



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:17 AM GMT

PDB ID : 3E0R
Title : Crystal structure of cppA protein from Streptococcus pneumoniae TIGR4
Authors : Nocek, B.; Mulligan, R.; Abdullah, J.; Otwinowski, Z.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2008-07-31
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

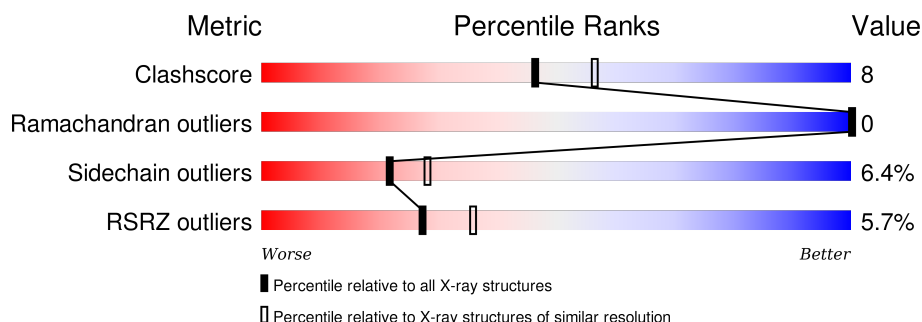
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	244	<div> <div>9%</div> <div> <div></div> <div>81%</div> <div>14%</div> <div>..</div> </div> </div>
1	B	244	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>18%</div> <div>...</div> </div> </div>
1	C	244	<div> <div>4%</div> <div> <div></div> <div>80%</div> <div>16%</div> <div>..</div> </div> </div>
1	D	244	<div> <div>6%</div> <div> <div></div> <div>79%</div> <div>16%</div> <div>..</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8192 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 C3-degrading proteinase (CppA protein).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	239	Total	C	N	O	Se	0	0	0
			1917	1228	308	377	4			
1	B	236	Total	C	N	O	Se	0	1	0
			1905	1219	307	375	4			
1	C	238	Total	C	N	O	Se	0	3	0
			1931	1235	312	380	4			
1	D	234	Total	C	N	O	Se	0	1	0
			1889	1211	307	367	4			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q9X4I9
A	-1	ASN	-	expression tag	UNP Q9X4I9
A	0	ALA	-	expression tag	UNP Q9X4I9
B	-2	SER	-	expression tag	UNP Q9X4I9
B	-1	ASN	-	expression tag	UNP Q9X4I9
B	0	ALA	-	expression tag	UNP Q9X4I9
C	-2	SER	-	expression tag	UNP Q9X4I9
C	-1	ASN	-	expression tag	UNP Q9X4I9
C	0	ALA	-	expression tag	UNP Q9X4I9
D	-2	SER	-	expression tag	UNP Q9X4I9
D	-1	ASN	-	expression tag	UNP Q9X4I9
D	0	ALA	-	expression tag	UNP Q9X4I9

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cl	0	0
			1	1		

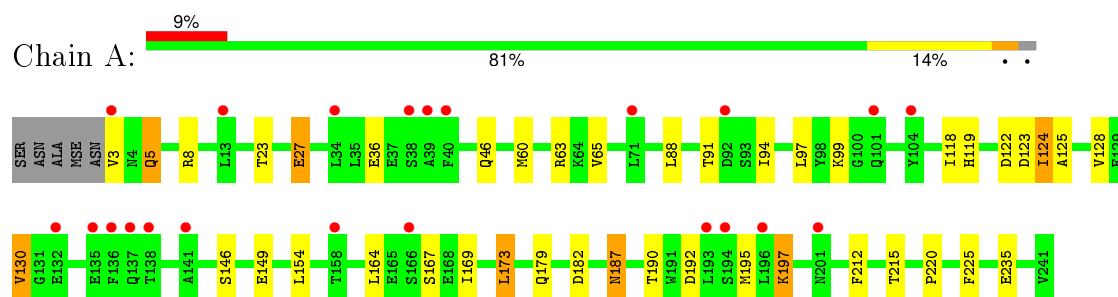
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	119	Total 119	O 119	0	0
3	B	147	Total 147	O 147	0	0
3	C	144	Total 144	O 144	0	0
3	D	139	Total 139	O 139	0	0

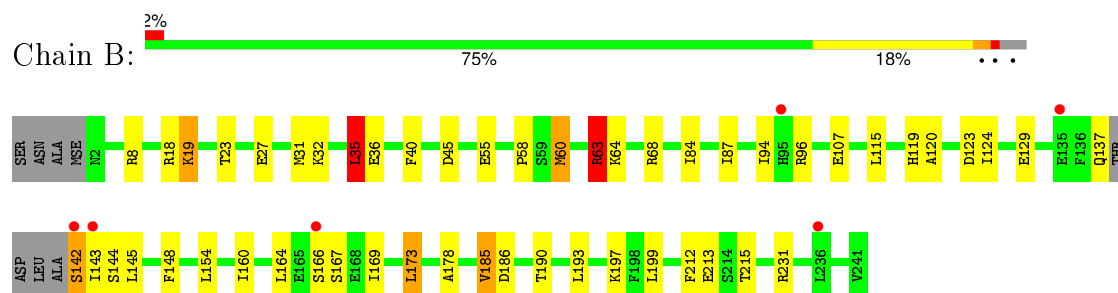
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

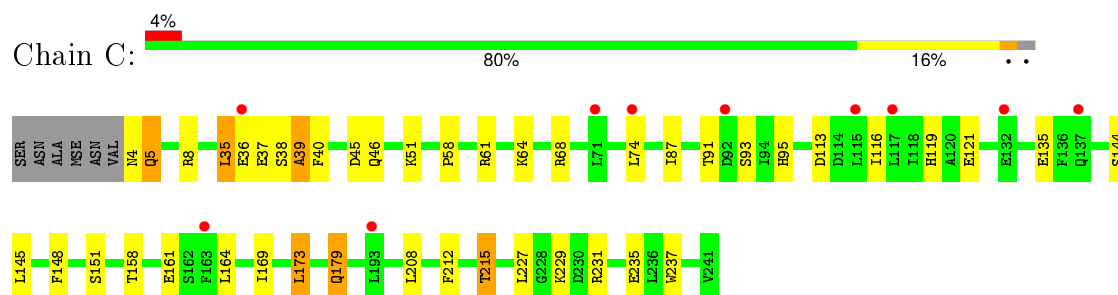
- Molecule 1: C3-degrading proteinase (CppA protein)



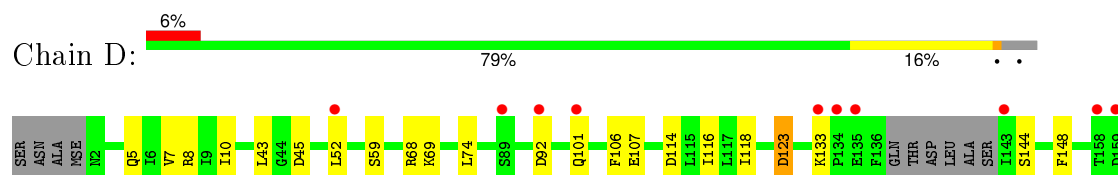
- Molecule 1: C3-degrading proteinase (CppA protein)



- Molecule 1: C3-degrading proteinase (CppA protein)



- Molecule 1: C3-degrading proteinase (CppA protein)





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	114.74Å 130.74Å 91.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.30 29.71 – 2.27	Depositor EDS
% Data completeness (in resolution range)	97.2 (40.00-2.30) 95.4 (29.71-2.27)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 2.26Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.189 , 0.256 0.198 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.482	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 35.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 61498 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8192	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.77 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 4.7482e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL

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	0.90	0/1945	0.85	3/2619 (0.1%)
1	B	0.89	0/1932	0.90	5/2599 (0.2%)
1	C	0.95	1/1965 (0.1%)	0.91	2/2646 (0.1%)
1	D	0.91	1/1916 (0.1%)	0.87	2/2577 (0.1%)
All	All	0.91	2/7758 (0.0%)	0.88	12/10441 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	39	ALA	CA-CB	6.96	1.67	1.52
1	D	197	LYS	CE-NZ	5.35	1.62	1.49

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	209	ARG	NE-CZ-NH1	5.79	123.19	120.30
1	C	8	ARG	NE-CZ-NH2	5.75	123.18	120.30
1	C	68	ARG	NE-CZ-NH1	5.75	123.17	120.30
1	B	63	ARG	NE-CZ-NH2	-5.73	117.44	120.30
1	B	35	LEU	CA-CB-CG	-5.64	102.33	115.30
1	B	45	ASP	CB-CG-OD2	-5.39	113.45	118.30
1	A	8	ARG	NE-CZ-NH1	-5.37	117.62	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	231	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	A	192	ASP	CB-CG-OD1	5.33	123.09	118.30
1	D	123	ASP	CB-CG-OD1	5.30	123.07	118.30
1	A	8	ARG	NE-CZ-NH2	5.13	122.87	120.30
1	B	63	ARG	NE-CZ-NH1	5.00	122.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	168	GLU	Peptide

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	1917	0	1928	25	0
1	B	1905	0	1909	34	0
1	C	1931	0	1942	34	0
1	D	1889	0	1901	25	0
2	B	1	0	0	0	0
3	A	119	0	0	4	0
3	B	147	0	0	3	0
3	C	144	0	0	6	0
3	D	139	0	0	2	0
All	All	8192	0	7680	116	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 8.

All (116) 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:8[B]:ARG:HH11	1:D:8[B]:ARG:CG	1.57	1.17
1:C:38:SER:HB3	1:C:39:ALA:HA	1.30	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:8[B]:ARG:HH11	1:D:8[B]:ARG:HG2	1.15	1.06
1:D:8[B]:ARG:HH11	1:D:8[B]:ARG:CB	1.74	1.00
1:D:8[B]:ARG:NH1	1:D:8[B]:ARG:CB	2.30	0.95
1:D:8[B]:ARG:HB3	1:D:8[B]:ARG:NH1	1.81	0.94
1:A:154:LEU:HD12	1:A:173:LEU:HD21	1.53	0.90
1:B:35:LEU:HD23	1:B:36:GLU:H	1.40	0.86
1:C:212:PHE:O	1:C:215:THR:HG22	1.77	0.85
1:A:212:PHE:O	1:A:215:THR:HG22	1.76	0.84
1:C:38:SER:HA	1:C:40:PHE:H	1.44	0.83
1:D:169:ILE:HG23	1:D:173:LEU:HB3	1.59	0.82
1:C:38:SER:CB	1:C:39:ALA:HA	2.00	0.80
1:B:60:MSE:HE3	1:B:60:MSE:HA	1.63	0.79
1:B:31:MSE:HE3	1:B:148:PHE:CZ	2.18	0.77
1:D:8[B]:ARG:NH1	1:D:8[B]:ARG:HG2	1.90	0.75
1:C:35:LEU:HD22	1:C:35:LEU:H	1.53	0.74
1:B:164:LEU:HB3	1:B:169:ILE:HG21	1.71	0.72
1:A:46:GLN:HG3	1:A:146:SER:HA	1.72	0.71
1:C:38:SER:HB3	1:C:39:ALA:CA	2.15	0.71
1:C:212:PHE:HB3	1:C:215:THR:CG2	2.22	0.69
1:B:60:MSE:O	1:B:60:MSE:HE2	1.93	0.68
1:C:212:PHE:HB3	1:C:215:THR:HG22	1.76	0.67
1:A:99:LYS:O	1:A:128:VAL:HG22	1.95	0.67
1:A:23:THR:HA	1:A:27:GLU:HG3	1.76	0.66
1:C:35:LEU:HD22	1:C:35:LEU:N	2.11	0.66
1:A:46:GLN:CG	1:A:146:SER:HA	2.25	0.66
1:A:119:HIS:CE1	1:A:124:ILE:HG22	2.31	0.66
1:C:164:LEU:HB3	1:C:169:ILE:CG2	2.27	0.65
1:A:154:LEU:CD1	1:A:173:LEU:HD21	2.25	0.64
1:A:164:LEU:HB3	1:A:169:ILE:HG21	1.80	0.64
1:D:43:LEU:HD12	1:D:52:LEU:HD23	1.79	0.64
1:B:212:PHE:O	1:B:215:THR:HG22	1.97	0.63
1:B:35:LEU:HD23	1:B:36:GLU:N	2.13	0.62
1:D:8[B]:ARG:HB3	1:D:8[B]:ARG:CZ	2.31	0.60
1:B:154:LEU:HD12	1:B:173:LEU:HD21	1.84	0.60
1:B:31:MSE:HE3	1:B:148:PHE:CE1	2.36	0.60
1:C:38:SER:HA	1:C:40:PHE:N	2.15	0.59
1:A:5:GLN:HE21	1:A:5:GLN:HA	1.69	0.58
1:A:187:ASN:ND2	3:A:270:HOH:O	2.37	0.58
1:A:88:LEU:CD2	1:A:94:ILE:HG21	2.35	0.57
1:D:92:ASP:O	1:D:133:LYS:NZ	2.36	0.56
1:B:60:MSE:O	1:B:60:MSE:CE	2.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:THR:HA	1:A:27:GLU:CG	2.36	0.55
1:C:45:ASP:OD2	1:C:51:LYS:NZ	2.37	0.55
1:B:107:GLU:HB3	1:B:115:LEU:HD11	1.89	0.54
1:B:197:LYS:HE2	1:B:199:LEU:HD21	1.89	0.54
1:B:123:ASP:OD2	1:C:179:GLN:OE1	2.26	0.54
1:B:32:LYS:NZ	3:B:332:HOH:O	2.41	0.54
1:D:181:GLN:HA	3:D:293:HOH:O	2.06	0.53
1:C:91:THR:HG23	1:C:91:THR:O	2.08	0.53
1:B:23:THR:HA	1:B:27:GLU:HG2	1.89	0.53
1:C:119:HIS:HD2	1:C:121:GLU:H	1.57	0.53
1:D:45:ASP:HB3	1:D:148:PHE:CE2	2.44	0.52
1:C:35:LEU:HD21	3:C:479:HOH:O	2.09	0.52
1:A:179:GLN:OE1	1:D:123:ASP:OD2	2.27	0.51
1:B:40:PHE:CE1	1:B:55:GLU:HG3	2.46	0.51
1:B:31:MSE:HE3	1:B:148:PHE:HZ	1.74	0.51
1:A:65:VAL:HG13	1:A:182:ASP:HB2	1.93	0.51
1:C:119:HIS:CD2	1:C:121:GLU:H	2.29	0.50
1:D:230:ASP:HB2	1:D:236:LEU:HD11	1.93	0.50
1:B:154:LEU:HD22	1:B:193:LEU:HD22	1.93	0.50
1:A:5:GLN:NE2	3:A:343:HOH:O	2.45	0.50
1:D:68:ARG:HD2	1:D:178:ALA:HB1	1.95	0.49
1:C:4:ASN:HD21	1:C:208:LEU:HG	1.78	0.49
1:D:7:VAL:HG12	1:D:8[B]:ARG:HG3	1.94	0.48
1:C:64:LYS:NZ	1:C:113:ASP:OD2	2.46	0.48
1:D:10:ILE:HD12	1:D:10:ILE:N	2.28	0.48
1:D:69:LYS:HZ3	1:D:114:ASP:CG	2.17	0.47
1:D:205:ILE:HG12	3:D:359:HOH:O	2.14	0.47
1:D:220:PRO:HG3	1:D:225:PHE:CE2	2.50	0.47
1:D:107:GLU:HA	1:D:116:ILE:O	2.15	0.47
1:B:18:ARG:HH21	1:B:36:GLU:HG3	1.80	0.46
1:A:235:GLU:OE2	3:A:254:HOH:O	2.21	0.46
1:B:137:GLN:HG3	3:B:387:HOH:O	2.15	0.46
1:B:119:HIS:CE1	1:B:124:ILE:HG22	2.51	0.46
1:C:179:GLN:NE2	3:C:410:HOH:O	2.49	0.46
1:B:169:ILE:HD12	1:B:173:LEU:HD22	1.97	0.45
1:C:95:HIS:ND1	3:C:477:HOH:O	2.36	0.45
1:D:106:PHE:CE1	1:D:118:ILE:HD13	2.50	0.45
1:C:58:PRO:HG2	1:C:61:ARG:HD2	1.98	0.45
1:D:74:LEU:HB3	1:D:116:ILE:HD12	1.99	0.45
1:B:87:ILE:HD11	1:B:145:LEU:HD21	1.99	0.45
1:C:158:THR:HG23	3:C:410:HOH:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:187:ASN:HD22	1:D:188:THR:N	2.15	0.45
1:B:185:VAL:HG13	1:B:186:ASP:O	2.18	0.44
1:D:45:ASP:HB3	1:D:148:PHE:CD2	2.52	0.44
1:C:45:ASP:HB3	1:C:148:PHE:CE2	2.51	0.44
1:C:39:ALA:HB3	3:C:395:HOH:O	2.17	0.44
1:C:35:LEU:CD2	1:C:35:LEU:N	2.80	0.44
1:A:195:MSE:CE	1:A:197:LYS:HZ3	2.30	0.44
1:C:46:GLN:HE21	1:C:144:SER:HB3	1.83	0.44
1:B:87:ILE:HG12	1:B:143:ILE:HG23	1.99	0.44
1:A:123:ASP:OD1	1:A:125:ALA:HB3	2.18	0.43
1:B:68:ARG:HD2	1:B:178:ALA:HB1	2.00	0.43
1:A:197:LYS:HE2	3:A:279:HOH:O	2.18	0.43
1:B:96:ARG:HD3	1:B:129:GLU:CD	2.38	0.43
1:A:128:VAL:O	1:A:128:VAL:HG23	2.18	0.43
1:A:220:PRO:HD2	1:A:225:PHE:O	2.19	0.42
1:C:87:ILE:HD11	1:C:145:LEU:HD21	2.01	0.42
1:C:91:THR:CG2	1:C:91:THR:O	2.66	0.42
1:B:19:LYS:HD2	1:B:19:LYS:O	2.19	0.42
1:C:5:GLN:NE2	3:C:485:HOH:O	2.44	0.42
1:C:74:LEU:HB3	1:C:116:ILE:HD12	2.01	0.42
1:B:84:ILE:CD1	1:B:120:ALA:HB2	2.50	0.42
1:B:63:ARG:O	1:B:190:THR:HA	2.20	0.41
1:B:31:MSE:CE	1:B:148:PHE:HZ	2.33	0.41
1:A:195:MSE:HE3	1:A:197:LYS:HZ3	1.85	0.41
1:A:63:ARG:O	1:A:190:THR:HA	2.19	0.41
1:C:169:ILE:HB	1:C:173:LEU:HB3	2.02	0.41
1:B:142:SER:N	3:B:347:HOH:O	2.54	0.41
1:A:97:LEU:HD23	1:A:130:VAL:CG2	2.51	0.41
1:C:227:LEU:HD11	1:C:235:GLU:HB3	2.03	0.41
1:B:60:MSE:HE3	1:B:60:MSE:CA	2.42	0.40
1:C:161:GLU:O	1:C:231:ARG:HD2	2.21	0.40
1:B:60:MSE:CE	1:B:60:MSE:HA	2.44	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	237/244 (97%)	230 (97%)	7 (3%)	0	100	100
1	B	233/244 (96%)	230 (99%)	3 (1%)	0	100	100
1	C	239/244 (98%)	232 (97%)	7 (3%)	0	100	100
1	D	231/244 (95%)	221 (96%)	10 (4%)	0	100	100
All	All	940/976 (96%)	913 (97%)	27 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	216/215 (100%)	201 (93%)	15 (7%)	19	24
1	B	215/215 (100%)	199 (93%)	16 (7%)	17	21
1	C	218/215 (101%)	206 (94%)	12 (6%)	27	36
1	D	212/215 (99%)	200 (94%)	12 (6%)	25	34
All	All	861/860 (100%)	806 (94%)	55 (6%)	22	28

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	VAL
1	A	5	GLN
1	A	27	GLU
1	A	36	GLU
1	A	60	MSE
1	A	91	THR
1	A	118	ILE
1	A	122	ASP

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Mol	Chain	Res	Type
1	A	124	ILE
1	A	130	VAL
1	A	149	GLU
1	A	167	SER
1	A	173	LEU
1	A	187	ASN
1	A	197	LYS
1	B	8	ARG
1	B	19	LYS
1	B	35	LEU
1	B	58	PRO
1	B	60	MSE
1	B	63	ARG
1	B	64	LYS
1	B	94	ILE
1	B	142	SER
1	B	144	SER
1	B	160	ILE
1	B	166	SER
1	B	167	SER
1	B	173	LEU
1	B	185	VAL
1	B	213	GLU
1	C	5	GLN
1	C	35	LEU
1	C	36	GLU
1	C	37	GLU
1	C	93	SER
1	C	135	GLU
1	C	151	SER
1	C	173	LEU
1	C	179	GLN
1	C	215	THR
1	C	229	LYS
1	C	237	TRP
1	D	5	GLN
1	D	59	SER
1	D	101	GLN
1	D	144	SER
1	D	165	GLU
1	D	167	SER
1	D	173	LEU

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Mol	Chain	Res	Type
1	D	185	VAL
1	D	187	ASN
1	D	207	SER
1	D	213	GLU
1	D	215	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	102	ASN
1	A	187	ASN
1	A	210	GLN
1	B	5	GLN
1	B	102	ASN
1	C	4	ASN
1	C	46	GLN
1	C	101	GLN
1	C	119	HIS
1	D	102	ASN
1	D	119	HIS
1	D	155	HIS
1	D	187	ASN
1	D	210	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	235/244 (96%)	0.25	22 (9%) 11 16	13, 26, 42, 45	0
1	B	232/244 (95%)	0.03	6 (2%) 59 68	11, 23, 36, 40	0
1	C	234/244 (95%)	0.09	10 (4%) 39 48	12, 22, 38, 42	0
1	D	230/244 (94%)	0.08	15 (6%) 22 30	15, 25, 36, 41	0
All	All	931/976 (95%)	0.11	53 (5%) 27 36	11, 24, 38, 45	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	VAL	7.2
1	A	137	GLN	5.4
1	B	143	ILE	4.7
1	D	92	ASP	4.7
1	A	141	ALA	4.1
1	D	167	SER	4.1
1	A	34	LEU	4.1
1	D	173	LEU	4.0
1	A	40	PHE	3.9
1	D	134	PRO	3.4
1	C	36	GLU	3.2
1	A	193	LEU	3.0
1	A	38	SER	3.0
1	D	159	ASP	2.9
1	A	138	THR	2.9
1	C	132	GLU	2.9
1	B	135	GLU	2.9
1	A	39	ALA	2.9
1	D	143	ILE	2.8
1	C	115	LEU	2.8
1	A	132	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	158	THR	2.7
1	A	136	PHE	2.7
1	D	166	SER	2.7
1	A	104	TYR	2.7
1	D	171	ALA	2.6
1	B	166	SER	2.5
1	C	193	LEU	2.5
1	B	236	LEU	2.5
1	C	117	LEU	2.5
1	D	52	LEU	2.5
1	A	135	GLU	2.5
1	B	95	HIS	2.5
1	B	142	SER	2.4
1	A	71	LEU	2.4
1	A	101	GLN	2.3
1	A	92	ASP	2.3
1	C	74	LEU	2.3
1	D	236	LEU	2.2
1	A	166	SER	2.2
1	A	194	SER	2.2
1	A	13	LEU	2.2
1	C	163	PHE	2.2
1	C	92	ASP	2.1
1	C	137	GLN	2.1
1	D	133	LYS	2.1
1	A	158	THR	2.0
1	D	101	GLN	2.0
1	A	196	LEU	2.0
1	A	201	ASN	2.0
1	D	135	GLU	2.0
1	C	71	LEU	2.0
1	D	89	SER	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 [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	CL	B	242	1/1	0.99	0.08	-2.89	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.