLU	C-N-CA	5.68	129.10	120.13
1	A	232	ILE	N-CA-CB	-5.62	104.63	111.21
1	F	235	LEU	CA-C-N	5.59	128.54	120.38
1	F	235	LEU	C-N-CA	5.59	128.54	120.38
1	D	235	LEU	CA-C-N	5.52	128.23	120.28
1	D	235	LEU	C-N-CA	5.52	128.23	120.28
1	C	208	ASN	CA-C-N	5.34	128.05	120.53
1	C	208	ASN	C-N-CA	5.34	128.05	120.53
1	C	155	TYR	CA-C-N	5.19	127.23	120.28
1	C	155	TYR	C-N-CA	5.19	127.23	120.28
1	A	155	TYR	CA-C-N	5.13	127.47	120.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	155	TYR	C-N-CA	5.13	127.47	120.54
1	A	73	GLN	CA-C-N	5.07	127.07	120.28
1	A	73	GLN	C-N-CA	5.07	127.07	120.28
1	E	208	ASN	CA-C-N	5.04	127.63	120.53
1	E	208	ASN	C-N-CA	5.04	127.63	120.53
1	B	27	SER	CA-C-N	5.03	129.47	122.08
1	B	27	SER	C-N-CA	5.03	129.47	122.08
1	C	122	GLU	CA-C-N	5.01	127.31	120.54
1	C	122	GLU	C-N-CA	5.01	127.31	120.54
1	C	133	LEU	CA-C-N	5.00	131.10	121.54
1	C	133	LEU	C-N-CA	5.00	131.10	121.54

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	2123	0	2132	35	0
1	B	2123	0	2132	24	0
1	C	2104	0	2112	21	0
1	D	2113	0	2125	20	0
1	E	2096	0	2100	18	0
1	F	2173	0	2167	19	1
All	All	12732	0	12768	135	1

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 5.

All (135) 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:A:49:ASP:HB2	1:A:53:GLN:HG3	1.51	0.92
1:A:224:PHE:HE1	1:A:231:PRO:HD2	1.43	0.83
1:A:93:PHE:HA	1:A:96:LEU:HD23	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:224:PHE:HB2	1:C:228:HIS:HB2	1.72	0.71
1:C:36:THR:HG21	1:C:41:GLU:HB3	1.75	0.68
1:E:220:LEU:HD13	1:E:238:ARG:HH22	1.61	0.65
1:E:36:THR:HG21	1:E:41:GLU:HB3	1.78	0.65
1:A:224:PHE:HE1	1:A:231:PRO:CD	2.10	0.64
1:B:161:ILE:HG12	1:B:172:ILE:HD13	1.80	0.63
1:E:224:PHE:HE1	1:E:231:PRO:HG2	1.64	0.63
1:B:45:TYR:HA	1:B:49:ASP:HB3	1.80	0.62
1:B:59:ILE:HG23	1:B:66:LYS:HA	1.82	0.61
1:D:138:VAL:HG23	1:D:139:VAL:HG22	1.82	0.61
1:A:223:VAL:HG22	1:A:229:ARG:HG2	1.83	0.61
1:B:5:ILE:HB	1:B:35:THR:HG22	1.82	0.61
1:C:55:TYR:HB3	1:C:57:LEU:HD13	1.83	0.61
1:F:230:CYS:H	1:F:231:PRO:HD2	1.66	0.59
1:B:38:LYS:HZ2	1:B:39:VAL:H	1.49	0.59
1:E:29:ILE:HG21	1:E:129:LYS:HD2	1.85	0.59
1:F:59:ILE:HD12	1:F:88:THR:HG21	1.84	0.59
1:A:199:TYR:HB2	1:A:209:ILE:HD11	1.86	0.57
1:D:230:CYS:H	1:D:231:PRO:HD2	1.69	0.57
1:A:220:LEU:HD13	1:A:238:ARG:HH22	1.70	0.56
1:D:134:GLU:HA	1:D:138:VAL:HG21	1.87	0.56
1:A:55:TYR:HB3	1:A:57:LEU:HD13	1.88	0.56
1:A:222:ILE:HD11	1:A:241:LYS:HE2	1.87	0.55
1:C:36:THR:HG22	1:C:38:LYS:H	1.70	0.55
1:E:209:ILE:HA	1:E:212:ILE:HD12	1.88	0.55
1:A:233:SER:HB3	1:A:238:ARG:HH21	1.70	0.55
1:C:50:GLU:HB2	1:C:53:GLN:HG2	1.87	0.55
1:C:214:GLU:HB3	1:C:223:VAL:HB	1.88	0.55
1:A:59:ILE:HA	1:A:68:GLY:HA3	1.89	0.55
1:C:93:PHE:HA	1:C:96:LEU:HD23	1.89	0.55
1:A:15:ARG:O	1:A:19:ILE:HG12	2.07	0.54
1:D:5:ILE:HB	1:D:35:THR:HG22	1.90	0.54
1:F:112:ILE:HD12	1:F:116:MSE:HB3	1.90	0.54
1:B:199:TYR:HB2	1:B:209:ILE:HD12	1.89	0.54
1:E:50:GLU:HB2	1:E:53:GLN:HG2	1.89	0.54
1:B:222:ILE:HB	1:B:231:PRO:HG2	1.90	0.54
1:A:224:PHE:CE1	1:A:231:PRO:HD2	2.33	0.53
1:C:217:ARG:HH11	1:C:238:ARG:HD2	1.73	0.52
1:D:161:ILE:HG12	1:D:172:ILE:HD13	1.91	0.52
1:B:164:THR:HG22	1:B:169:LYS:O	2.10	0.51
1:B:87:ILE:HG22	1:B:110:LYS:HD3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:50:GLU:H	1:E:53:GLN:HG3	1.75	0.51
1:E:224:PHE:CE1	1:E:231:PRO:HG2	2.46	0.51
1:A:230:CYS:HB2	1:A:231:PRO:HD3	1.93	0.50
1:D:139:VAL:HG23	1:D:141:TYR:CE1	2.46	0.50
1:C:88:THR:HA	1:C:110:LYS:HE3	1.94	0.50
1:F:222:ILE:HB	1:F:231:PRO:HG2	1.93	0.50
1:E:4:LEU:HD13	1:E:53:GLN:HE22	1.75	0.49
1:E:201:PRO:HA	1:E:237:ILE:HG21	1.94	0.49
1:F:155:TYR:HA	1:F:158:ILE:HD12	1.93	0.49
1:A:232:ILE:HD12	1:A:232:ILE:H	1.77	0.49
1:C:49:ASP:HB2	1:C:53:GLN:HG3	1.93	0.49
1:B:212:ILE:HG23	1:B:222:ILE:HG23	1.94	0.49
1:D:59:ILE:HD12	1:D:88:THR:HG21	1.94	0.49
1:B:127:TYR:O	1:B:131:MSE:HG2	2.12	0.49
1:F:20:LEU:HD22	1:F:31:ILE:HG21	1.95	0.49
1:A:8:ASP:HB3	1:A:61:ILE:HG23	1.95	0.49
1:A:51:VAL:HG22	1:A:179:LYS:HG2	1.94	0.49
1:D:19:ILE:HG23	1:D:118:LYS:HG3	1.95	0.49
1:E:224:PHE:HB2	1:E:228:HIS:HB2	1.95	0.49
1:A:158:ILE:HG12	1:A:172:ILE:HD11	1.95	0.48
1:C:223:VAL:HG22	1:C:229:ARG:HG2	1.94	0.48
1:D:76:ARG:HH21	1:D:84:ILE:HG12	1.79	0.48
1:C:209:ILE:HA	1:C:212:ILE:HD12	1.94	0.48
1:D:222:ILE:HB	1:D:231:PRO:HG2	1.94	0.48
1:A:224:PHE:HB2	1:A:228:HIS:HB2	1.95	0.48
1:D:158:ILE:HG23	1:D:172:ILE:HG23	1.96	0.48
1:D:2:LYS:H	1:D:53:GLN:HG2	1.77	0.48
1:E:36:THR:HG22	1:E:38:LYS:H	1.78	0.47
1:F:15:ARG:HH11	1:F:110:LYS:HE3	1.79	0.47
1:D:38:LYS:HZ2	1:D:39:VAL:H	1.62	0.47
1:C:4:LEU:HD13	1:C:53:GLN:HE22	1.77	0.47
1:E:8:ASP:HB3	1:E:61:ILE:HG23	1.95	0.47
1:F:79:ASN:HB3	1:F:82:ALA:HB2	1.97	0.47
1:C:8:ASP:HB3	1:C:61:ILE:HG23	1.96	0.46
1:E:240:LEU:HD13	1:E:243:ILE:HD11	1.97	0.46
1:E:171:ARG:HG3	1:E:180:GLU:HG2	1.96	0.46
1:F:230:CYS:H	1:F:231:PRO:CD	2.29	0.46
1:F:222:ILE:HG12	1:F:241:LYS:HE3	1.98	0.46
1:B:141:TYR:HA	1:B:154:PRO:HA	1.96	0.46
1:F:161:ILE:HG12	1:F:172:ILE:HD13	1.97	0.46
1:E:43:GLU:HA	1:E:46:ILE:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:PHE:HE1	1:B:97:THR:HG22	1.80	0.45
1:F:145:ASN:HD22	1:F:150:ASP:HB3	1.81	0.45
1:B:19:ILE:HG23	1:B:118:LYS:HG3	1.98	0.45
1:F:59:ILE:HA	1:F:68:GLY:HA3	1.98	0.45
1:D:87:ILE:HG13	1:D:108:VAL:HB	1.98	0.45
1:F:38:LYS:HE3	1:F:40:ARG:HG3	1.98	0.45
1:B:2:LYS:H	1:B:53:GLN:HG2	1.82	0.45
1:B:226:GLU:O	1:B:228:HIS:N	2.50	0.45
1:F:235:LEU:HD12	1:F:238:ARG:HH22	1.80	0.45
1:A:34:LYS:HB3	1:A:45:TYR:CE2	2.53	0.44
1:B:76:ARG:NH2	1:B:84:ILE:HG12	2.32	0.44
1:D:87:ILE:HG23	1:D:110:LYS:HD3	1.99	0.44
1:A:220:LEU:HA	1:A:238:ARG:NH2	2.32	0.44
1:C:226:GLU:HG3	1:D:134:GLU:HB2	2.00	0.44
1:F:76:ARG:HD2	1:F:102:VAL:HA	2.00	0.44
1:A:106:ASP:OD1	1:A:120:ARG:NH2	2.51	0.44
1:D:69:PHE:HE1	1:D:97:THR:HG22	1.81	0.44
1:A:220:LEU:HD13	1:A:238:ARG:HH12	1.82	0.43
1:F:69:PHE:HE1	1:F:97:THR:HG22	1.84	0.43
1:A:232:ILE:HD12	1:A:232:ILE:N	2.33	0.43
1:B:4:LEU:HD23	1:B:34:LYS:HB3	2.00	0.43
1:C:129:LYS:HE3	1:C:133:LEU:HD13	1.99	0.43
1:C:155:TYR:HA	1:C:158:ILE:HD12	2.00	0.43
1:A:138:VAL:HG21	1:A:152:LYS:HE3	2.01	0.43
1:F:8:ASP:HB3	1:F:61:ILE:HG23	2.01	0.43
1:C:220:LEU:HD13	1:C:238:ARG:HH12	1.84	0.42
1:A:36:THR:HG21	1:A:41:GLU:HB3	2.01	0.42
1:A:4:LEU:HD21	1:A:45:TYR:HB3	2.01	0.42
1:B:134:GLU:HA	1:B:138:VAL:CG2	2.49	0.42
1:C:85:VAL:HG13	1:C:106:ASP:HB3	2.00	0.42
1:A:217:ARG:HD2	1:A:238:ARG:HD2	2.01	0.42
1:B:69:PHE:CE1	1:B:97:THR:HG22	2.54	0.42
1:E:52:ASN:HD21	1:E:152:LYS:H	1.66	0.42
1:A:88:THR:C	1:A:110:LYS:HG2	2.45	0.42
1:F:161:ILE:HD12	1:F:206:LEU:HD12	2.01	0.42
1:D:222:ILE:HD11	1:D:233:SER:HB2	2.02	0.42
1:A:88:THR:HA	1:A:110:LYS:HE3	2.02	0.41
1:A:155:TYR:HA	1:A:158:ILE:HD12	2.02	0.41
1:B:166:VAL:HG13	1:B:169:LYS:HB3	2.02	0.41
1:B:174:GLY:HA3	1:B:177:PHE:CE1	2.55	0.41
1:E:19:ILE:HG23	1:E:118:LYS:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:134:GLU:HA	1:B:138:VAL:HG22	2.02	0.41
1:B:155:TYR:CZ	1:B:197:ARG:HD3	2.56	0.41
1:A:3:VAL:HG11	1:A:20:LEU:HD21	2.03	0.41
1:A:171:ARG:NH1	1:A:180:GLU:OE2	2.54	0.41
1:D:185:MSE:HA	1:D:188:ILE:HD12	2.04	0.40
1:C:93:PHE:HD1	1:C:96:LEU:HD23	1.86	0.40
1:C:225:TYR:HB3	1:D:134:GLU:O	2.20	0.40
1:A:207:VAL:HG12	1:A:231:PRO:HG2	2.03	0.40
1:A:209:ILE:HA	1:A:212:ILE:HD12	2.03	0.40

All (1) 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	Interatomic distance (Å)	Clash overlap (Å)
1:F:116:MSE:CE	1:F:116:MSE:CE[3_655]	0.63	1.57

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	249/256 (97%)	236 (95%)	11 (4%)	2 (1%)	16	44
1	B	249/256 (97%)	235 (94%)	12 (5%)	2 (1%)	16	44
1	C	247/256 (96%)	231 (94%)	12 (5%)	4 (2%)	7	29
1	D	248/256 (97%)	239 (96%)	8 (3%)	1 (0%)	30	59
1	E	246/256 (96%)	232 (94%)	12 (5%)	2 (1%)	16	44
1	F	254/256 (99%)	242 (95%)	10 (4%)	2 (1%)	16	44
All	All	1493/1536 (97%)	1415 (95%)	65 (4%)	13 (1%)	14	42

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	51	VAL
1	B	227	ASP
1	C	134	GLU
1	A	229	ARG
1	F	49	ASP
1	A	230	CYS
1	E	131	MSE
1	C	135	ASN
1	C	226	GLU
1	F	230	CYS
1	C	139	VAL
1	D	230	CYS
1	E	227	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	237/238 (100%)	218 (92%)	19 (8%)	11	36
1	B	237/238 (100%)	214 (90%)	23 (10%)	8	28
1	C	235/238 (99%)	213 (91%)	22 (9%)	8	29
1	D	236/238 (99%)	224 (95%)	12 (5%)	21	48
1	E	234/238 (98%)	215 (92%)	19 (8%)	11	36
1	F	242/238 (102%)	232 (96%)	10 (4%)	27	52
All	All	1421/1428 (100%)	1316 (93%)	105 (7%)	13	38

All (105) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	SER
1	A	36	THR
1	A	64	ILE
1	A	87	ILE
1	A	95	THR
1	A	106	ASP

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Mol	Chain	Res	Type
1	A	121	ILE
1	A	131	MSE
1	A	147	LYS
1	A	150	ASP
1	A	166	VAL
1	A	172	ILE
1	A	173	ILE
1	A	177	PHE
1	A	195	THR
1	A	197	ARG
1	A	206	LEU
1	A	220	LEU
1	A	245	GLU
1	B	16	LEU
1	B	23	ILE
1	B	36	THR
1	B	38	LYS
1	B	59	ILE
1	B	71	VAL
1	B	74	LEU
1	B	125	ILE
1	B	132	LEU
1	B	138	VAL
1	B	151	LEU
1	B	153	ILE
1	B	180	GLU
1	B	185	MSE
1	B	195	THR
1	B	206	LEU
1	B	209	ILE
1	B	222	ILE
1	B	229	ARG
1	B	233	SER
1	B	235	LEU
1	B	237	ILE
1	B	242	ASP
1	C	4	LEU
1	C	20	LEU
1	C	53	GLN
1	C	64	ILE
1	C	67	LYS
1	C	87	ILE

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Mol	Chain	Res	Type
1	C	95	THR
1	C	102	VAL
1	C	121	ILE
1	C	125	ILE
1	C	131	MSE
1	C	132	LEU
1	C	133	LEU
1	C	150	ASP
1	C	177	PHE
1	C	195	THR
1	C	197	ARG
1	C	206	LEU
1	C	215	ILE
1	C	230	CYS
1	C	235	LEU
1	C	244	LEU
1	D	38	LYS
1	D	44	GLU
1	D	52	ASN
1	D	74	LEU
1	D	87	ILE
1	D	125	ILE
1	D	139	VAL
1	D	151	LEU
1	D	195	THR
1	D	229	ARG
1	D	238	ARG
1	D	240	LEU
1	E	4	LEU
1	E	20	LEU
1	E	29	ILE
1	E	53	GLN
1	E	64	ILE
1	E	74	LEU
1	E	87	ILE
1	E	95	THR
1	E	121	ILE
1	E	132	LEU
1	E	141	TYR
1	E	177	PHE
1	E	195	THR
1	E	197	ARG

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Mol	Chain	Res	Type
1	E	206	LEU
1	E	235	LEU
1	E	238	ARG
1	E	241	LYS
1	E	244	LEU
1	F	9	VAL
1	F	16	LEU
1	F	44	GLU
1	F	74	LEU
1	F	87	ILE
1	F	125	ILE
1	F	195	THR
1	F	206	LEU
1	F	229	ARG
1	F	233	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	HIS
1	A	13	GLN
1	A	123	GLN
1	A	168	HIS
1	B	101	GLN
1	B	156	HIS
1	B	219	ASN
1	B	249	GLN
1	C	12	HIS
1	C	13	GLN
1	C	28	ASN
1	C	53	GLN
1	C	62	HIS
1	C	168	HIS
1	C	208	ASN
1	C	228	HIS
1	D	13	GLN
1	D	28	ASN
1	D	62	HIS
1	D	123	GLN
1	D	145	ASN
1	D	156	HIS
1	D	176	ASN

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Mol	Chain	Res	Type
1	D	219	ASN
1	E	13	GLN
1	E	52	ASN
1	E	53	GLN
1	E	145	ASN
1	E	228	HIS
1	F	145	ASN
1	F	219	ASN

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

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	247/256 (96%)	-0.31	3 (1%) 76 63	35, 60, 104, 150	0
1	B	247/256 (96%)	-0.18	6 (2%) 59 45	35, 67, 109, 184	0
1	C	245/256 (95%)	0.05	3 (1%) 76 63	74, 116, 163, 206	0
1	D	246/256 (96%)	0.28	8 (3%) 49 36	86, 140, 185, 212	0
1	E	245/256 (95%)	0.26	4 (1%) 70 56	119, 158, 192, 220	0
1	F	252/256 (98%)	0.02	3 (1%) 76 63	94, 125, 159, 171	0
All	All	1482/1536 (96%)	0.02	27 (1%) 67 53	35, 118, 179, 220	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	233	SER	4.1
1	B	230	CYS	3.3
1	D	141	TYR	3.3
1	D	232	ILE	3.0
1	E	221	GLU	3.0
1	C	231	PRO	2.8
1	D	225	TYR	2.8
1	C	232	ILE	2.7
1	E	220	LEU	2.6
1	A	238	ARG	2.4
1	F	235	LEU	2.4
1	F	238	ARG	2.4
1	D	235	LEU	2.4
1	B	48	ASN	2.3
1	C	230	CYS	2.3
1	A	140	ASP	2.3
1	F	241	LYS	2.3
1	B	241	LYS	2.3
1	E	132	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	239	LYS	2.2
1	E	235	LEU	2.1
1	B	231	PRO	2.1
1	D	230	CYS	2.1
1	B	245	GLU	2.1
1	B	249	GLN	2.0
1	A	229	ARG	2.0
1	D	219	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.