



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 25, 2024 – 10:12 AM EDT

PDB ID : 6I07
Title : Crystal structure of EpCAM in complex with scFv
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Deposited on : 2018-10-25
Resolution : 2.35 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	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
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)	:	2.37.1

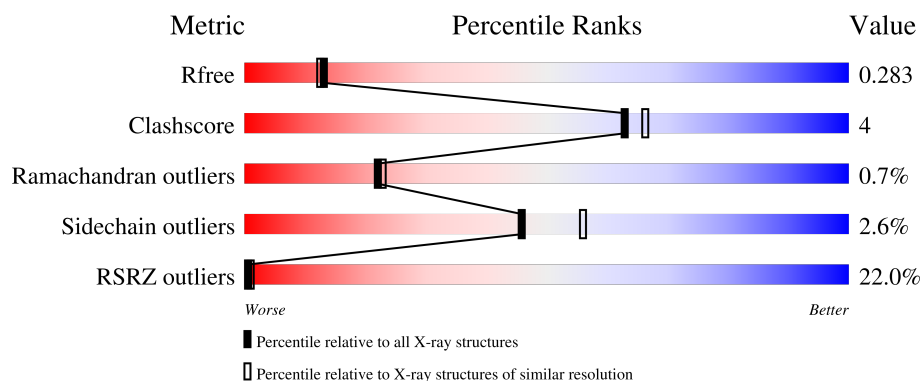
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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	262	<div> <div>8%</div> <div>77%</div> <div>9%</div> <div>13%</div> </div>
1	B	262	<div> <div>27%</div> <div>74%</div> <div>12%</div> <div>14%</div> </div>
2	C	253	<div> <div>18%</div> <div>75%</div> <div>13%</div> <div>11%</div> </div>
2	D	253	<div> <div>25%</div> <div>75%</div> <div>15%</div> <div>10%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7241 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 Single chain Fv.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	228	Total	C	N	O	S	0	0	0
			1767	1122	290	346	9			
1	B	226	Total	C	N	O	S	0	0	0
			1752	1113	287	343	9			

- Molecule 2 is a protein called Epithelial cell adhesion molecule.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	225	Total	C	N	O	S	0	0	0
			1792	1114	307	355	16			
2	D	227	Total	C	N	O	S	0	0	0
			1807	1123	311	358	15			

There are 28 discrepancies between the modelled and reference sequences:

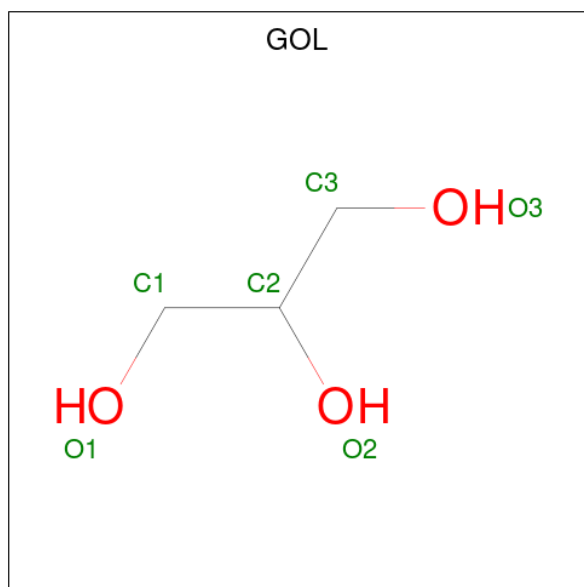
Chain	Residue	Modelled	Actual	Comment	Reference
C	74	GLN	ASN	engineered mutation	UNP P16422
C	111	GLN	ASN	engineered mutation	UNP P16422
C	198	GLN	ASN	engineered mutation	UNP P16422
C	266	GLY	-	expression tag	UNP P16422
C	267	GLY	-	expression tag	UNP P16422
C	268	GLY	-	expression tag	UNP P16422
C	269	GLY	-	expression tag	UNP P16422
C	270	SER	-	expression tag	UNP P16422
C	271	HIS	-	expression tag	UNP P16422
C	272	HIS	-	expression tag	UNP P16422
C	273	HIS	-	expression tag	UNP P16422
C	274	HIS	-	expression tag	UNP P16422
C	275	HIS	-	expression tag	UNP P16422
C	276	HIS	-	expression tag	UNP P16422
D	74	GLN	ASN	engineered mutation	UNP P16422
D	111	GLN	ASN	engineered mutation	UNP P16422

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Chain	Residue	Modelled	Actual	Comment	Reference
D	198	GLN	ASN	engineered mutation	UNP P16422
D	266	GLY	-	expression tag	UNP P16422
D	267	GLY	-	expression tag	UNP P16422
D	268	GLY	-	expression tag	UNP P16422
D	269	GLY	-	expression tag	UNP P16422
D	270	SER	-	expression tag	UNP P16422
D	271	HIS	-	expression tag	UNP P16422
D	272	HIS	-	expression tag	UNP P16422
D	273	HIS	-	expression tag	UNP P16422
D	274	HIS	-	expression tag	UNP P16422
D	275	HIS	-	expression tag	UNP P16422
D	276	HIS	-	expression tag	UNP P16422

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

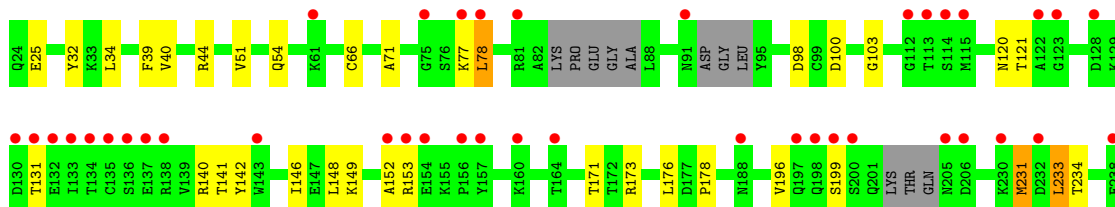
- Molecule 4 is water.

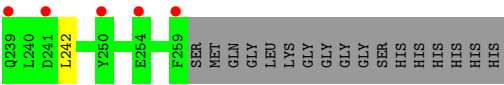
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	95	Total	O	0	0
			95	95		
4	B	13	Total	O	0	0
			13	13		

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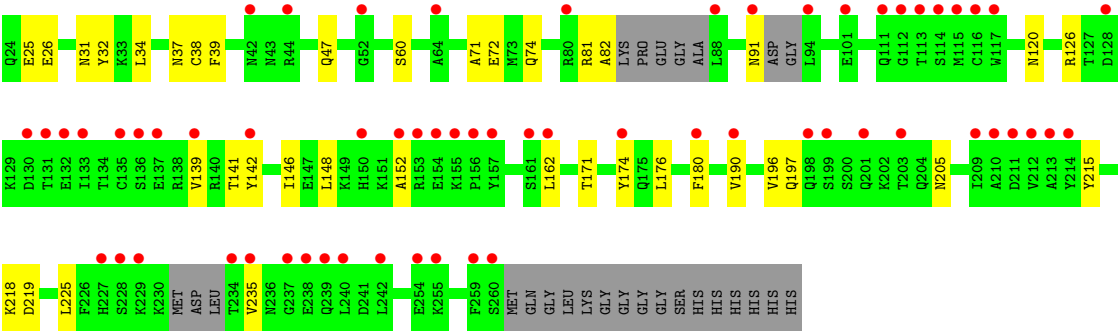
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	8	Total	O	0	0
			8	8		
4	D	1	Total	O	0	0
			1	1		





● Molecule 2: Epithelial cell adhesion molecule



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.89Å 91.07Å 181.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.70 – 2.35 28.69 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.2 (28.70-2.35) 99.3 (28.69-2.35)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.10 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.230 , 0.279 0.235 , 0.283	Depositor DCC
R_{free} test set	2851 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	58.3	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 50.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7241	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.05% 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: PCA, 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	0.70	0/1808	0.89	0/2452
1	B	0.70	0/1793	0.80	0/2433
2	C	0.68	0/1808	0.79	0/2436
2	D	0.69	0/1823	0.74	0/2456
All	All	0.69	0/7232	0.81	0/9777

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	A	1767	0	1717	11	0
1	B	1752	0	1699	13	0
2	C	1792	0	1751	21	0
2	D	1807	0	1771	20	0
3	A	6	0	8	0	0
4	A	95	0	0	1	0
4	B	13	0	0	0	0
4	C	8	0	0	1	0
4	D	1	0	0	0	0
All	All	7241	0	6946	60	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 (60) 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:C:120:ASN:ND2	2:C:141:THR:OG1	2.15	0.79
1:A:191:PHE:CZ	1:A:193:GLY:HA2	2.29	0.68
2:C:173:ARG:HH12	2:C:231:MET:HB2	1.62	0.63
2:D:39:PHE:CZ	2:D:47:GLN:NE2	2.67	0.62
2:D:31:ASN:ND2	2:D:60:SER:O	2.34	0.61
2:C:54:GLN:NE2	4:C:301:HOH:O	2.34	0.60
2:C:148:LEU:HD23	2:C:242:LEU:HD22	1.84	0.58
2:D:72:GLU:OE1	2:D:218:LYS:NZ	2.36	0.55
1:B:179:ASN:HA	2:D:37:ASN:OD1	2.07	0.55
1:A:227:ALA:HB3	1:A:230:GLY:O	2.08	0.54
2:C:233:LEU:HD12	2:C:234:THR:N	2.23	0.53
2:D:71:ALA:O	2:D:74:GLN:O	2.26	0.53
1:A:138:VAL:O	1:A:139:LYS:HG2	2.09	0.53
2:C:171:THR:HG22	2:C:176:LEU:O	2.09	0.52
2:C:173:ARG:NH1	2:C:231:MET:HB2	2.25	0.52
2:C:146:ILE:HG22	2:C:148:LEU:CD1	2.40	0.50
1:B:72:SER:OG	1:B:73:GLY:N	2.43	0.50
1:A:169:GLY:O	1:A:170:GLN:HB2	2.11	0.50
2:C:77:LYS:HB3	2:C:78:LEU:HA	1.95	0.49
2:C:171:THR:HA	2:C:176:LEU:O	2.12	0.48
2:D:162:LEU:HD12	2:D:235:VAL:HG21	1.95	0.48
2:D:81:ARG:HG2	2:D:82:ALA:N	2.28	0.48
1:B:31:HIS:HB3	1:B:33:ASP:OD1	2.14	0.47
1:A:99:ILE:HD11	2:C:40:VAL:O	2.14	0.47
1:B:40:TRP:HB2	1:B:53:ILE:HB	1.96	0.47
2:D:215:TYR:CE2	2:D:225:LEU:HB2	2.50	0.47
2:D:32:TYR:CE1	2:D:34:LEU:HB2	2.50	0.47
2:D:120:ASN:ND2	2:D:141:THR:OG1	2.48	0.46
1:A:4:MET:SD	1:A:25:SER:HB3	2.56	0.46
1:A:97:LEU:O	2:C:44:ARG:NH1	2.50	0.44
1:A:146:LYS:HE3	4:A:456:HOH:O	2.18	0.44
2:C:121:THR:HG23	2:C:140:ARG:HA	2.00	0.44
2:C:66:CYS:HB3	2:C:103:GLY:O	2.18	0.44
1:B:155:THR:HB	1:B:158:ASN:ND2	2.33	0.43
2:C:142:TYR:O	2:C:196:VAL:HA	2.18	0.43
2:D:146:ILE:HG22	2:D:148:LEU:HD11	1.99	0.43
2:C:171:THR:HG21	2:C:178:PRO:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:99:ILE:HA	1:B:100:PRO:HA	1.77	0.43
2:D:142:TYR:O	2:D:196:VAL:HA	2.17	0.43
2:D:180:PHE:CE1	2:D:197:GLN:HG3	2.53	0.43
1:B:51:LEU:HD23	1:B:230:GLY:HA2	2.01	0.43
1:B:131:LEU:HD12	1:B:232:TYR:O	2.18	0.43
1:B:227:ALA:HA	2:D:26:GLU:HB2	2.00	0.42
2:D:38:CYS:HA	2:D:47:GLN:O	2.19	0.42
1:B:160:GLY:HA3	1:B:177:TRP:NE1	2.34	0.42
1:B:92:TYR:HD2	1:B:104:GLY:O	2.03	0.42
2:D:25:GLU:O	2:D:39:PHE:HA	2.20	0.42
2:C:51:VAL:HG22	2:C:71:ALA:HB1	2.02	0.42
1:B:174:TRP:CZ2	1:B:176:GLY:HA2	2.55	0.42
1:B:218:THR:HG23	1:B:240:THR:HA	2.02	0.41
1:A:174:TRP:CZ2	1:A:176:GLY:HA2	2.55	0.41
2:C:120:ASN:HD22	2:C:141:THR:HG1	1.58	0.41
2:D:174:TYR:OH	2:D:219:ASP:OD2	2.26	0.41
2:C:32:TYR:CE1	2:C:34:LEU:HB2	2.56	0.41
1:A:40:TRP:CE2	1:A:78:LEU:HB2	2.56	0.41
2:D:171:THR:HG22	2:D:176:LEU:O	2.20	0.41
2:C:25:GLU:O	2:C:39:PHE:HA	2.21	0.41
2:C:78:LEU:O	2:D:190:VAL:HG21	2.22	0.40
2:D:126:ARG:NE	2:D:139:VAL:HG11	2.36	0.40
1:A:180:THR:HA	1:A:199:LEU:HD11	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	A	224/262 (86%)	215 (96%)	8 (4%)	1 (0%)	34	38
1	B	222/262 (85%)	201 (90%)	21 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	217/253 (86%)	195 (90%)	19 (9%)	3 (1%)	11	9
2	D	219/253 (87%)	194 (89%)	23 (10%)	2 (1%)	17	17
All	All	882/1030 (86%)	805 (91%)	71 (8%)	6 (1%)	22	23

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	231	MET
2	C	152	ALA
2	D	152	ALA
2	D	205	ASN
1	A	170	GLN
2	C	131	THR

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	195/208 (94%)	189 (97%)	6 (3%)	40	48
1	B	193/208 (93%)	186 (96%)	7 (4%)	35	43
2	C	202/222 (91%)	195 (96%)	7 (4%)	36	44
2	D	204/222 (92%)	203 (100%)	1 (0%)	88	94
All	All	794/860 (92%)	773 (97%)	21 (3%)	46	56

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	ASP
1	A	14	THR
1	A	108	LYS
1	A	152	SER
1	A	173	LYS
1	A	209	GLN

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Mol	Chain	Res	Type
1	B	20	SER
1	B	48	SER
1	B	57	SER
1	B	108	LYS
1	B	167	GLN
1	B	209	GLN
1	B	228	ILE
2	C	78	LEU
2	C	98	ASP
2	C	100	ASP
2	C	149	LYS
2	C	153	ARG
2	C	199	SER
2	C	233	LEU
2	D	91	ASN

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

Mol	Chain	Res	Type
2	D	55	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
2	PCA	D	24	2	7,8,9	0.63	0	9,10,12	0.62	0
2	PCA	C	24	2	7,8,9	0.75	0	9,10,12	0.62	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
2	PCA	D	24	2	-	0/0/11/13	0/1/1/1
2	PCA	C	24	2	-	0/0/11/13	0/1/1/1

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.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
3	GOL	A	301	-	5,5,5	0.12	0	5,5,5	0.31	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
3	GOL	A	301	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	GOL	C1-C2-C3-O3
3	A	301	GOL	O2-C2-C3-O3

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	228/262 (87%)	0.46	20 (8%)	10 15	32, 46, 77, 111	0
1	B	226/262 (86%)	1.58	72 (31%)	0 0	48, 101, 163, 196	0
2	C	224/253 (88%)	1.11	45 (20%)	1 2	38, 105, 160, 184	0
2	D	226/253 (89%)	1.32	62 (27%)	0 0	71, 116, 160, 183	0
All	All	904/1030 (87%)	1.12	199 (22%)	0 1	32, 94, 159, 196	0

All (199) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	112	GLY	11.8
2	C	113	THR	9.5
2	D	113	THR	8.9
1	B	85	ALA	7.7
1	B	82	ARG	7.2
1	B	14	THR	7.0
1	B	61	SER	6.8
2	D	112	GLY	6.7
1	B	15	PRO	6.3
2	C	135	CYS	6.3
1	B	81	SER	6.3
1	B	94	ALA	6.1
1	B	40	TRP	6.1
1	B	39	TYR	6.1
2	C	114	SER	5.7
2	D	130	ASP	5.7
1	B	16	GLY	5.5
1	B	80	ILE	5.5
1	B	33	ASP	5.4
2	D	153	ARG	5.3
1	B	66	ARG	5.2

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Mol	Chain	Res	Type	RSRZ
1	B	83	VAL	5.2
1	B	35	ILE	5.1
2	C	131	THR	4.8
2	D	152	ALA	4.7
2	D	131	THR	4.7
1	B	41	TYR	4.6
1	B	29	LEU	4.6
2	C	241	ASP	4.5
1	B	2	ILE	4.5
2	D	132	GLU	4.5
2	C	232	ASP	4.5
1	B	18	PRO	4.4
2	C	200	SER	4.4
2	D	190	VAL	4.4
2	D	114	SER	4.4
1	B	84	GLU	4.4
1	B	111	ILE	4.4
2	D	239	GLN	4.3
1	B	23	CYS	4.3
2	C	152	ALA	4.3
1	B	21	ILE	4.3
1	B	62	GLY	4.3
2	D	133	ILE	4.2
2	D	210	ALA	4.2
1	B	8	PRO	4.2
2	D	212	VAL	4.2
1	B	65	ASP	4.2
1	B	67	PHE	4.1
2	C	136	SER	4.1
1	B	86	GLU	4.1
2	C	160	LYS	4.1
1	A	164	VAL	4.0
1	B	45	PRO	3.9
2	C	115	MET	3.8
2	D	209	ILE	3.8
2	D	115	MET	3.8
2	C	138	ARG	3.7
2	C	198	GLN	3.7
2	D	260	SER	3.7
2	D	80	ARG	3.7
2	C	130	ASP	3.6
1	B	34	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	224	ALA	3.6
2	D	180	PHE	3.5
1	B	226	PHE	3.5
2	C	205	ASN	3.5
2	D	42	ASN	3.5
1	B	109	LEU	3.5
2	D	240	LEU	3.5
2	C	254	GLU	3.4
2	C	199	SER	3.4
1	B	93	CYS	3.4
2	D	111	GLN	3.4
2	D	142	TYR	3.4
2	C	259	PHE	3.4
2	D	201	GLN	3.4
1	A	208	LEU	3.3
1	B	13	VAL	3.3
1	B	46	GLY	3.3
2	D	203	THR	3.3
2	D	213	ALA	3.2
1	B	37	TYR	3.2
2	D	157	TYR	3.2
1	B	51	LEU	3.2
1	B	32	SER	3.2
2	D	162	LEU	3.1
2	C	250	TYR	3.1
1	A	163	TRP	3.1
2	D	101	GLU	3.1
1	A	233	TRP	3.1
2	D	154	GLU	3.0
1	B	64	PRO	3.0
2	D	136	SER	3.0
2	D	238	GLU	3.0
1	A	127	SER	3.0
2	D	117	TRP	3.0
1	A	172	LEU	3.0
1	B	52	LEU	3.0
2	D	259	PHE	3.0
2	D	150	HIS	2.9
1	B	161	MET	2.9
2	C	239	GLN	2.9
2	C	134	THR	2.9
2	D	235	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
2	D	229	LYS	2.9
1	B	12	PRO	2.9
1	B	73	GLY	2.8
2	D	214	TYR	2.8
1	B	88	GLU	2.8
2	D	255	LYS	2.8
1	B	110	GLU	2.8
2	C	153	ARG	2.8
1	B	38	LEU	2.7
1	B	27	LYS	2.7
2	C	188	ASN	2.7
2	D	128	ASP	2.7
2	C	156	PRO	2.7
1	B	190	ASP	2.7
1	B	31	HIS	2.7
1	B	79	LYS	2.7
1	B	160	GLY	2.7
2	C	78	LEU	2.7
2	C	164	THR	2.7
2	D	91	ASN	2.6
2	C	75	GLY	2.6
1	A	92	TYR	2.6
1	B	168	PRO	2.6
2	D	116	CYS	2.6
1	A	103	PHE	2.6
2	D	137	GLU	2.6
1	B	178	ILE	2.6
2	D	155	LYS	2.6
2	C	230	LYS	2.5
2	D	228	SER	2.5
1	A	168	PRO	2.5
2	C	154	GLU	2.5
2	D	242	LEU	2.5
2	D	135	CYS	2.5
2	D	199	SER	2.5
2	D	52	GLY	2.5
1	A	112	LYS	2.5
1	B	231	ASP	2.5
1	B	132	VAL	2.5
1	A	161	MET	2.4
2	C	132	GLU	2.4
2	D	234	THR	2.4

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Mol	Chain	Res	Type	RSRZ
2	C	123	GLY	2.4
2	C	81	ARG	2.4
2	D	94	LEU	2.4
1	B	92	TYR	2.4
2	C	137	GLU	2.4
2	C	143	TRP	2.4
1	B	11	LEU	2.4
2	D	254	GLU	2.4
2	C	61	LYS	2.4
2	C	122	ALA	2.4
1	A	197	PHE	2.4
1	A	41	TYR	2.3
2	D	198	GLN	2.3
1	B	229	LYS	2.3
2	C	157	TYR	2.3
2	C	197	GLN	2.3
2	D	44	ARG	2.3
2	D	211	ASP	2.3
2	D	161	SER	2.3
1	A	94	ALA	2.3
1	A	224	ALA	2.3
2	D	156	PRO	2.2
1	B	101	ARG	2.2
1	A	196	ALA	2.2
1	A	39	TYR	2.2
1	B	97	LEU	2.2
2	D	174	TYR	2.2
1	B	25	SER	2.2
1	B	153	GLY	2.2
1	A	51	LEU	2.2
2	C	206	ASP	2.2
1	A	178	ILE	2.2
1	B	56	LEU	2.1
1	B	58	ASN	2.1
2	D	88	LEU	2.1
1	B	63	VAL	2.1
1	B	1	ASP	2.1
2	D	227	HIS	2.1
1	B	196	ALA	2.1
2	D	237	GLY	2.1
2	C	128	ASP	2.0
2	C	133	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
2	C	77	LYS	2.0
1	A	226	PHE	2.0
2	C	238	GLU	2.0
2	D	139	VAL	2.0
1	B	163	TRP	2.0
1	B	232	TYR	2.0
1	B	233	TRP	2.0
2	C	91	ASN	2.0
1	B	230	GLY	2.0
2	D	64	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
2	PCA	D	24	8/9	0.93	0.34	96,100,104,109	0
2	PCA	C	24	8/9	0.99	0.20	37,43,47,49	0

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, 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
3	GOL	A	301	6/6	0.92	0.16	75,77,82,88	0

6.5 Other polymers [i](#)

There are no such residues in this entry.