



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 06:31 AM UTC

PDB ID : 7NXA / pdb_00007nxa
Title : Crystal structure of the receptor binding domain of SARS-CoV-2 B.1.351 variant Spike glycoprotein in complex with COVOX-222 and EY6A Fabs
Authors : Zhou, D.; Ren, J.; Stuart, D.
Deposited on : 2021-03-17
Resolution : 2.50 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

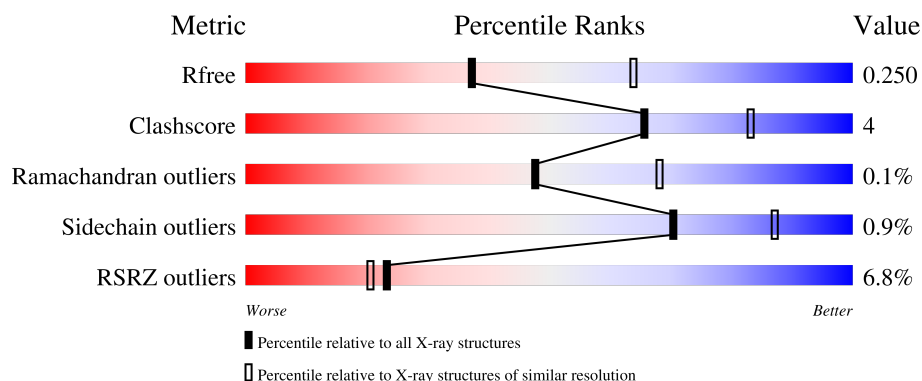
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	H	226	17% 83% 12% 5%
2	L	215	11% 90% 9%
3	E	205	3% 85% 9% 6%
4	A	224	% 87% 8% .
5	B	214	89% 10%

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 8206 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 EY6A Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	215	Total	C	N	O	S	0	0	0
			1637	1041	273	317	6			

- Molecule 2 is a protein called EY6A Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	214	Total	C	N	O	S	0	0	0
			1631	1019	272	335	5			

- Molecule 3 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	193	Total	C	N	O	S	0	0	0
			1532	984	255	285	8			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	324	GLU	-	expression tag	UNP P0DTC2
E	325	THR	-	expression tag	UNP P0DTC2
E	326	GLY	-	expression tag	UNP P0DTC2
E	327	HIS	-	expression tag	UNP P0DTC2
E	328	HIS	-	expression tag	UNP P0DTC2
E	329	HIS	-	expression tag	UNP P0DTC2
E	330	HIS	-	expression tag	UNP P0DTC2
E	331	HIS	-	expression tag	UNP P0DTC2
E	332	HIS	-	expression tag	UNP P0DTC2
E	417	ASN	LYS	variant	UNP P0DTC2
E	484	LYS	GLU	variant	UNP P0DTC2
E	501	TYR	ASN	variant	UNP P0DTC2
E	527	LYS	PRO	variant	UNP P0DTC2

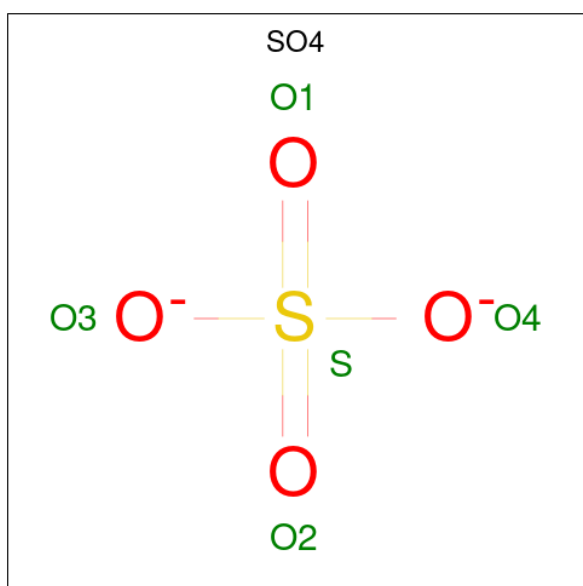
- Molecule 4 is a protein called COVOX-222 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	214	Total	C	N	O	S	0	0	0
			1577	995	263	313	6			

- Molecule 5 is a protein called COVOX-222 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	213	Total	C	N	O	S	0	1	0
			1637	1023	279	330	5			

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



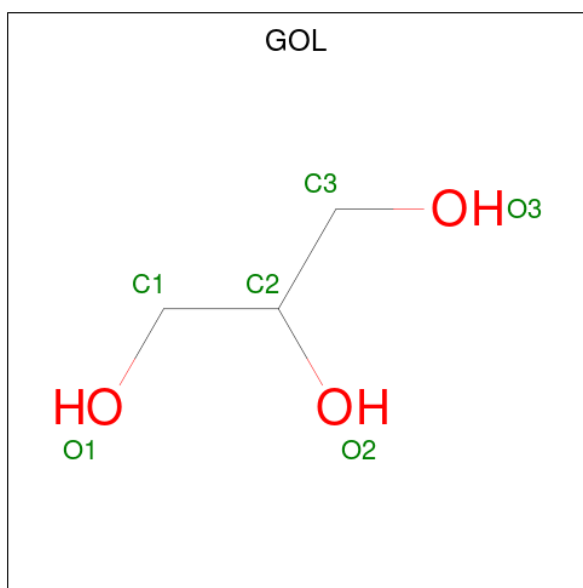
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	L	1	Total	O	S	0	0
			5	4	1		
6	L	1	Total	O	S	0	0
			5	4	1		
6	L	1	Total	O	S	0	0
			5	4	1		
6	L	1	Total	O	S	0	0
			5	4	1		
6	E	1	Total	O	S	0	0
			5	4	1		
6	E	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	E	1	Total	O	S	0	0
			5	4	1		
6	E	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	E	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	E	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 9 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	E	1	Total	C	O	0	0
			7	4	3		
9	E	1	Total	C	O	0	0
			7	4	3		

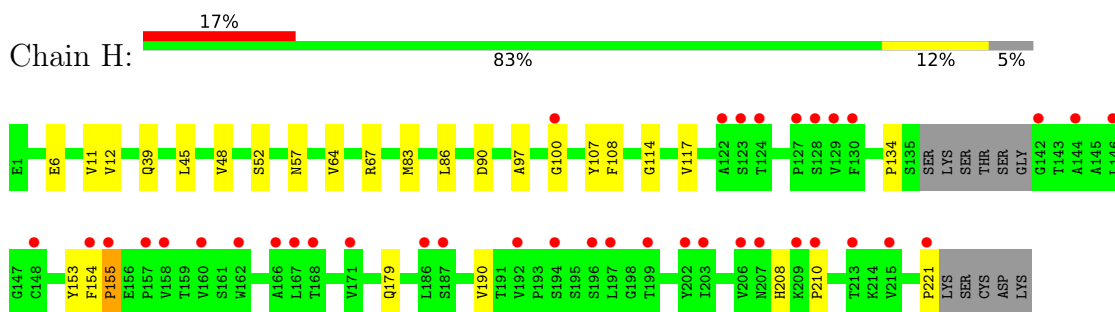
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	H	8	Total	O	0	0
			8	8		
10	L	15	Total	O	0	0
			15	15		
10	E	11	Total	O	0	0
			11	11		
10	A	11	Total	O	0	0
			11	11		
10	B	12	Total	O	0	0
			12	12		

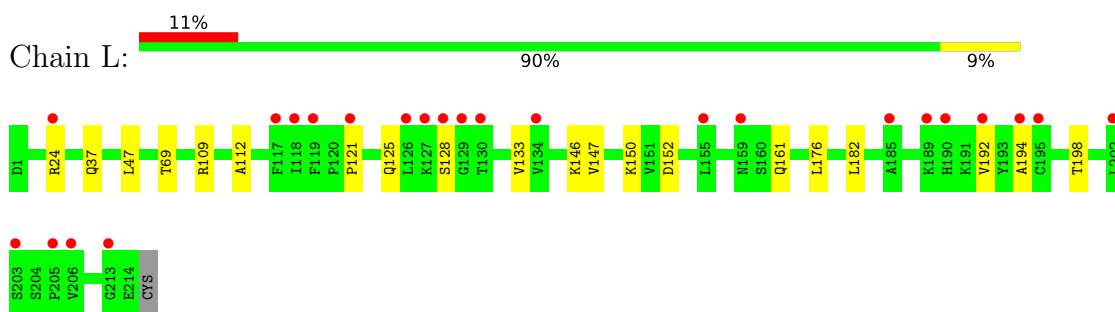
3 Residue-property plots [i](#)

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.

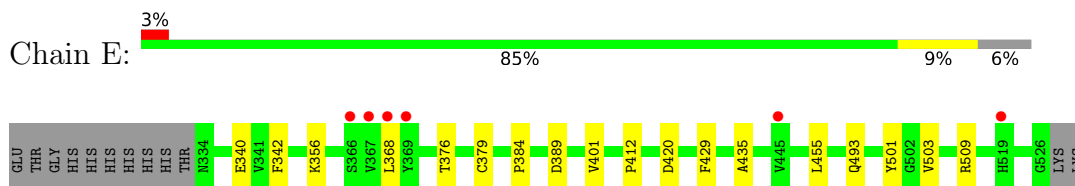
- Molecule 1: EY6A Fab heavy chain



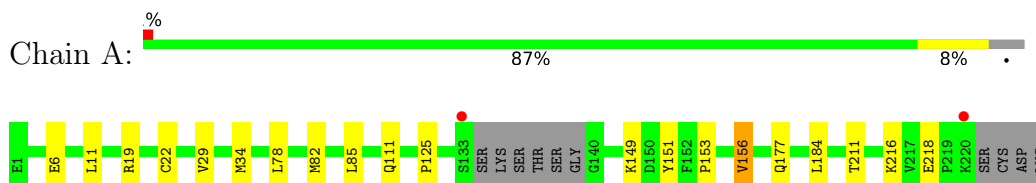
- Molecule 2: EY6A Fab light chain



- Molecule 3: Spike protein S1



- Molecule 4: COVOX-222 Fab heavy chain

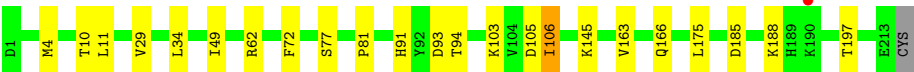


- Molecule 5: COVOX-222 Fab light chain

Chain B:

89%

10%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.17Å 120.41Å 211.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	60.86 – 2.50 60.86 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.8 (60.86-2.50) 98.8 (60.86-2.50)	Depositor EDS
R_{merge}	0.40	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.19_4092	Depositor
R, R_{free}	0.205 , 0.253 0.205 , 0.250	Depositor DCC
R_{free} test set	2422 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	61.5	Xtriage
Anisotropy	0.079	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 53.1	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	8206	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.44% 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: SO4, GOL, PEG, NAG

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	H	0.12	0/1679	0.31	0/2288
2	L	0.10	0/1664	0.31	0/2258
3	E	0.11	0/1576	0.27	0/2145
4	A	0.11	0/1615	0.30	0/2203
5	B	0.11	0/1677	0.31	0/2279
All	All	0.11	0/8211	0.30	0/11173

There are no bond length outliers.

There are no bond angle outliers.

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	H	1637	0	1591	15	0
2	L	1631	0	1591	12	0
3	E	1532	0	1448	10	0
4	A	1577	0	1534	11	0
5	B	1637	0	1590	14	0
6	A	30	0	0	0	0
6	B	20	0	0	0	0
6	E	20	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	L	25	0	0	0	0
7	A	6	0	8	0	0
7	E	6	0	8	0	0
8	E	14	0	13	0	0
9	E	14	0	20	1	0
10	A	11	0	0	0	0
10	B	12	0	0	1	0
10	E	11	0	0	2	0
10	H	8	0	0	0	0
10	L	15	0	0	0	0
All	All	8206	0	7803	61	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 (61) 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)
3:E:420:ASP:OD1	10:E:801:HOH:O	1.95	0.85
1:H:83:MET:HB3	1:H:86:LEU:HD21	1.73	0.70
3:E:389:ASP:OD2	10:E:802:HOH:O	2.14	0.65
3:E:412:PRO:HG3	3:E:429:PHE:HB3	1.79	0.63
5:B:10:THR:HG22	5:B:103:LYS:HB3	1.81	0.63
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.80	0.62
5:B:4:MET:HG3	5:B:91:HIS:CD2	2.35	0.61
3:E:376:THR:HB	3:E:435:ALA:HB3	1.80	0.61
3:E:340:GLU:OE1	3:E:356:LYS:NZ	2.35	0.59
2:L:146:LYS:HB3	2:L:198:THR:HB	1.84	0.58
2:L:152:ASP:OD1	2:L:192:VAL:N	2.38	0.57
5:B:62:ARG:HB2	5:B:77:SER:O	2.07	0.55
4:A:22:CYS:HB3	4:A:78:LEU:HB3	1.89	0.53
4:A:6:GLU:H	4:A:111:GLN:HE22	1.57	0.52
5:B:81:PRO:HA	5:B:106:ILE:HD13	1.90	0.52
4:A:216:LYS:NZ	4:A:218:GLU:OE2	2.41	0.52
5:B:106:ILE:O	5:B:166:GLN:NE2	2.44	0.51
4:A:82:MET:HB3	4:A:85:LEU:HD21	1.93	0.51
4:A:34:MET:HB3	4:A:78:LEU:HD22	1.93	0.51
5:B:93:ASP:OD1	5:B:94:THR:N	2.40	0.51
1:H:12:VAL:HG21	1:H:86:LEU:HD12	1.93	0.50
2:L:125:GLN:O	2:L:128:SER:OG	2.27	0.49
4:A:125:PRO:HB3	4:A:151:TYR:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:149:LYS:NZ	4:A:177:GLN:OE1	2.46	0.48
1:H:39:GLN:HB2	1:H:45:LEU:HD23	1.94	0.48
1:H:208:HIS:CD2	1:H:210:PRO:HD2	2.48	0.48
5:B:11:LEU:O	5:B:105:ASP:N	2.45	0.48
4:A:156:VAL:HG22	4:A:184:LEU:HD21	1.96	0.47
5:B:145:LYS:HB3	5:B:197:THR:OG1	2.15	0.47
3:E:379:CYS:SG	3:E:384:PRO:HG3	2.54	0.47
5:B:4:MET:HE2	5:B:29:VAL:HG21	1.96	0.47
1:H:6:GLU:OE1	1:H:114:GLY:N	2.32	0.46
4:A:125:PRO:HD2	4:A:211:THR:HG21	1.96	0.46
2:L:121:PRO:HD3	2:L:133:VAL:HG22	1.96	0.46
2:L:109:ARG:NH1	2:L:112:ALA:HB2	2.31	0.45
1:H:48:VAL:HG13	1:H:64:VAL:HG21	1.98	0.45
5:B:163[A]:VAL:HG22	5:B:175:LEU:HD12	1.98	0.45
5:B:188:LYS:NZ	10:B:405:HOH:O	2.50	0.45
2:L:109:ARG:HH12	2:L:112:ALA:HB2	1.82	0.45
3:E:501:TYR:OH	9:E:704:PEG:H22	2.16	0.45
2:L:152:ASP:HA	2:L:192:VAL:HB	1.98	0.44
3:E:401:VAL:HG22	3:E:509:ARG:HG2	1.99	0.44
5:B:163[B]:VAL:HG22	5:B:175:LEU:HD12	1.99	0.44
4:A:29:VAL:HG13	4:A:34:MET:HG3	2.00	0.44
3:E:342:PHE:CE1	3:E:368:LEU:HD11	2.53	0.43
1:H:67:ARG:NH1	1:H:90:ASP:OD2	2.46	0.43
2:L:150:LYS:HB2	2:L:194:ALA:HB3	2.00	0.43
2:L:147:VAL:HG21	2:L:176:LEU:HD22	2.00	0.43
1:H:179:GLN:HB3	2:L:161:GLN:HE22	1.83	0.43
1:H:153:TYR:HB2	1:H:208:HIS:CE1	2.54	0.42
5:B:185:ASP:HA	5:B:188:LYS:HD3	2.01	0.42
1:H:52:SER:HB3	1:H:57:ASN:HB2	2.00	0.42
1:H:97:ALA:HB1	1:H:108:PHE:HB3	2.01	0.42
1:H:100:GLY:HA3	1:H:107:TYR:CZ	2.55	0.41
1:H:83:MET:HE1	1:H:117:VAL:HG21	2.01	0.41
1:H:154:PHE:HA	1:H:155:PRO:HA	1.79	0.41
4:A:11:LEU:HB2	4:A:153:PRO:HG3	2.02	0.41
5:B:34:LEU:HD13	5:B:72:PHE:CG	2.56	0.41
2:L:24:ARG:HA	2:L:69:THR:O	2.20	0.41
1:H:134:PRO:HD2	1:H:221:PRO:HA	2.03	0.41
3:E:455:LEU:HD22	3:E:493:GLN:HG3	2.03	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	H	211/226 (93%)	199 (94%)	11 (5%)	1 (0%)	24	43
2	L	212/215 (99%)	203 (96%)	9 (4%)	0	100	100
3	E	191/205 (93%)	183 (96%)	8 (4%)	0	100	100
4	A	210/224 (94%)	202 (96%)	8 (4%)	0	100	100
5	B	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
All	All	1036/1084 (96%)	991 (96%)	44 (4%)	1 (0%)	48	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	155	PRO

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	H	181/191 (95%)	179 (99%)	2 (1%)	65	84
2	L	154/188 (82%)	153 (99%)	1 (1%)	78	91
3	E	166/177 (94%)	165 (99%)	1 (1%)	78	91
4	A	165/186 (89%)	163 (99%)	2 (1%)	63	83
5	B	185/185 (100%)	183 (99%)	2 (1%)	65	84
All	All	851/927 (92%)	843 (99%)	8 (1%)	70	87

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	11	VAL
1	H	190	VAL
2	L	182	LEU
3	E	503	VAL
4	A	19	ARG
4	A	156	VAL
5	B	49	ILE
5	B	106	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	77	ASN
2	L	200	GLN
3	E	360	ASN
3	E	370	ASN
5	B	189	HIS

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](#)

24 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	$\# Z > 2$
6	SO4	L	302	-	4,4,4	0.26	0	6,6,6	0.15	0
6	SO4	A	407	-	4,4,4	0.23	0	6,6,6	0.08	0
6	SO4	L	304	-	4,4,4	0.25	0	6,6,6	0.07	0
9	PEG	E	704	-	6,6,6	0.10	0	5,5,5	0.09	0
7	GOL	A	401	-	5,5,5	0.88	0	5,5,5	1.12	0
9	PEG	E	703	-	6,6,6	0.12	0	5,5,5	0.09	0
6	SO4	E	708	-	4,4,4	0.23	0	6,6,6	0.12	0
6	SO4	E	705	-	4,4,4	0.24	0	6,6,6	0.10	0
6	SO4	B	301	-	4,4,4	0.24	0	6,6,6	0.09	0
7	GOL	E	701	-	5,5,5	0.91	0	5,5,5	1.12	0
6	SO4	A	405	-	4,4,4	0.23	0	6,6,6	0.08	0
6	SO4	L	301	-	4,4,4	0.24	0	6,6,6	0.07	0
6	SO4	A	403	-	4,4,4	0.25	0	6,6,6	0.09	0
6	SO4	B	302	-	4,4,4	0.23	0	6,6,6	0.08	0
6	SO4	A	402	-	4,4,4	0.23	0	6,6,6	0.09	0
6	SO4	E	707	-	4,4,4	0.24	0	6,6,6	0.10	0
6	SO4	E	706	-	4,4,4	0.24	0	6,6,6	0.08	0
6	SO4	B	303	-	4,4,4	0.24	0	6,6,6	0.07	0
8	NAG	E	702	3	14,14,15	0.36	0	17,19,21	0.46	0
6	SO4	B	304	-	4,4,4	0.23	0	6,6,6	0.09	0
6	SO4	A	406	-	4,4,4	0.25	0	6,6,6	0.10	0
6	SO4	A	404	-	4,4,4	0.24	0	6,6,6	0.09	0
6	SO4	L	303	-	4,4,4	0.25	0	6,6,6	0.08	0
6	SO4	L	305	-	4,4,4	0.26	0	6,6,6	0.07	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
9	PEG	E	703	-	-	1/4/4/4	-
8	NAG	E	702	3	-	0/6/23/26	0/1/1/1
7	GOL	E	701	-	-	2/4/4/4	-
9	PEG	E	704	-	-	3/4/4/4	-
7	GOL	A	401	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	E	701	GOL	C1-C2-C3-O3
7	E	701	GOL	O2-C2-C3-O3
7	A	401	GOL	O1-C1-C2-O2
7	A	401	GOL	O1-C1-C2-C3
9	E	704	PEG	O1-C1-C2-O2
9	E	704	PEG	C4-C3-O2-C2
9	E	703	PEG	C4-C3-O2-C2
7	A	401	GOL	O2-C2-C3-O3
9	E	704	PEG	O2-C3-C4-O4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	E	704	PEG	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	H	215/226 (95%)	0.86	38 (17%) 4 3	50, 80, 142, 165	0
2	L	214/215 (99%)	0.70	24 (11%) 10 8	47, 83, 138, 159	0
3	E	193/205 (94%)	0.27	6 (3%) 51 47	46, 65, 94, 121	0
4	A	214/224 (95%)	0.16	2 (0%) 81 78	51, 68, 93, 116	0
5	B	213/214 (99%)	0.13	1 (0%) 87 85	43, 68, 89, 105	1 (0%)
All	All	1049/1084 (96%)	0.43	71 (6%) 23 20	43, 69, 132, 165	1 (0%)

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	369	TYR	4.9
2	L	119	PHE	4.4
2	L	130	THR	4.3
2	L	185	ALA	4.0
1	H	210	PRO	4.0
1	H	215	VAL	3.9
1	H	129	VAL	3.7
4	A	133	SER	3.7
1	H	206	VAL	3.6
1	H	127	PRO	3.6
1	H	167	LEU	3.5
2	L	118	ILE	3.4
1	H	166	ALA	3.3
2	L	189	LYS	3.3
2	L	192	VAL	3.2
4	A	220	LYS	3.2
1	H	160	VAL	3.2
1	H	199	THR	3.0
2	L	194	ALA	3.0
2	L	155	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	H	123	SER	2.9
1	H	192	VAL	2.8
2	L	195	CYS	2.8
1	H	213	THR	2.7
1	H	142	GLY	2.7
1	H	122	ALA	2.7
3	E	519	HIS	2.6
3	E	367	VAL	2.6
2	L	121	PRO	2.6
1	H	197	LEU	2.6
1	H	168	THR	2.6
1	H	128	SER	2.6
1	H	144	ALA	2.5
2	L	205	PRO	2.5
2	L	134	VAL	2.5
1	H	157	PRO	2.5
2	L	129	GLY	2.5
1	H	162	TRP	2.5
1	H	124	THR	2.5
1	H	194	SER	2.5
2	L	128	SER	2.4
2	L	213	GLY	2.4
1	H	171	VAL	2.4
1	H	130	PHE	2.4
2	L	127	LYS	2.4
2	L	117	PHE	2.4
2	L	202	LEU	2.3
3	E	368	LEU	2.3
1	H	202	TYR	2.3
1	H	146	LEU	2.3
1	H	203	ILE	2.3
2	L	190	HIS	2.2
1	H	196	SER	2.2
1	H	187	SER	2.2
2	L	24	ARG	2.2
1	H	155	PRO	2.2
1	H	158	VAL	2.2
1	H	221	PRO	2.2
2	L	126	LEU	2.2
1	H	148	CYS	2.2
1	H	186	LEU	2.1
3	E	366	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	H	100	GLY	2.1
5	B	190	LYS	2.1
2	L	206	VAL	2.1
3	E	445	VAL	2.1
1	H	207	ASN	2.1
1	H	209	LYS	2.0
1	H	154	PHE	2.0
2	L	159	ASN	2.0
2	L	203	SER	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](#)

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(Å ²)	Q<0.9
6	SO4	B	301	5/5	0.65	0.09	114,120,145,153	0
6	SO4	B	304	5/5	0.66	0.11	115,117,142,154	0
6	SO4	A	405	5/5	0.69	0.10	102,111,135,146	0
6	SO4	E	707	5/5	0.71	0.12	94,100,119,127	0
6	SO4	B	302	5/5	0.74	0.08	95,102,122,128	0
6	SO4	E	708	5/5	0.75	0.12	97,101,128,146	0
6	SO4	A	402	5/5	0.76	0.08	100,116,124,124	0
8	NAG	E	702	14/15	0.76	0.15	83,105,121,122	0
6	SO4	B	303	5/5	0.78	0.11	87,87,114,122	0
9	PEG	E	704	7/7	0.81	0.18	74,86,96,96	0
6	SO4	A	406	5/5	0.82	0.12	100,116,147,160	0
7	GOL	E	701	6/6	0.83	0.14	60,77,79,84	0
6	SO4	A	403	5/5	0.83	0.16	77,78,80,115	0
6	SO4	A	407	5/5	0.83	0.12	109,114,151,172	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	SO4	L	305	5/5	0.84	0.17	94,114,135,155	0
6	SO4	E	705	5/5	0.84	0.09	96,100,118,121	0
9	PEG	E	703	7/7	0.85	0.15	68,71,76,77	0
6	SO4	L	303	5/5	0.86	0.08	104,111,144,156	0
6	SO4	L	301	5/5	0.87	0.16	70,84,88,92	0
6	SO4	A	404	5/5	0.88	0.14	92,94,108,127	0
6	SO4	E	706	5/5	0.89	0.08	98,100,136,141	0
6	SO4	L	304	5/5	0.89	0.11	77,117,125,143	0
7	GOL	A	401	6/6	0.89	0.13	69,75,82,83	0
6	SO4	L	302	5/5	0.93	0.14	63,78,84,96	0

6.5 Other polymers [i](#)

There are no such residues in this entry.