



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 01:07 PM UTC

PDB ID : 4XAK / pdb_00004xak
Title : Crystal structure of potent neutralizing antibody m336 in complex with MERS Co-V RBD
Authors : Zhou, T.; Dimtrov, D.S.; Ying, T.
Deposited on : 2014-12-15
Resolution : 2.45 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

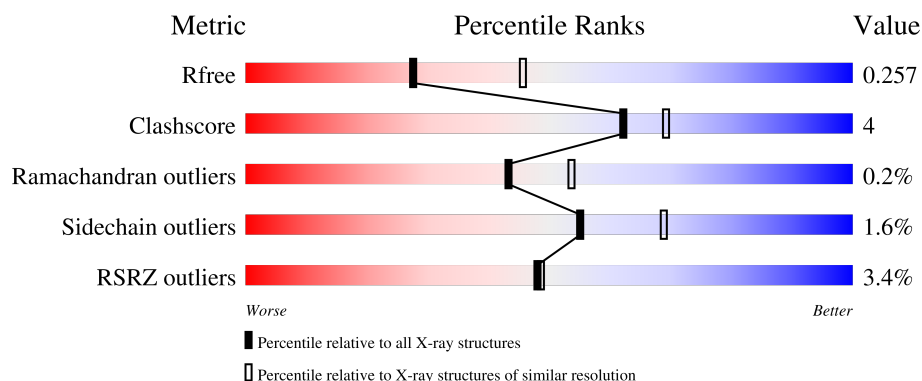
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

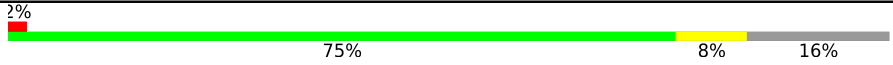
The reported resolution of this entry is 2.45 Å.

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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	252	
1	B	252	
2	D	252	
2	H	252	
3	E	214	

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Mol	Chain	Length	Quality of chain
3	L	214	% 90% 9%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10049 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	211	Total	C	N	O	S	0	0	0
			1636	1046	259	320	11			
1	B	211	Total	C	N	O	S	0	0	0
			1636	1046	259	320	11			

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	602	GLY	-	expression tag	UNP K9N5Q8
A	603	SER	-	expression tag	UNP K9N5Q8
A	604	LEU	-	expression tag	UNP K9N5Q8
A	605	GLU	-	expression tag	UNP K9N5Q8
A	606	VAL	-	expression tag	UNP K9N5Q8
A	607	LEU	-	expression tag	UNP K9N5Q8
A	608	PHE	-	expression tag	UNP K9N5Q8
A	609	GLN	-	expression tag	UNP K9N5Q8
A	610	GLY	-	expression tag	UNP K9N5Q8
A	611	PRO	-	expression tag	UNP K9N5Q8
A	612	GLY	-	expression tag	UNP K9N5Q8
A	613	HIS	-	expression tag	UNP K9N5Q8
A	614	HIS	-	expression tag	UNP K9N5Q8
A	615	HIS	-	expression tag	UNP K9N5Q8
A	616	HIS	-	expression tag	UNP K9N5Q8
A	617	HIS	-	expression tag	UNP K9N5Q8
A	618	HIS	-	expression tag	UNP K9N5Q8
B	602	GLY	-	expression tag	UNP K9N5Q8
B	603	SER	-	expression tag	UNP K9N5Q8
B	604	LEU	-	expression tag	UNP K9N5Q8
B	605	GLU	-	expression tag	UNP K9N5Q8
B	606	VAL	-	expression tag	UNP K9N5Q8
B	607	LEU	-	expression tag	UNP K9N5Q8
B	608	PHE	-	expression tag	UNP K9N5Q8
B	609	GLN	-	expression tag	UNP K9N5Q8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	610	GLY	-	expression tag	UNP K9N5Q8
B	611	PRO	-	expression tag	UNP K9N5Q8
B	612	GLY	-	expression tag	UNP K9N5Q8
B	613	HIS	-	expression tag	UNP K9N5Q8
B	614	HIS	-	expression tag	UNP K9N5Q8
B	615	HIS	-	expression tag	UNP K9N5Q8
B	616	HIS	-	expression tag	UNP K9N5Q8
B	617	HIS	-	expression tag	UNP K9N5Q8
B	618	HIS	-	expression tag	UNP K9N5Q8

- Molecule 2 is a protein called Heavy chain of neutralizing antibody m336.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	227	Total	C	N	O	S	0	0	0
			1664	1045	279	331	9			
2	D	218	Total	C	N	O	S	0	0	0
			1610	1016	269	316	9			

- Molecule 3 is a protein called Light chain of neutralizing antibody m336.

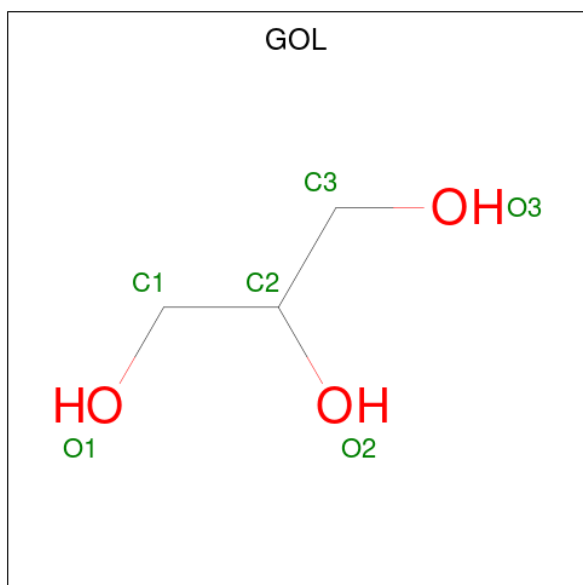
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	212	Total	C	N	O	S	0	0	0
			1616	1010	274	328	4			
3	E	207	Total	C	N	O	S	0	0	0
			1583	991	268	320	4			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	L	1	Total	C	O	0	0
			6	3	3		
5	L	1	Total	C	O	0	0
			6	3	3		

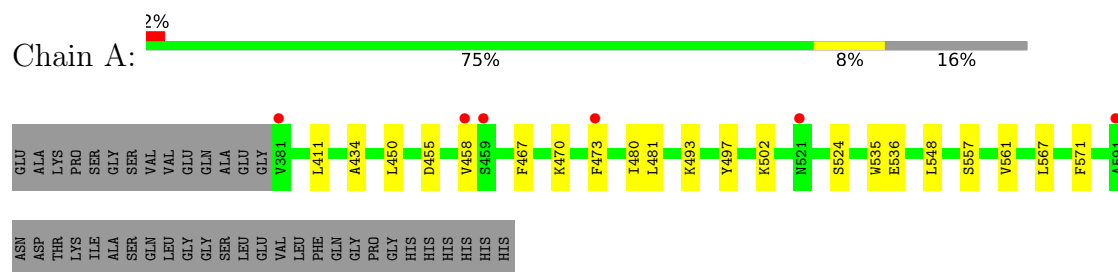
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	48	Total	O	0	0
			48	48		
6	H	56	Total	O	0	0
			56	56		
6	L	79	Total	O	0	0
			79	79		
6	B	31	Total	O	0	0
			31	31		
6	D	11	Total	O	0	0
			11	11		
6	E	11	Total	O	0	0
			11	11		

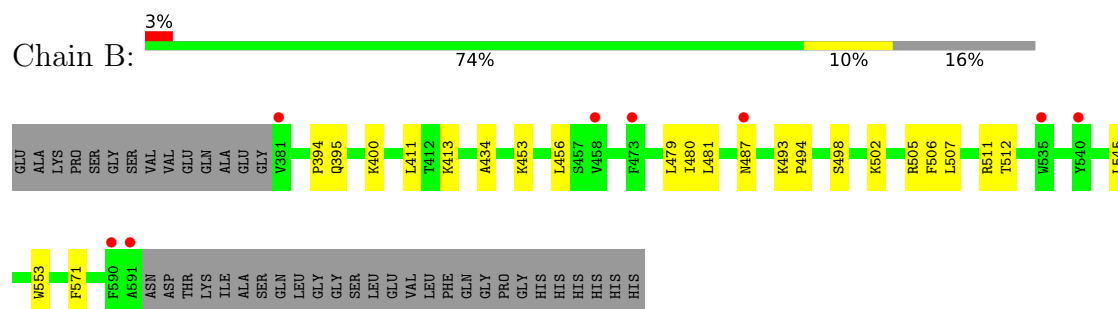
3 Residue-property plots [i](#)

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.

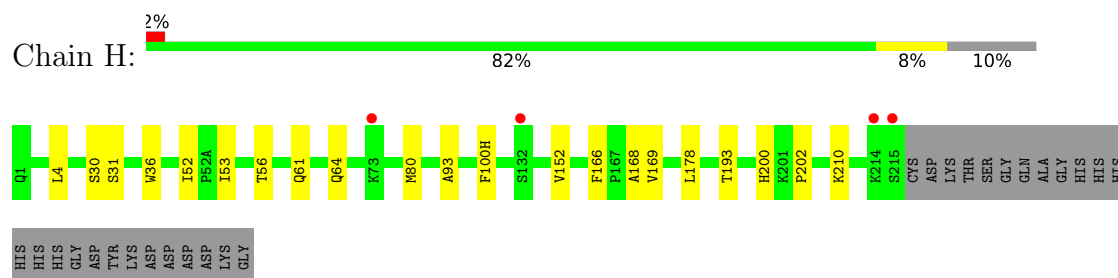
• Molecule 1: Spike glycoprotein



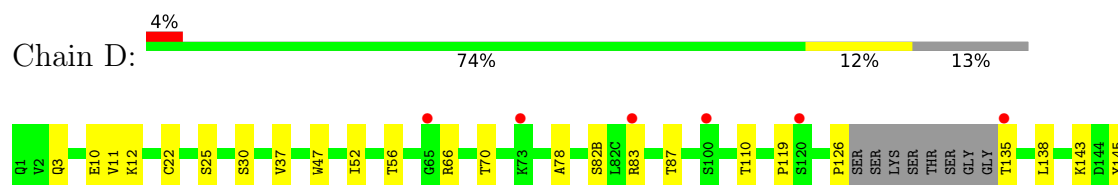
• Molecule 1: Spike glycoprotein

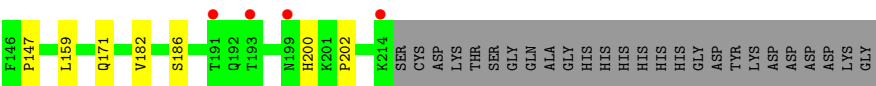


• Molecule 2: Heavy chain of neutralizing antibody m336

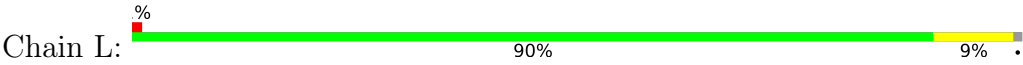


• Molecule 2: Heavy chain of neutralizing antibody m336

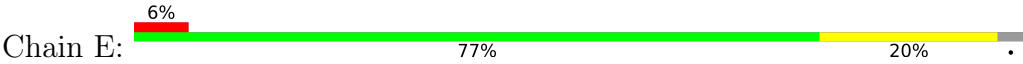




● Molecule 3: Light chain of neutralizing antibody m336



● Molecule 3: Light chain of neutralizing antibody m336



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	47.80Å 146.88Å 200.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.45 – 2.45 45.45 – 2.45	Depositor EDS
% Data completeness (in resolution range)	91.5 (45.45-2.45) 86.5 (45.45-2.45)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.45Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1702)	Depositor
R, R_{free}	0.198 , 0.249 0.207 , 0.257	Depositor DCC
R_{free} test set	2480 reflections (4.65%)	wwPDB-VP
Wilson B-factor (Å ²)	43.2	Xtriage
Anisotropy	0.203	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10049	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% 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

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

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	0.27	0/1677	0.65	0/2289
1	B	0.27	0/1677	0.66	0/2289
2	D	0.25	0/1646	0.66	1/2239 (0.0%)
2	H	0.28	0/1701	0.68	1/2313 (0.0%)
3	E	0.26	0/1615	0.70	1/2190 (0.0%)
3	L	0.28	0/1649	0.68	0/2238
All	All	0.27	0/9965	0.67	3/13558 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	30	SER	CB-CA-C	-5.33	110.40	116.54
2	D	30	SER	CB-CA-C	-5.15	110.62	116.54
3	E	30	ARG	CB-CA-C	-5.05	110.36	117.23

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	1636	0	1590	10	0
1	B	1636	0	1590	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1610	0	1593	14	0
2	H	1664	0	1645	12	0
3	E	1583	0	1552	24	0
3	L	1616	0	1582	9	0
4	A	28	0	26	0	0
4	B	28	0	26	1	0
5	L	12	0	16	0	0
6	A	48	0	0	1	0
6	B	31	0	0	0	0
6	D	11	0	0	1	0
6	E	11	0	0	0	0
6	H	56	0	0	0	0
6	L	79	0	0	0	0
All	All	10049	0	9620	79	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 (79) 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)
2:D:135:THR:N	2:D:186:SER:HG	1.91	0.68
3:E:4:LEU:HD11	3:E:90:GLN:HB2	1.77	0.67
1:B:394:PRO:HG3	1:B:400:LYS:HG3	1.79	0.65
3:L:120:PRO:HD3	3:L:132:VAL:HG22	1.78	0.65
3:E:189:HIS:O	3:E:211:ARG:NH1	2.30	0.64
1:B:411:LEU:HD23	1:B:434:ALA:HB2	1.82	0.62
3:E:21:ILE:HD12	3:E:102:THR:HG21	1.83	0.61
1:B:506:PHE:HB3	1:B:553:TRP:HB2	1.82	0.60
2:D:52:ILE:HD12	2:D:56:THR:HB	1.84	0.60
1:A:497:TYR:HB2	1:A:561:VAL:HB	1.85	0.59
2:H:52:ILE:HD12	2:H:56:THR:HB	1.85	0.58
2:H:61:GLN:HA	2:H:64:GLN:HG3	1.85	0.58
1:B:480:ILE:HB	1:B:571:PHE:HB2	1.86	0.58
1:A:493:LYS:HG2	1:A:567:LEU:HB2	1.86	0.58
2:D:10:GLU:OE1	2:D:12:LYS:NZ	2.36	0.57
3:E:116:PHE:HB2	3:E:135:LEU:HB3	1.86	0.57
2:H:169:VAL:HG21	3:L:160:GLN:HB3	1.89	0.55
2:H:53:ILE:HD12	2:H:53:ILE:H	1.72	0.54
3:E:198:HIS:HB3	3:E:201:LEU:HG	1.89	0.54
3:E:115:VAL:O	3:E:207:LYS:NZ	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:200:HIS:CD2	2:H:202:PRO:HD2	2.44	0.52
2:D:66:ARG:NH1	2:D:82(B):SER:O	2.42	0.52
3:E:186:TYR:O	3:E:192:TYR:OH	2.28	0.52
3:E:37:GLN:HB2	3:E:47:LEU:HD11	1.91	0.51
3:L:39:LYS:HD3	3:L:84:ALA:HB2	1.93	0.51
1:A:470:LYS:NZ	6:A:834:HOH:O	2.44	0.50
3:L:37:GLN:HB2	3:L:47:LEU:HD11	1.93	0.50
2:D:126:PRO:HG3	2:D:138:LEU:HB3	1.94	0.50
2:H:36:TRP:CE2	2:H:80:MET:HB2	2.47	0.50
3:E:142:ARG:CZ	3:E:163:VAL:HG21	2.41	0.50
2:D:143:LYS:NZ	2:D:171:GLN:OE1	2.42	0.49
1:A:411:LEU:HD22	1:A:434:ALA:HB2	1.94	0.48
1:A:450:LEU:HD12	1:A:481:LEU:HD23	1.96	0.48
3:L:124:GLN:O	3:L:127:SER:OG	2.28	0.48
2:H:31:SER:HA	2:H:53:ILE:HD11	1.96	0.48
1:A:502:LYS:HB2	1:A:557:SER:HB3	1.96	0.48
3:E:166:GLN:NE2	3:E:171:SER:OG	2.46	0.48
2:H:168:ALA:HA	2:H:178:LEU:HB3	1.96	0.48
1:B:456:LEU:HG	1:B:479:LEU:HD21	1.96	0.47
2:D:119:PRO:HB3	2:D:145:TYR:HB3	1.97	0.47
3:E:140:TYR:CG	3:E:141:PRO:HA	2.50	0.46
3:E:35:TRP:HB2	3:E:48:ILE:HB	1.96	0.46
3:E:136:LEU:HB2	3:E:175:LEU:HB3	1.96	0.46
3:E:80:PRO:HA	3:E:83:PHE:HD2	1.80	0.46
2:D:3:GLN:HB2	2:D:25:SER:HB3	1.99	0.45
1:A:470:LYS:HE2	1:A:473:PHE:CZ	2.51	0.45
1:A:467:PHE:O	1:A:524:SER:HB2	2.16	0.45
2:H:93:ALA:HB1	2:H:100(H):PHE:HB3	1.99	0.45
2:D:200:HIS:CD2	2:D:202:PRO:HD2	2.52	0.45
2:H:168:ALA:HB2	2:H:178:LEU:HD23	1.99	0.45
2:D:22:CYS:HB3	2:D:78:ALA:HB3	1.99	0.44
3:E:35:TRP:CE2	3:E:73:LEU:HB2	2.53	0.44
3:E:90:GLN:OE1	3:E:93:SER:N	2.46	0.44
3:L:33:LEU:HD11	3:L:88:CYS:SG	2.58	0.44
2:D:11:VAL:HG21	2:D:147:PRO:HG3	2.00	0.44
3:E:80:PRO:HA	3:E:83:PHE:CD2	2.52	0.44
1:B:456:LEU:HD23	1:B:481:LEU:HD21	1.98	0.44
3:E:140:TYR:O	3:E:198:HIS:HE1	2.00	0.44
1:B:413:LYS:HA	4:B:701:NAG:H61	2.00	0.44
2:D:87:THR:HG23	2:D:110:THR:HA	1.99	0.43
2:H:166:PHE:CD2	3:L:164:THR:HG23	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:505:ARG:HH11	1:B:545:LEU:HD12	1.84	0.43
2:H:193:THR:HG23	2:H:210:LYS:HE3	2.00	0.42
1:B:502:LYS:HE2	1:B:502:LYS:HB3	1.91	0.42
3:L:122:ASP:O	3:L:126:LYS:HG2	2.20	0.42
3:E:90:GLN:HE21	3:E:90:GLN:HB3	1.66	0.42
3:E:140:TYR:CD1	3:E:141:PRO:HA	2.55	0.42
1:B:395:GLN:HG3	1:B:498:SER:HB2	2.00	0.41
1:B:493:LYS:HA	1:B:494:PRO:HD3	1.92	0.41
2:D:83:ARG:NE	6:D:309:HOH:O	2.53	0.41
3:E:82:ASP:O	3:E:86:TYR:OH	2.25	0.41
1:A:480:ILE:HB	1:A:571:PHE:HB2	2.02	0.41
1:A:535:TRP:CD1	1:A:536:GLU:HG2	2.55	0.41
3:E:24:ARG:NE	3:E:70:ASP:OD1	2.46	0.41
3:L:35:TRP:CE2	3:L:73:LEU:HB2	2.56	0.41
2:D:37:VAL:HG22	2:D:47:TRP:HA	2.03	0.41
3:E:16:GLY:HA2	3:E:77:SER:HB3	2.02	0.41
1:B:453:LYS:HE2	1:B:453:LYS:HB3	1.94	0.40
3:E:39:LYS:HG2	3:E:84:ALA:HB2	2.03	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	209/252 (83%)	202 (97%)	7 (3%)	0	100	100
1	B	209/252 (83%)	204 (98%)	5 (2%)	0	100	100
2	D	214/252 (85%)	199 (93%)	15 (7%)	0	100	100
2	H	225/252 (89%)	218 (97%)	7 (3%)	0	100	100
3	E	203/214 (95%)	185 (91%)	17 (8%)	1 (0%)	24	32
3	L	210/214 (98%)	201 (96%)	8 (4%)	1 (0%)	24	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1270/1436 (88%)	1209 (95%)	59 (5%)	2 (0%)	43	54

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	L	211	ARG
3	E	204	PRO

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	192/224 (86%)	189 (98%)	3 (2%)	55	69
1	B	192/224 (86%)	188 (98%)	4 (2%)	47	62
2	D	181/208 (87%)	178 (98%)	3 (2%)	53	67
2	H	188/208 (90%)	186 (99%)	2 (1%)	65	76
3	E	181/186 (97%)	177 (98%)	4 (2%)	45	60
3	L	184/186 (99%)	182 (99%)	2 (1%)	65	76
All	All	1118/1236 (90%)	1100 (98%)	18 (2%)	55	69

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	455	ASP
1	A	458	VAL
1	A	548	LEU
2	H	4	LEU
2	H	152	VAL
3	L	91	LEU
3	L	201	LEU
1	B	487	ASN
1	B	507	LEU
1	B	511	ARG

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Mol	Chain	Res	Type
1	B	512	THR
2	D	70	THR
2	D	159	LEU
2	D	182	VAL
3	E	17	ASP
3	E	54	LEU
3	E	146	VAL
3	E	211	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	475	ASN
1	A	486	HIS
1	A	516	GLN
2	H	3	GLN
3	L	79	GLN
3	L	155	GLN
2	D	164	HIS
3	E	155	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](#)

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	B	701	1	14,14,15	0.25	0	17,19,21	0.46	0
4	NAG	A	702	1	14,14,15	0.25	0	17,19,21	0.36	0
4	NAG	B	702	1	14,14,15	0.27	0	17,19,21	0.53	0
5	GOL	L	500	-	5,5,5	0.38	0	5,5,5	0.35	0
4	NAG	A	701	1	14,14,15	0.26	0	17,19,21	0.49	0
5	GOL	L	501	-	5,5,5	0.38	0	5,5,5	0.39	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	B	701	1	-	3/6/23/26	0/1/1/1
4	NAG	A	702	1	-	2/6/23/26	0/1/1/1
4	NAG	B	702	1	-	2/6/23/26	0/1/1/1
5	GOL	L	500	-	-	2/4/4/4	-
4	NAG	A	701	1	-	2/6/23/26	0/1/1/1
5	GOL	L	501	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	L	500	GOL	O1-C1-C2-O2
5	L	500	GOL	O1-C1-C2-C3
4	A	701	NAG	O5-C5-C6-O6
4	A	701	NAG	C4-C5-C6-O6
4	A	702	NAG	O5-C5-C6-O6
4	B	701	NAG	C8-C7-N2-C2
4	B	701	NAG	O7-C7-N2-C2
4	B	702	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
5	L	501	GOL	O1-C1-C2-C3
5	L	501	GOL	O1-C1-C2-O2
4	B	701	NAG	O5-C5-C6-O6
4	B	702	NAG	C4-C5-C6-O6
4	A	702	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	701	NAG	1	0

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	211/252 (83%)	0.09	6 (2%) 55 56	37, 51, 84, 116	0
1	B	211/252 (83%)	0.32	8 (3%) 44 44	39, 63, 106, 146	0
2	D	218/252 (86%)	0.73	10 (4%) 37 36	58, 83, 115, 142	0
2	H	227/252 (90%)	-0.13	4 (1%) 67 69	35, 47, 81, 115	0
3	E	207/214 (96%)	0.90	13 (6%) 26 23	64, 98, 128, 150	0
3	L	212/214 (99%)	-0.10	3 (1%) 73 75	32, 47, 71, 89	0
All	All	1286/1436 (89%)	0.30	44 (3%) 48 48	32, 62, 115, 150	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	65	GLY	3.9
1	B	381	VAL	3.8
1	A	458	VAL	3.6
1	B	591	ALA	3.6
3	E	76	SER	3.6
3	E	2	ILE	3.3
2	D	191	THR	3.2
3	E	150	VAL	3.1
3	E	80	PRO	3.1
1	B	590	PHE	3.0
2	D	83	ARG	3.0
3	E	191	VAL	3.0
1	B	535	TRP	2.9
1	A	473	PHE	2.9
2	H	215	SER	2.8
2	D	193	THR	2.8
3	E	157	GLY	2.7
2	H	214	LYS	2.6
1	A	381	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
3	E	156	SER	2.6
3	E	155	GLN	2.6
2	H	73	LYS	2.5
1	B	458	VAL	2.5
3	E	13	ALA	2.5
3	L	212	GLY	2.4
2	D	73	LYS	2.4
3	E	75	ILE	2.4
3	L	76	SER	2.4
1	B	487	ASN	2.3
1	A	459	SER	2.3
2	H	132	SER	2.3
2	D	199	ASN	2.2
3	E	62	PHE	2.2
1	A	521	ASN	2.2
1	A	591	ALA	2.2
2	D	135	THR	2.2
2	D	100	SER	2.2
3	L	88	CYS	2.2
1	B	473	PHE	2.2
1	B	540	TYR	2.1
2	D	120	SER	2.1
3	E	112	ALA	2.1
3	E	106	ILE	2.1
2	D	214	LYS	2.1

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 oligosaccharides in this entry.

6.4 Ligands ⓘ

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. 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	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	A	702	14/15	0.59	0.17	79,87,97,97	0
4	NAG	B	702	14/15	0.63	0.15	71,85,87,92	0
4	NAG	A	701	14/15	0.74	0.12	64,74,78,78	0
4	NAG	B	701	14/15	0.84	0.11	49,61,70,78	0
5	GOL	L	501	6/6	0.89	0.13	59,67,71,71	0
5	GOL	L	500	6/6	0.94	0.11	53,56,61,68	0

6.5 Other polymers [i](#)

There are no such residues in this entry.