



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:55 PM GMT

PDB ID : 1VQQ
Title : Structure of Penicillin binding protein 2a from methicillin resistant Staphylococcus aureus strain 27r at 1.80 Å resolution.
Authors : Lim, D.; Strynadka, N.C.J.
Deposited on : 2004-12-17
Resolution : 1.80 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

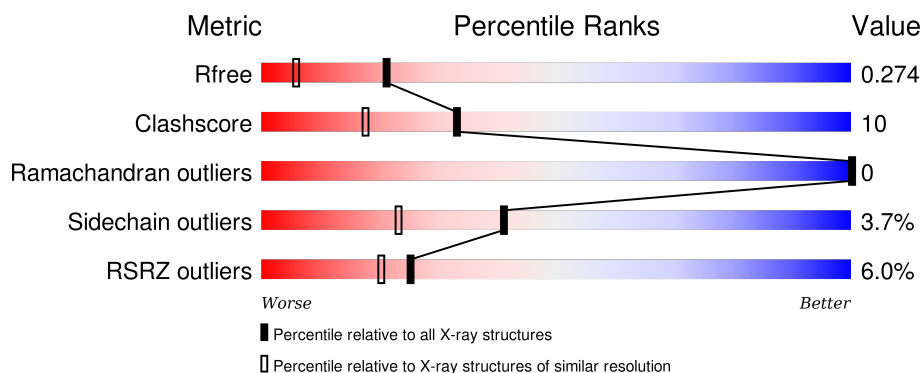
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


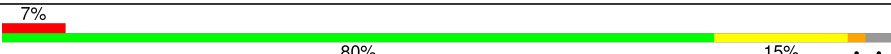
The reported resolution of this entry is 1.80 Å.

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}	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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	646	 4% 76% 20% . .
1	B	646	 7% 80% 15% . .

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 10644 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 penicillin-binding protein mecA, low-affinity.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	635	Total	C	N	O	S	0	0	0
			5102	3218	860	1009	15			
1	B	625	Total	C	N	O	S	0	0	0
			5023	3171	843	994	15			

- Molecule 2 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	5	Total	Cd	0	0
			5	5		
2	A	2	Total	Cd	0	0
			2	2		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total	Cl	0	0
			3	3		
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	246	Total	O	0	0
			246	246		
4	B	262	Total	O	0	0
			262	262		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.87Å 100.61Å 186.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.92 – 1.80 24.92 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.3 (24.92-1.80) 97.4 (24.92-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 1.80Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.237 , 0.274 0.237 , 0.274	Depositor DCC
R_{free} test set	6974 reflections (5.08%)	DCC
Wilson B-factor (Å ²)	23.9	Xtriage
Anisotropy	0.804	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 48.6	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	0 of 137299 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10644	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% of the height of the origin peak. No significant pseudotranslation is detected.*

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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.47	0/5186	0.70	2/6971 (0.0%)
1	B	0.46	0/5105	0.69	1/6862 (0.0%)
All	All	0.47	0/10291	0.69	3/13833 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	252	LEU	CA-CB-CG	5.83	128.72	115.30
1	A	174	VAL	N-CA-C	-5.42	96.35	111.00
1	B	174	VAL	N-CA-C	-5.06	97.35	111.00

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	5102	0	5099	122	0
1	B	5023	0	5008	88	0
2	A	2	0	0	0	0
2	B	5	0	0	0	0
3	A	1	0	0	0	0
3	B	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	246	0	0	5	0
4	B	262	0	0	6	0
All	All	10644	0	10107	209	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 10.

All (209) 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:87:LYS:H	1:A:87:LYS:HE3	1.14	1.08
1:B:267:LYS:H	1:B:267:LYS:HD3	1.21	1.06
1:A:611:GLY:HA3	1:A:635:ASP:OD1	1.56	1.04
1:A:436:LYS:HD3	1:A:436:LYS:H	1.23	1.03
1:B:267:LYS:HD3	1:B:267:LYS:N	1.89	0.86
1:A:87:LYS:H	1:A:87:LYS:CE	1.92	0.82
1:B:87:LYS:HD3	1:B:87:LYS:N	1.93	0.82
1:A:138:LYS:H	1:A:138:LYS:HD2	1.43	0.81
1:A:122:MET:HG3	1:A:124:LYS:NZ	1.95	0.81
1:B:226:ASP:O	1:B:230:LYS:HG2	1.82	0.79
1:A:28:LYS:HD2	1:A:28:LYS:N	1.97	0.79
1:A:87:LYS:HE3	1:A:87:LYS:N	1.96	0.78
1:B:510:ASN:HB3	1:B:513:LEU:HD12	1.65	0.77
1:A:436:LYS:CD	1:A:436:LYS:H	1.96	0.77
1:A:70:TYR:HB3	1:A:75:VAL:CG2	2.15	0.76
1:A:138:LYS:CD	1:A:138:LYS:H	1.99	0.74
1:B:387:LYS:HE2	1:B:387:LYS:HA	1.69	0.73
1:A:70:TYR:HB3	1:A:75:VAL:HG21	1.69	0.73
1:A:557:VAL:HG11	1:A:560:LYS:HG2	1.71	0.73
1:A:112:VAL:CG1	1:A:134:PRO:HB3	2.19	0.72
1:A:485:LYS:HE3	4:A:1170:HOH:O	1.90	0.72
1:A:613:GLN:HG2	1:A:641:MET:SD	2.30	0.71
1:B:256:VAL:HG22	4:B:1059:HOH:O	1.90	0.71
1:B:426:LYS:HG2	1:B:452:ASN:OD1	1.91	0.70
1:B:267:LYS:HA	1:B:270:LYS:HE3	1.73	0.70
1:B:122:MET:HG3	1:B:124:LYS:HE2	1.73	0.70
1:A:536:SER:HA	1:A:628:MET:HE3	1.73	0.70
1:A:77:ASP:HB2	1:A:102:LYS:HD2	1.74	0.68
1:B:138:LYS:H	1:B:138:LYS:HE2	1.58	0.68
1:B:220:MET:HE1	1:B:224:LEU:HD23	1.75	0.68
1:B:378:GLU:HG3	1:B:382:LYS:NZ	2.08	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112:VAL:CG1	1:B:134:PRO:HB3	2.25	0.67
1:B:603:LEU:HD23	1:B:604:LYS:N	2.11	0.66
1:A:268:GLU:HG3	1:A:269:TYR:CD1	2.31	0.65
1:A:133:ILE:HB	1:A:136:MET:CE	2.27	0.65
1:B:167:THR:HG23	1:B:237:GLU:HG3	1.80	0.64
1:A:176:LYS:HG3	1:A:208:ASP:O	1.98	0.64
1:B:112:VAL:HG13	1:B:134:PRO:HB3	1.80	0.64
1:A:171:ILE:HD11	1:A:217:VAL:HG13	1.79	0.64
1:A:436:LYS:N	1:A:436:LYS:HD3	2.06	0.63
1:A:614:ILE:HD11	1:A:634:LYS:HG3	1.79	0.63
1:A:171:ILE:HD11	1:A:217:VAL:CG1	2.29	0.63
1:A:176:LYS:HD2	1:B:113:GLN:NE2	2.15	0.62
1:B:627:MET:O	1:B:627:MET:HG3	1.98	0.62
1:A:420:ASP:OD1	4:A:1011:HOH:O	2.16	0.62
1:B:100:LYS:HG2	1:B:109:ASP:OD2	2.00	0.62
1:A:138:LYS:N	1:A:138:LYS:HD2	2.12	0.61
1:A:598:SER:HB3	1:A:617:PHE:CD1	2.36	0.61
1:A:602:GLU:OE1	1:A:613:GLN:NE2	2.29	0.61
1:B:29:GLU:OE1	1:B:123:TRP:HD1	1.84	0.61
1:A:408:LEU:HD22	1:A:534:ILE:HG21	1.83	0.61
1:B:99:TYR:HD1	1:B:112:VAL:HG11	1.66	0.60
1:A:46:TYR:O	1:A:54:LYS:HD3	2.01	0.60
1:B:186:ILE:HD13	1:B:233:LEU:HD21	1.84	0.60
1:B:226:ASP:HB3	1:B:230:LYS:HE3	1.83	0.60
1:B:220:MET:CE	1:B:224:LEU:HD23	2.32	0.60
1:A:133:ILE:HB	1:A:136:MET:HE2	1.84	0.60
1:A:261:SER:O	1:A:265:LYS:HE3	2.02	0.59
1:B:261:SER:HA	1:B:264:LEU:HD12	1.84	0.59
1:A:658:GLU:HB2	1:A:662:LYS:HG2	1.85	0.59
1:B:50:SER:O	1:B:54:LYS:HD2	2.02	0.59
1:A:503:ILE:O	1:A:524:ILE:HG12	2.04	0.58
1:B:277:VAL:HG23	4:B:1057:HOH:O	2.04	0.58
1:A:136:MET:HE2	1:A:142:ILE:HD11	1.85	0.58
1:A:290:LYS:HG3	4:A:1144:HOH:O	2.03	0.58
1:B:260:ASN:O	1:B:264:LEU:HG	2.05	0.57
1:B:449:VAL:HG23	1:B:449:VAL:O	2.04	0.57
1:A:89:SER:OG	1:A:92:LYS:HB3	2.05	0.56
1:A:612:ARG:HH11	1:A:612:ARG:HG3	1.69	0.56
1:A:70:TYR:HB3	1:A:75:VAL:HG22	1.87	0.56
1:A:425:TYR:OH	1:A:473:GLU:HG3	2.06	0.56
1:B:86:LYS:HG2	1:B:87:LYS:N	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:378:GLU:HG3	1:B:382:LYS:HZ3	1.70	0.56
1:B:125:LEU:HD13	1:B:127:TRP:N	2.21	0.56
1:A:28:LYS:CD	1:A:28:LYS:N	2.69	0.56
1:A:112:VAL:HG11	1:A:134:PRO:HB3	1.86	0.55
1:B:554:LYS:HG2	4:B:1196:HOH:O	2.06	0.55
1:A:219:LYS:HD2	1:A:219:LYS:H	1.71	0.55
1:A:277:VAL:HG23	4:A:1055:HOH:O	2.06	0.55
1:A:136:MET:CE	1:A:142:ILE:HD11	2.38	0.54
1:A:290:LYS:HB2	1:A:324:ILE:HD11	1.89	0.54
1:B:82:ASP:O	1:B:82:ASP:OD1	2.26	0.54
1:A:460:GLU:OE1	1:A:581:LYS:HE3	2.07	0.54
1:B:221:ASP:OD2	1:B:224:LEU:HB2	2.08	0.53
1:A:658:GLU:HG3	1:A:662:LYS:HD3	1.90	0.53
1:A:302:VAL:CG1	1:A:307:ASN:HA	2.39	0.53
1:A:122:MET:HG3	1:A:124:LYS:HZ1	1.71	0.53
1:B:484:LYS:NZ	1:B:484:LYS:HB2	2.22	0.53
1:A:614:ILE:CD1	1:A:634:LYS:HA	2.39	0.52
1:B:82:ASP:O	1:B:84:LYS:HG3	2.09	0.52
1:A:639:LYS:HD3	1:A:644:TYR:CE1	2.44	0.52
1:A:298:ARG:HD3	1:A:315:GLU:OE1	2.10	0.52
1:A:189:GLU:HG2	1:A:227:PHE:CE1	2.45	0.52
1:A:614:ILE:CD1	1:A:634:LYS:HG3	2.39	0.52
1:B:87:LYS:HD3	1:B:87:LYS:H	1.72	0.51
1:A:217:VAL:HG21	1:A:224:LEU:HD13	1.92	0.51
1:B:86:LYS:CG	1:B:87:LYS:N	2.73	0.51
1:B:424:SER:OG	1:B:452:ASN:HB3	2.10	0.51
1:A:64:GLU:O	1:A:67:ILE:HB	2.10	0.51
1:B:99:TYR:HB2	1:B:112:VAL:CG2	2.41	0.50
1:B:386:ASP:HB3	1:B:390:PRO:HD3	1.92	0.50
1:B:516:ASP:HA	1:B:519:TYR:CE2	2.46	0.50
1:A:70:TYR:CB	1:A:75:VAL:HG21	2.40	0.50
1:A:268:GLU:HG3	1:A:269:TYR:CE1	2.47	0.50
1:A:598:SER:HB3	1:A:617:PHE:CE1	2.47	0.50
1:A:180:LYS:HA	1:A:183:TYR:CE1	2.47	0.50
1:B:565:LYS:HE2	4:B:1262:HOH:O	2.11	0.50
1:B:125:LEU:CD1	1:B:127:TRP:HA	2.42	0.49
1:B:658:GLU:HG3	1:B:662:LYS:HE2	1.94	0.49
1:A:60:VAL:HG13	1:A:64:GLU:OE1	2.12	0.49
1:B:587:ILE:HG12	1:B:587:ILE:O	2.12	0.49
1:B:390:PRO:HD2	4:B:1085:HOH:O	2.10	0.49
1:A:189:GLU:HG2	1:A:227:PHE:CZ	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:ILE:HB	1:A:136:MET:HE3	1.94	0.49
1:B:378:GLU:HG3	1:B:382:LYS:HZ1	1.78	0.49
1:A:220:MET:SD	1:A:224:LEU:HD23	2.52	0.49
1:A:262:GLU:CD	1:A:262:GLU:H	2.13	0.49
1:B:192:ILE:HD12	1:B:196:TYR:HD2	1.78	0.49
1:A:98:GLN:NE2	1:A:109:ASP:OD2	2.42	0.49
1:A:536:SER:HA	1:A:628:MET:CE	2.41	0.48
1:A:180:LYS:HA	1:A:183:TYR:CD1	2.48	0.48
1:B:86:LYS:CG	1:B:87:LYS:H	2.27	0.48
1:B:289:LYS:HB2	1:B:289:LYS:NZ	2.28	0.48
1:B:194:GLU:O	1:B:198:LYS:HG3	2.14	0.48
1:A:261:SER:HB2	1:A:262:GLU:OE1	2.14	0.48
1:A:352:PRO:HA	1:A:536:SER:HB2	1.95	0.48
1:A:277:VAL:HG23	1:A:277:VAL:O	2.14	0.48
1:B:369:TYR:HB2	1:B:370:PRO:HD3	1.96	0.48
1:B:191:SER:HB3	1:B:376:SER:HB3	1.96	0.47
1:B:604:LYS:HA	1:B:604:LYS:HE3	1.96	0.47
1:B:665:ASP:HB3	1:B:668:GLU:HB2	1.97	0.47
1:B:668:GLU:OXT	1:B:668:GLU:HG2	2.15	0.47
1:A:222:GLU:O	1:A:226:ASP:HB2	2.14	0.47
1:B:364:PRO:HG2	1:B:388:LYS:HD3	1.96	0.47
1:A:331:LYS:NZ	1:A:668:GLU:OXT	2.47	0.47
1:B:370:PRO:HB2	1:B:375:MET:HE2	1.97	0.47
1:A:166:GLY:HA3	1:A:242:ASN:HB2	1.97	0.46
1:A:471:ALA:HB1	1:A:514:LEU:HD22	1.97	0.46
1:B:138:LYS:H	1:B:138:LYS:CE	2.26	0.46
1:A:182:ASP:N	1:A:182:ASP:OD1	2.49	0.46
1:B:119:GLU:O	1:B:120:ASP:C	2.53	0.46
1:B:220:MET:HA	1:B:220:MET:HE2	1.97	0.46
1:B:290:LYS:HB2	1:B:324:ILE:HD11	1.98	0.46
1:A:173:ILE:CD1	1:A:214:LEU:HD11	2.45	0.46
1:A:187:ALA:HB1	1:A:192:ILE:O	2.16	0.46
1:A:197:ILE:O	1:A:201:MET:HG2	2.16	0.46
1:B:387:LYS:CE	1:B:387:LYS:HA	2.41	0.45
1:A:93:LYS:HE3	1:A:123:TRP:CZ2	2.51	0.45
1:B:510:ASN:CB	1:B:513:LEU:HD12	2.40	0.45
1:A:167:THR:CG2	1:A:237:GLU:HG3	2.47	0.45
1:B:407:ILE:O	1:B:411:MET:HG3	2.15	0.45
1:B:302:VAL:CG1	1:B:307:ASN:HA	2.47	0.45
1:A:262:GLU:OE1	1:A:262:GLU:N	2.40	0.45
1:A:614:ILE:HD12	1:A:634:LYS:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:566:GLU:HG2	4:B:1188:HOH:O	2.16	0.45
1:B:363:THR:HA	1:B:364:PRO:C	2.37	0.45
1:A:297:TYR:CE1	1:A:316:LYS:HD3	2.51	0.45
1:A:100:LYS:HA	1:A:108:ILE:O	2.17	0.45
1:B:54:LYS:HB3	1:B:54:LYS:HE2	1.73	0.44
1:A:595:ILE:HD11	1:A:620:TYR:CZ	2.52	0.44
1:A:39:ASP:O	1:A:40:LYS:HB2	2.17	0.44
1:B:245:LEU:HD13	1:B:334:LYS:HG3	1.99	0.44
1:B:267:LYS:H	1:B:267:LYS:CD	2.08	0.44
1:A:557:VAL:HG11	1:A:560:LYS:CG	2.45	0.44
1:B:125:LEU:HD11	1:B:127:TRP:HA	2.00	0.44
1:B:658:GLU:CD	1:B:662:LYS:HG2	2.38	0.44
1:B:267:LYS:HG2	1:B:268:GLU:HG2	1.99	0.43
1:A:112:VAL:CG1	1:A:134:PRO:CB	2.94	0.43
1:A:490:GLU:OE1	1:A:559:LYS:NZ	2.39	0.43
1:A:138:LYS:CE	1:A:138:LYS:H	2.30	0.43
1:A:559:LYS:HB3	1:A:562:ILE:HD11	2.00	0.43
1:A:154:ILE:HB	1:A:163:ALA:HB3	2.00	0.43
1:A:415:ASN:HD21	1:A:485:LYS:HE2	1.84	0.43
1:A:363:THR:HA	1:A:364:PRO:C	2.38	0.43
1:A:498:PHE:CE2	1:A:529:VAL:HG21	2.53	0.43
1:A:658:GLU:CG	1:A:662:LYS:HD3	2.49	0.43
1:A:99:TYR:HD1	1:A:112:VAL:HG11	1.84	0.43
1:A:298:ARG:HG2	1:A:300:THR:HG23	2.01	0.43
1:A:70:TYR:CG	1:A:75:VAL:HG21	2.54	0.43
1:A:93:LYS:HG3	1:A:123:TRP:CH2	2.54	0.42
1:B:167:THR:CG2	1:B:237:GLU:HG3	2.47	0.42
1:A:112:VAL:HG12	1:A:134:PRO:CB	2.49	0.42
1:A:453:ILE:HG23	1:A:457:GLN:CG	2.49	0.42
1:B:51:TYR:O	1:B:54:LYS:HG2	2.20	0.42
1:A:645:ASN:HD22	1:A:645:ASN:H	1.67	0.42
1:B:430:LYS:HG3	1:B:448:VAL:CG2	2.49	0.42
1:A:74:GLY:O	1:A:76:LYS:HD3	2.19	0.42
1:A:50:SER:O	1:A:54:LYS:HG3	2.20	0.42
1:B:82:ASP:OD1	1:B:84:LYS:HD2	2.20	0.42
1:A:415:ASN:ND2	1:A:485:LYS:HE2	2.35	0.41
1:B:154:ILE:HB	1:B:163:ALA:HB3	2.02	0.41
1:A:435:ASP:HB2	1:A:436:LYS:HD3	2.02	0.41
1:A:138:LYS:HB3	1:A:138:LYS:HE3	1.86	0.41
1:A:112:VAL:HG12	1:A:134:PRO:HB3	2.01	0.41
1:A:502:GLN:O	1:A:502:GLN:HG3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:LYS:N	1:A:265:LYS:HD3	2.36	0.41
1:B:259:ILE:HG12	1:B:260:ASN:N	2.35	0.41
1:A:222:GLU:OE2	1:A:222:GLU:HA	2.20	0.41
1:B:633:VAL:CG2	1:B:645:ASN:HD21	2.34	0.41
1:B:367:ASP:OD1	1:B:369:TYR:CD1	2.74	0.41
1:B:424:SER:HG	1:B:452:ASN:HB3	1.84	0.41
1:A:228:ALA:HA	1:A:233:LEU:HB2	2.02	0.41
1:A:42:PHE:HB3	1:A:63:THR:HA	2.03	0.41
1:B:327:THR:OG1	1:B:549:LEU:HA	2.22	0.40
1:A:663:LYS:HE2	4:A:1216:HOH:O	2.20	0.40
1:A:600:THR:HG21	1:A:641:MET:HB3	2.03	0.40
1:B:186:ILE:CD1	1:B:233:LEU:HD21	2.50	0.40
1:A:91:ASN:ND2	1:A:118:LYS:HB3	2.36	0.40
1:A:491:ASP:OD1	1:A:500:ASN:ND2	2.54	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	629/646 (97%)	612 (97%)	17 (3%)	0	100	100
1	B	615/646 (95%)	595 (97%)	20 (3%)	0	100	100
All	All	1244/1292 (96%)	1207 (97%)	37 (3%)	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	567/576 (98%)	546 (96%)	21 (4%)	41	23
1	B	557/576 (97%)	536 (96%)	21 (4%)	40	22
All	All	1124/1152 (98%)	1082 (96%)	42 (4%)	41	23

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LYS
1	A	38	GLU
1	A	76	LYS
1	A	77	ASP
1	A	87	LYS
1	A	99	TYR
1	A	125	LEU
1	A	138	LYS
1	A	141	SER
1	A	156	ASP
1	A	182	ASP
1	A	204	ASN
1	A	219	LYS
1	A	252	LEU
1	A	352	PRO
1	A	391	LEU
1	A	419	LEU
1	A	436	LYS
1	A	513	LEU
1	A	514	LEU
1	A	554	LYS
1	B	54	LYS
1	B	87	LYS
1	B	99	TYR
1	B	102	LYS
1	B	112	VAL
1	B	120	ASP
1	B	122	MET
1	B	156	ASP
1	B	252	LEU
1	B	267	LYS
1	B	268	GLU
1	B	377	ASN

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Mol	Chain	Res	Type
1	B	391	LEU
1	B	392	LEU
1	B	419	LEU
1	B	446	TYR
1	B	514	LEU
1	B	532	LEU
1	B	570	LEU
1	B	627	MET
1	B	662	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	ASN
1	A	81	GLN
1	A	91	ASN
1	A	113	GLN
1	A	115	ASN
1	A	203	GLN
1	A	207	GLN
1	A	266	GLN
1	A	415	ASN
1	A	645	ASN
1	B	32	ASN
1	B	81	GLN
1	B	111	ASN
1	B	377	ASN
1	B	433	GLN
1	B	632	ASN
1	B	645	ASN

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 11 are 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 [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	635/646 (98%)	0.27	27 (4%) 39 32	17, 31, 51, 62	0
1	B	625/646 (96%)	0.32	48 (7%) 16 13	19, 31, 53, 62	0
All	All	1260/1292 (97%)	0.30	75 (5%) 25 20	17, 31, 52, 62	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	223	TYR	7.4
1	B	223	TYR	6.4
1	A	120	ASP	5.4
1	A	611	GLY	5.2
1	B	120	ASP	4.8
1	B	261	SER	4.3
1	B	204	ASN	4.3
1	A	222	GLU	4.2
1	B	603	LEU	4.0
1	B	267	LYS	4.0
1	B	28	LYS	3.8
1	B	51	TYR	3.7
1	A	204	ASN	3.5
1	A	226	ASP	3.5
1	B	264	LEU	3.3
1	B	122	MET	3.2
1	B	274	ASP	3.1
1	B	272	TYR	3.1
1	A	509	ASP	3.1
1	B	86	LYS	3.1
1	B	76	LYS	3.0
1	B	85	ILE	3.0
1	A	508	LEU	3.0
1	A	229	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	133	ILE	3.0
1	B	266	GLN	2.9
1	A	267	LYS	2.9
1	B	604	LYS	2.9
1	B	121	GLY	2.9
1	A	87	LYS	2.8
1	B	123	TRP	2.8
1	B	270	LYS	2.8
1	A	179	SER	2.8
1	B	265	LYS	2.8
1	B	271	GLY	2.8
1	A	360	LEU	2.7
1	B	273	LYS	2.7
1	B	262	GLU	2.6
1	A	184	LYS	2.6
1	A	185	ALA	2.6
1	B	87	LYS	2.6
1	B	222	GLU	2.6
1	B	252	LEU	2.5
1	A	274	ASP	2.5
1	A	612	ARG	2.5
1	B	532	LEU	2.5
1	B	205	TRP	2.5
1	B	94	ARG	2.4
1	B	269	TYR	2.4
1	B	29	GLU	2.4
1	A	272	TYR	2.3
1	B	131	VAL	2.3
1	B	268	GLU	2.3
1	B	531	ILE	2.3
1	A	505	ASN	2.3
1	B	513	LEU	2.3
1	A	84	LYS	2.3
1	B	662	LYS	2.3
1	A	122	MET	2.3
1	B	27	ASP	2.2
1	B	132	ILE	2.2
1	A	262	GLU	2.2
1	B	408	LEU	2.2
1	A	85	ILE	2.1
1	B	37	ILE	2.1
1	B	230	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	407	ILE	2.1
1	B	534	ILE	2.1
1	A	532	LEU	2.1
1	A	407	ILE	2.1
1	B	509	ASP	2.1
1	B	259	ILE	2.0
1	A	220	MET	2.0
1	A	273	LYS	2.0
1	B	184	LYS	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 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(Å ²)	Q<0.9
3	CL	A	1009	1/1	0.98	0.10	0.86	27,27,27,27	0
3	CL	B	1011	1/1	0.98	0.09	-0.22	27,27,27,27	0
2	CD	B	1001	1/1	1.00	0.08	-0.55	25,25,25,25	0
2	CD	B	1002	1/1	1.00	0.08	-0.62	24,24,24,24	0
2	CD	A	1005	1/1	1.00	0.07	-1.19	27,27,27,27	0
2	CD	B	1003	1/1	0.99	0.09	-1.22	27,27,27,27	0
3	CL	B	1010	1/1	0.97	0.06	-1.65	29,29,29,29	0
3	CL	B	1008	1/1	0.98	0.06	-1.66	27,27,27,27	0
2	CD	B	1007	1/1	0.99	0.04	-2.07	31,31,31,31	0
2	CD	A	1004	1/1	0.99	0.05	-2.15	50,50,50,50	0
2	CD	B	1006	1/1	0.93	0.08	-	57,57,57,57	0

6.5 Other polymers

There are no such residues in this entry.