



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 31, 2021 – 09:10 pm BST

PDB ID : 7NXA  
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 wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.18  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.18

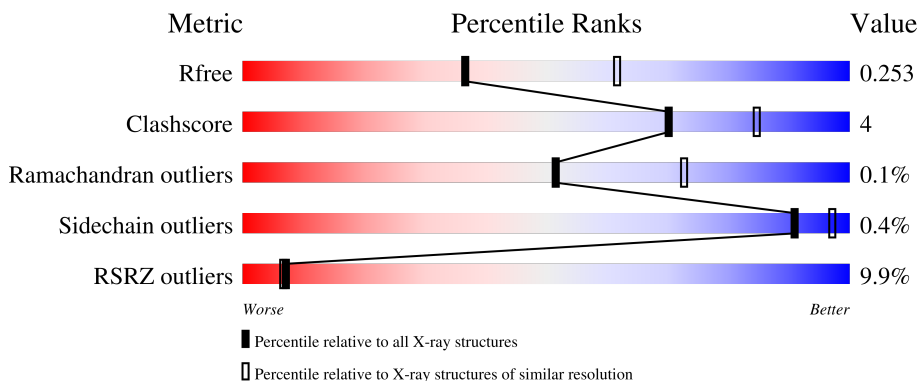
# 1 Overall quality at a glance

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))
$R_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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  $\geq 3$ , 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	 22% (Poor fit), 84% (0-3 outliers), 11% (1 outlier), 5% (2-3 outliers)
2	L	215	 21% (Poor fit), 90% (0-3 outliers), 9% (1 outlier)
3	E	205	 2% (Poor fit), 85% (0-3 outliers), 9% (1 outlier), 6% (2-3 outliers)
4	A	224	 % (Poor fit), 88% (0-3 outliers), 8% (1 outlier), . (2-3 outliers)
5	B	214	 2% (Poor fit), 90% (0-3 outliers), 9% (1 outlier)

## 2 Entry composition

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
			Total	C	N	O	S			
1	H	215	1637	1041	273	317	6	0	0	0

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

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

- Molecule 3 is a protein called Spike protein S1.

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

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

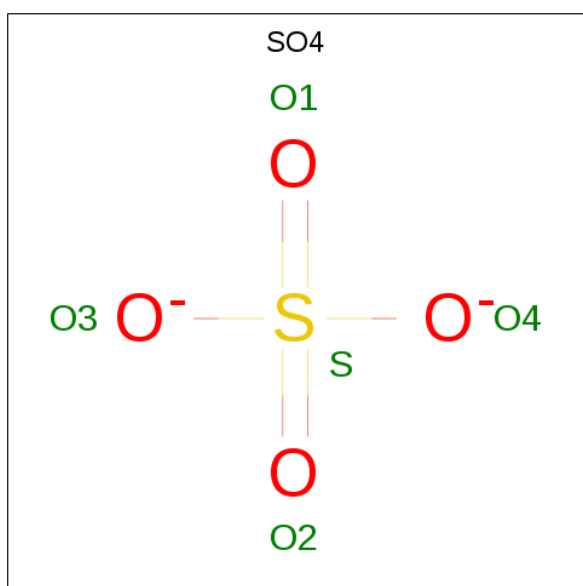
- Molecule 4 is a protein called COVOX-222 Fab heavy chain.

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

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

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

- Molecule 6 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



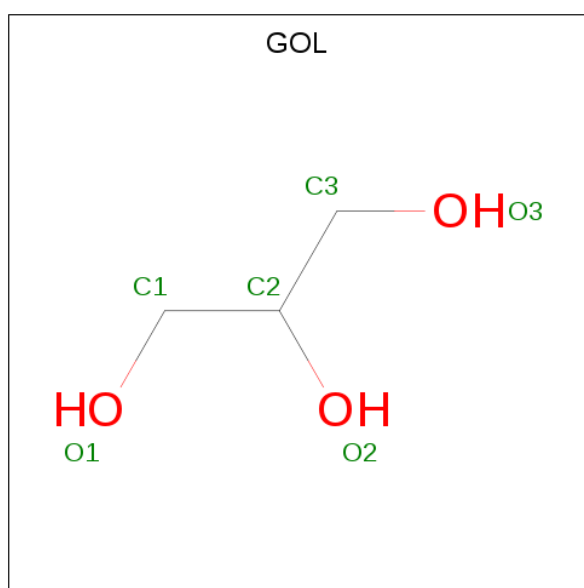
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
6	L	1	5	4	1	0	0
6	L	1	5	4	1	0	0
6	L	1	5	4	1	0	0
6	L	1	5	4	1	0	0
6	L	1	5	4	1	0	0
6	E	1	5	4	1	0	0
6	E	1	5	4	1	0	0

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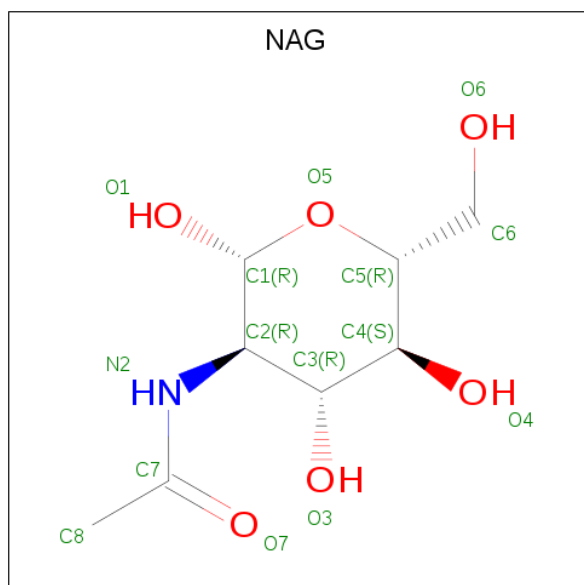
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	E	1	Total	O	S	0	0
			5	4	1		
6	E	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	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 (three-letter code: 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 (three-letter code: 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 (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).



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

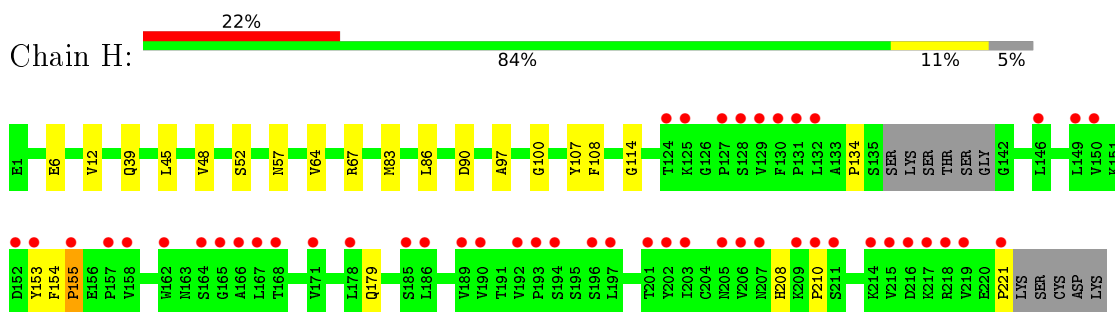
- Molecule 10 is water.

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

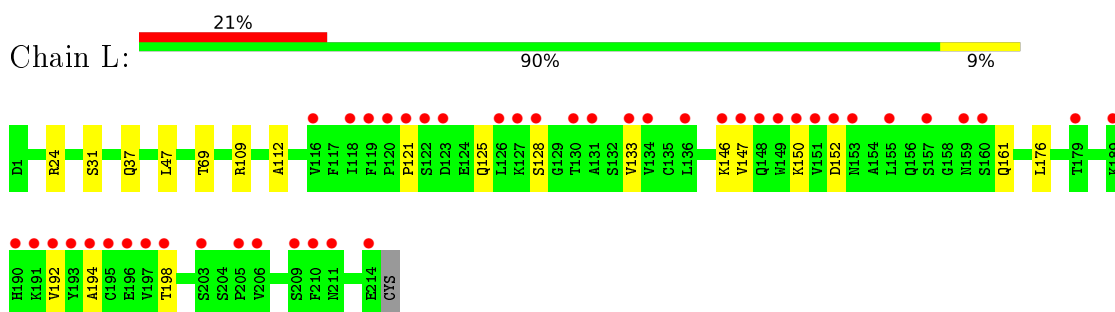
### 3 Residue-property plots [i](#)

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.

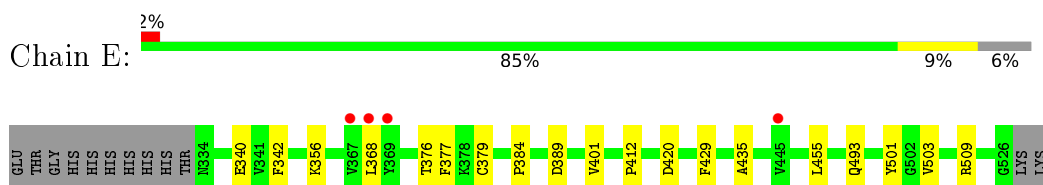
- Molecule 1: EY6A Fab heavy chain



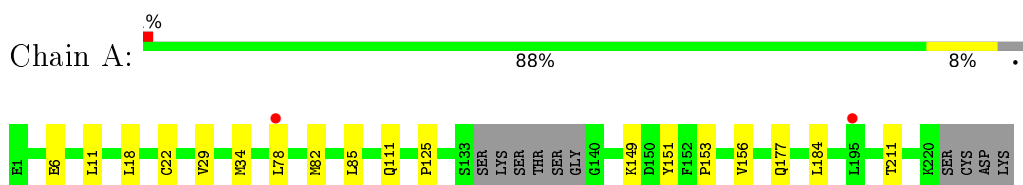
- Molecule 2: EY6A Fab light chain



- Molecule 3: Spike protein S1

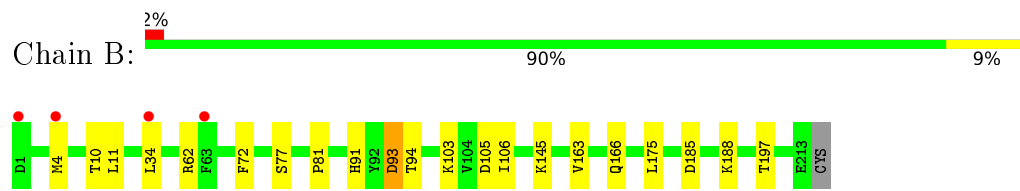


- Molecule 4: COVOX-222 Fab heavy chain



- Molecule 5: COVOX-222 Fab light chain





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	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) 98.9 (60.86-2.50)	Depositor EDS
$R_{merge}$	0.40	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.97 (at 2.51Å)	Xtrriage
Refinement program	PHENIX 1.19_4092	Depositor
R, $R_{free}$	0.205 , 0.253 0.207 , 0.253	Depositor DCC
$R_{free}$ test set	2396 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	61.5	Xtrriage
Anisotropy	0.079	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 51.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8206	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtrriage'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.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, PEG, NAG, SO4

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	0.26	0/1679	0.50	0/2288
2	L	0.25	0/1664	0.48	0/2258
3	E	0.26	0/1576	0.48	0/2145
4	A	0.26	0/1615	0.50	0/2203
5	B	0.26	0/1677	0.51	0/2279
All	All	0.26	0/8211	0.49	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 [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	H	1637	0	1591	14	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	12	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	0	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	58	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.

The worst 5 of 58 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

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%)	29	48
2	L	212/215 (99%)	203 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	51	73

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%)	181 (100%)	0	100	100
2	L	187/188 (100%)	186 (100%)	1 (0%)	88	96
3	E	166/177 (94%)	164 (99%)	2 (1%)	71	88
4	A	176/186 (95%)	176 (100%)	0	100	100
5	B	185/185 (100%)	184 (100%)	1 (0%)	88	96
All	All	895/927 (96%)	891 (100%)	4 (0%)	91	97

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	31	SER
3	E	377	PHE
3	E	503	VAL
5	B	93	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
5	B	91	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 monosaccharides 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	A	402	-	4,4,4	0.13	0	6,6,6	0.07	0
6	SO4	A	405	-	4,4,4	0.13	0	6,6,6	0.06	0
6	SO4	A	406	-	4,4,4	0.14	0	6,6,6	0.07	0
6	SO4	L	302	-	4,4,4	0.16	0	6,6,6	0.12	0
6	SO4	L	303	-	4,4,4	0.14	0	6,6,6	0.06	0
6	SO4	A	404	-	4,4,4	0.14	0	6,6,6	0.06	0
6	SO4	A	403	-	4,4,4	0.14	0	6,6,6	0.07	0
6	SO4	E	706	-	4,4,4	0.14	0	6,6,6	0.06	0
6	SO4	B	302	-	4,4,4	0.13	0	6,6,6	0.07	0
9	PEG	E	703	-	6,6,6	0.12	0	5,5,5	0.09	0
6	SO4	E	705	-	4,4,4	0.14	0	6,6,6	0.07	0
7	GOL	A	401	-	5,5,5	0.85	0	5,5,5	1.04	0
8	NAG	E	702	3	14,14,15	0.34	0	17,19,21	0.45	0
6	SO4	B	301	-	4,4,4	0.14	0	6,6,6	0.07	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	SO4	L	301	-	4,4,4	0.14	0	6,6,6	0.07	0
6	SO4	B	303	-	4,4,4	0.14	0	6,6,6	0.06	0
6	SO4	L	304	-	4,4,4	0.14	0	6,6,6	0.11	0
6	SO4	E	708	-	4,4,4	0.13	0	6,6,6	0.09	0
6	SO4	A	407	-	4,4,4	0.13	0	6,6,6	0.08	0
6	SO4	E	707	-	4,4,4	0.14	0	6,6,6	0.08	0
6	SO4	B	304	-	4,4,4	0.14	0	6,6,6	0.07	0
6	SO4	L	305	-	4,4,4	0.15	0	6,6,6	0.04	0
7	GOL	E	701	-	5,5,5	0.88	0	5,5,5	1.04	0
9	PEG	E	704	-	6,6,6	0.10	0	5,5,5	0.09	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
7	GOL	E	701	-	-	2/4/4/4	-
9	PEG	E	703	-	-	1/4/4/4	-
9	PEG	E	704	-	-	3/4/4/4	-
7	GOL	A	401	-	-	3/4/4/4	-
8	NAG	E	702	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 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

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

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q < 0.9
1	H	215/226 (95%)	1.23	49 (22%) 0 0	50, 80, 142, 165	0
2	L	214/215 (99%)	1.29	45 (21%) 1 0	47, 83, 138, 159	0
3	E	193/205 (94%)	0.57	4 (2%) 63 66	46, 65, 94, 121	0
4	A	214/224 (95%)	0.37	2 (0%) 84 86	51, 68, 93, 116	0
5	B	213/214 (99%)	0.43	4 (1%) 66 69	52, 68, 89, 105	0
All	All	1049/1084 (96%)	0.78	104 (9%) 7 7	46, 68, 132, 165	0

The worst 5 of 104 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	210	PRO	11.2
2	L	189	LYS	8.6
2	L	194	ALA	8.5
2	L	119	PHE	7.9
1	H	215	VAL	7.4

### 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 monosaccharides 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
6	SO4	B	301	5/5	0.70	0.20	114,120,145,153	0
6	SO4	E	708	5/5	0.75	0.23	97,101,128,146	0
6	SO4	B	302	5/5	0.78	0.16	95,102,122,128	0
9	PEG	E	704	7/7	0.78	0.14	74,86,96,96	0
8	NAG	E	702	14/15	0.79	0.27	83,105,121,122	0
6	SO4	E	707	5/5	0.81	0.20	94,100,119,127	0
6	SO4	L	305	5/5	0.81	0.20	94,114,135,155	0
6	SO4	B	304	5/5	0.82	0.41	115,117,142,154	0
6	SO4	A	406	5/5	0.82	0.27	100,116,147,160	0
6	SO4	A	407	5/5	0.82	0.37	109,114,151,172	0
7	GOL	E	701	6/6	0.86	0.12	60,77,79,84	0
9	PEG	E	703	7/7	0.87	0.14	68,71,76,77	0
7	GOL	A	401	6/6	0.87	0.12	69,75,82,83	0
6	SO4	A	404	5/5	0.88	0.31	92,94,108,127	0
6	SO4	A	405	5/5	0.88	0.17	102,111,135,146	0
6	SO4	E	705	5/5	0.88	0.17	96,100,118,121	0
6	SO4	L	304	5/5	0.89	0.32	77,117,125,143	0
6	SO4	E	706	5/5	0.89	0.18	98,100,136,141	0
6	SO4	B	303	5/5	0.89	0.19	87,87,114,122	0
6	SO4	L	303	5/5	0.90	0.13	104,111,144,156	0
6	SO4	L	302	5/5	0.92	0.17	63,78,84,96	0
6	SO4	A	403	5/5	0.93	0.18	77,78,80,115	0
6	SO4	A	402	5/5	0.93	0.12	100,116,124,124	0
6	SO4	L	301	5/5	0.94	0.17	70,84,88,92	0

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.