



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 10:19 AM GMT

PDB ID : 3U4E
Title : Crystal Structure of PG9 Fab in Complex with V1V2 Region from HIV-1 strain CAP45
Authors : Gorman, J.; McLellan, J.; Pancera, M.; Kwong, P.D.
Deposited on : 2011-10-07
Resolution : 2.19 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

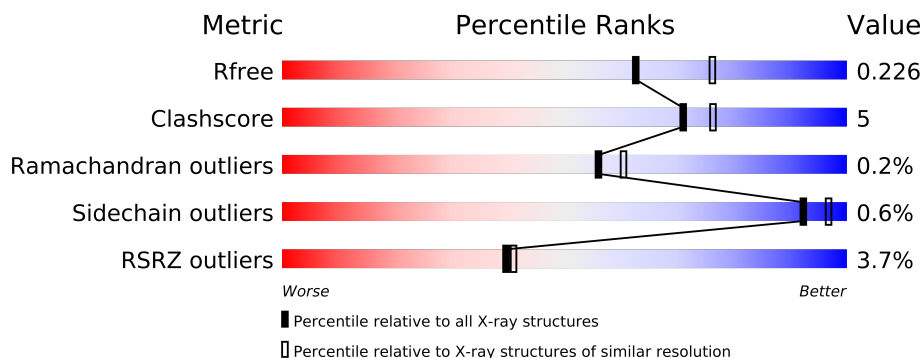
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.19 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}	66092	3841 (2.20-2.16)
Clashscore	79885	4835 (2.20-2.16)
Ramachandran outliers	78287	4740 (2.20-2.16)
Sidechain outliers	78261	4741 (2.20-2.16)
RSRZ outliers	66119	3842 (2.20-2.16)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	G	124	
1	J	124	
2	A	248	
2	H	248	
3	B	216	
3	L	216	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 17692 atoms, of which 8372 are hydrogens and 0 are deuterium.

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 V1V2 region of HIV-1 on 1FD6 scaffold.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	G	108	Total	C	H	N	O	S	0	0	0
			1647	529	805	136	172	5			
1	J	109	Total	C	H	N	O	S	0	0	0
			1659	537	806	137	175	4			

- Molecule 2 is a protein called PG9 Heavy Chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	H	239	Total	C	H	N	O	S	0	0	0
			3577	1155	1738	309	365	10			
2	A	230	Total	C	H	N	O	S	0	1	0
			3476	1127	1688	301	351	9			

- Molecule 3 is a protein called PG9 Light Chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	L	214	Total	C	H	N	O	S	0	0	0
			3138	988	1547	271	328	4			
3	B	212	Total	C	H	N	O	S	0	0	0
			3114	978	1541	268	323	4			

- Molecule 4 is a polymer of unknown type called SUGAR (7-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	G	7	Total	C	H	N	O	0	0
			154	46	71	2	35		
4	J	7	Total	C	H	N	O	0	0
			154	46	71	2	35		

- Molecule 5 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	G	6	Total	C	H	N	O	0	0
			133	40	61	2	30		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	G	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	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	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		

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

- Molecule 7 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	J	2	Total	C	H	N	O	0	0
			54	16	26	2	10		

- Molecule 8 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	2	Total	C	H	O	0	0
			40	12	18	10		

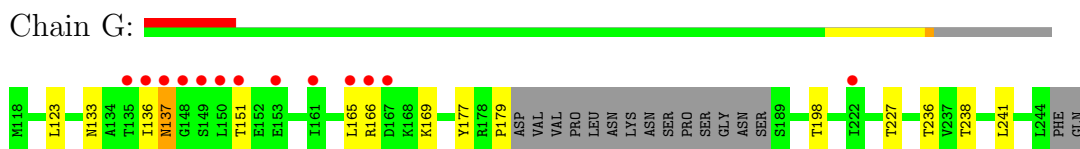
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	G	21	Total	O	0	0
			21	21		
9	J	19	Total	O	0	0
			19	19		
9	H	123	Total	O	0	0
			123	123		
9	L	135	Total	O	0	0
			135	135		
9	A	109	Total	O	0	0
			109	109		
9	B	79	Total	O	0	0
			79	79		

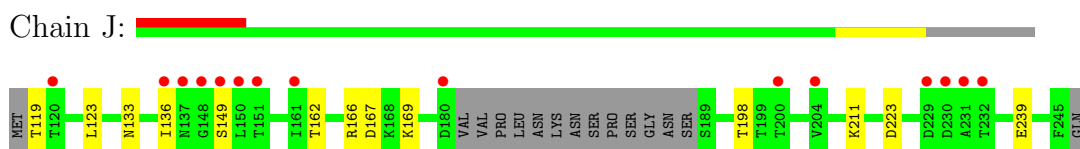
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

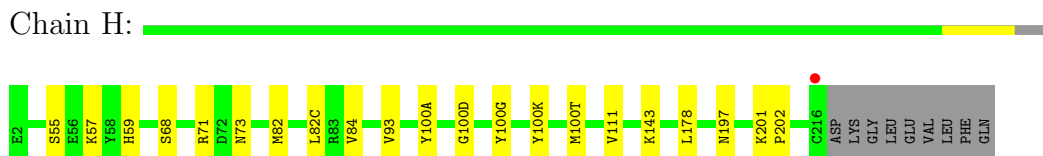
- Molecule 1: V1V2 region of HIV-1 on 1FD6 scaffold



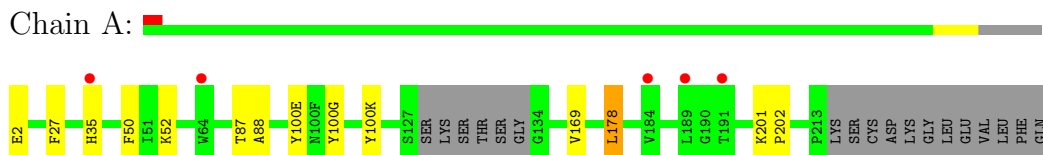
- Molecule 1: V1V2 region of HIV-1 on 1FD6 scaffold



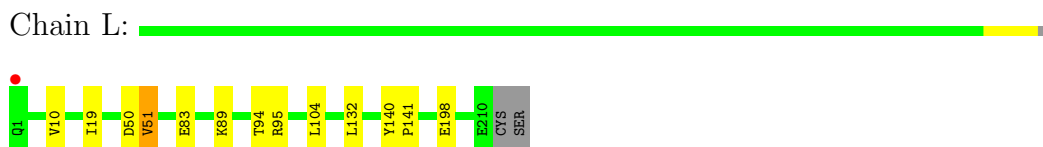
- Molecule 2: PG9 Heavy Chain



- Molecule 2: PG9 Heavy Chain

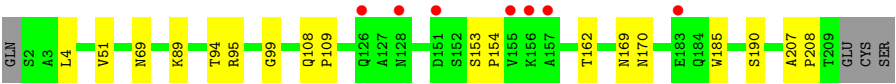


- Molecule 3: PG9 Light Chain



- Molecule 3: PG9 Light Chain





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.03Å 103.55Å 186.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.69 – 2.19 27.69 – 2.18	Depositor EDS
% Data completeness (in resolution range)	91.5 (27.69-2.19) 91.1 (27.69-2.18)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.18Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.182 , 0.234 0.175 , 0.226	Depositor DCC
R_{free} test set	3444 reflections (5.09%)	DCC
Wilson B-factor (Å ²)	34.9	Xtriage
Anisotropy	0.395	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 32.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 67685 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	17692	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.92% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, TYS, SO4, PCA, MAN

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	G	0.28	0/853	0.50	0/1157
1	J	0.26	0/865	0.48	0/1174
2	A	0.27	0/1798	0.48	0/2446
2	H	0.30	0/1847	0.51	0/2512
3	B	0.29	0/1608	0.50	0/2190
3	L	0.30	0/1626	0.52	0/2214
All	All	0.29	0/8597	0.50	0/11693

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	J	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	J	136	ILE	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit,

and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	842	805	4	10	0
1	J	853	806	0	9	0
2	A	1788	1688	0	14	0
2	H	1839	1738	0	17	0
3	B	1573	1541	0	16	0
3	L	1591	1547	0	9	0
4	G	83	71	6	0	0
4	J	83	71	6	3	0
5	G	72	61	5	9	0
6	B	20	0	0	1	0
6	G	5	0	0	0	0
6	L	35	0	0	0	0
7	J	28	26	0	8	0
8	A	22	18	3	7	0
9	A	109	0	0	1	0
9	B	79	0	0	1	0
9	G	21	0	0	1	0
9	H	123	0	0	0	0
9	J	19	0	0	3	0
9	L	135	0	0	2	0
All	All	9320	8372	24	78	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

The worst 5 of 78 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:J:1657:NAG:O4	8:A:1658:BMA:C1	1.68	1.39
7:J:1657:NAG:O4	8:A:1658:BMA:C2	1.91	1.18
5:G:658:BMA:H61	5:G:660:MAN:H5	1.43	1.00
7:J:1657:NAG:C4	8:A:1658:BMA:C1	2.44	0.94
5:G:659:MAN:H61	2:H:57:LYS:HE3	1.51	0.90

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	G	104/124 (84%)	99 (95%)	5 (5%)	0	100	100
1	J	105/124 (85%)	103 (98%)	2 (2%)	0	100	100
2	A	225/248 (91%)	220 (98%)	5 (2%)	0	100	100
2	H	235/248 (95%)	229 (97%)	6 (3%)	0	100	100
3	B	210/216 (97%)	203 (97%)	6 (3%)	1 (0%)	38	36
3	L	212/216 (98%)	206 (97%)	5 (2%)	1 (0%)	38	36
All	All	1091/1176 (93%)	1060 (97%)	29 (3%)	2 (0%)	56	60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	L	51	VAL
3	B	51	VAL

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	G	92/107 (86%)	90 (98%)	2 (2%)	64	75
1	J	93/107 (87%)	92 (99%)	1 (1%)	84	91
2	A	192/207 (93%)	191 (100%)	1 (0%)	94	97
2	H	199/207 (96%)	197 (99%)	2 (1%)	85	92
3	B	179/183 (98%)	179 (100%)	0	100	100
3	L	181/183 (99%)	181 (100%)	0	100	100
All	All	936/994 (94%)	930 (99%)	6 (1%)	92	97

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	149	SER
2	A	178	LEU
2	H	143	LYS
1	G	151	THR
2	H	197	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
3	L	37	GLN
3	B	194	GLN
2	A	171	GLN
2	H	32	GLN
2	A	32	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

6 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	TYS	A	100(G)	-	16,16,17	5.72	3 (18%)	20,22,24	1.20	2 (10%)
2	TYS	A	100(H)	2	16,16,17	6.04	3 (18%)	20,22,24	1.27	2 (10%)
2	PCA	A	2	2	8,8,9	6.41	2 (25%)	8,10,12	7.40	4 (50%)
2	TYS	H	100(G)	-	16,16,17	5.71	2 (12%)	20,22,24	1.33	3 (15%)
2	TYS	H	100(H)	2	16,16,17	5.83	3 (18%)	20,22,24	1.20	2 (10%)
2	PCA	H	2	2	8,8,9	6.41	2 (25%)	8,10,12	7.36	4 (50%)

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	TYS	A	100(G)	-	-	0/9/11/13	0/1/1/1
2	TYS	A	100(H)	2	-	0/9/11/13	0/1/1/1
2	PCA	A	2	2	-	0/0/11/13	0/1/1/1
2	TYS	H	100(G)	-	-	0/9/11/13	0/1/1/1
2	TYS	H	100(H)	2	-	0/9/11/13	0/1/1/1
2	PCA	H	2	2	-	0/0/11/13	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	100(H)	TYS	O-C	22.55	1.27	1.11
2	H	100(H)	TYS	O-C	21.69	1.26	1.11
2	A	100(G)	TYS	O-C	21.17	1.26	1.11
2	H	100(G)	TYS	O-C	21.15	1.26	1.11
2	A	2	PCA	O-C	17.02	1.23	1.11

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2	PCA	C-CA-N	-16.20	107.05	110.71
2	H	2	PCA	C-CA-N	-16.08	107.08	110.71
2	A	2	PCA	CA-N-CD	-12.57	104.55	114.37
2	H	2	PCA	CA-N-CD	-12.56	104.55	114.37
2	A	100(H)	TYS	C-CA-N	-3.55	110.28	113.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

24 carbohydrates 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	$\# Z > 2$
8	BMA	A	1658	8	10,11,12	0.69	0	11,15,17	1.61	1 (9%)
8	MAN	A	1659	8	10,11,12	0.71	0	11,15,17	1.68	1 (9%)
4	NAG	G	560	1,4	12,14,15	1.54	4 (33%)	15,19,21	2.30	3 (20%)
4	NAG	G	561	4	12,14,15	1.54	4 (33%)	15,19,21	2.09	3 (20%)
4	BMA	G	562	4	10,11,12	1.78	2 (20%)	11,15,17	1.26	1 (9%)
4	MAN	G	563	4	10,11,12	1.74	2 (20%)	11,15,17	1.84	4 (36%)
4	MAN	G	564	4	10,11,12	1.84	3 (30%)	11,15,17	1.33	2 (18%)
4	MAN	G	565	4	10,11,12	1.91	3 (30%)	11,15,17	1.39	1 (9%)
4	MAN	G	566	4	10,11,12	1.64	2 (20%)	11,15,17	1.17	1 (9%)
5	NAG	G	656	1,5	12,14,15	1.53	4 (33%)	15,19,21	2.08	2 (13%)
5	NAG	G	657	5	12,14,15	1.54	4 (33%)	15,19,21	2.13	4 (26%)
5	BMA	G	658	5	10,11,12	0.70	0	11,15,17	1.61	1 (9%)
5	MAN	G	659	5	10,11,12	0.70	0	11,15,17	1.69	1 (9%)
5	MAN	G	660	5	10,11,12	0.84	1 (10%)	11,15,17	1.30	2 (18%)
5	MAN	G	662	5	10,11,12	0.95	1 (10%)	11,15,17	1.06	1 (9%)
4	NAG	J	1560	1,4	12,14,15	1.54	4 (33%)	15,19,21	1.87	4 (26%)
4	NAG	J	1561	4	12,14,15	1.53	3 (25%)	15,19,21	2.58	4 (26%)
4	BMA	J	1562	4	10,11,12	1.77	2 (20%)	11,15,17	1.40	2 (18%)
4	MAN	J	1563	4	10,11,12	1.73	2 (20%)	11,15,17	2.84	4 (36%)
4	MAN	J	1564	4	10,11,12	1.72	2 (20%)	11,15,17	1.16	0
4	MAN	J	1565	4	10,11,12	1.81	3 (30%)	11,15,17	1.30	2 (18%)
4	MAN	J	1566	4	10,11,12	1.62	2 (20%)	11,15,17	1.24	0
7	NAG	J	1656	1,7	12,14,15	1.53	3 (25%)	15,19,21	2.25	3 (20%)
7	NAG	J	1657	7	12,14,15	1.60	3 (25%)	15,19,21	1.94	3 (20%)

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
8	BMA	A	1658	8	-	0/2/19/22	0/1/1/1
8	MAN	A	1659	8	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	G	560	1,4	-	0/6/23/26	0/1/1/1
4	NAG	G	561	4	-	0/6/23/26	0/1/1/1
4	BMA	G	562	4	-	0/2/19/22	0/1/1/1
4	MAN	G	563	4	-	0/2/19/22	0/1/1/1
4	MAN	G	564	4	-	0/2/19/22	0/1/1/1
4	MAN	G	565	4	-	0/2/19/22	0/1/1/1
4	MAN	G	566	4	-	0/2/19/22	0/1/1/1
5	NAG	G	656	1,5	-	0/6/23/26	0/1/1/1
5	NAG	G	657	5	-	0/6/23/26	0/1/1/1
5	BMA	G	658	5	-	0/2/19/22	0/1/1/1
5	MAN	G	659	5	-	0/2/19/22	0/1/1/1
5	MAN	G	660	5	-	0/2/19/22	0/1/1/1
5	MAN	G	662	5	-	0/2/19/22	0/1/1/1
4	NAG	J	1560	1,4	-	0/6/23/26	0/1/1/1
4	NAG	J	1561	4	-	0/6/23/26	0/1/1/1
4	BMA	J	1562	4	-	0/2/19/22	0/1/1/1
4	MAN	J	1563	4	-	0/2/19/22	0/1/1/1
4	MAN	J	1564	4	-	0/2/19/22	0/1/1/1
4	MAN	J	1565	4	-	0/2/19/22	0/1/1/1
4	MAN	J	1566	4	-	0/2/19/22	0/1/1/1
7	NAG	J	1656	1,7	-	0/6/23/26	0/1/1/1
7	NAG	J	1657	7	-	0/6/23/26	0/1/1/1

The worst 5 of 54 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	565	MAN	C4-C3	-3.86	1.42	1.52
4	J	1562	BMA	C4-C3	-3.83	1.42	1.52
4	G	562	BMA	C4-C3	-3.82	1.42	1.52
4	G	564	MAN	C4-C3	-3.79	1.42	1.52
4	J	1565	MAN	C4-C3	-3.77	1.42	1.52

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	1561	NAG	O5-C5-C6	8.01	115.39	106.98
7	J	1656	NAG	O5-C5-C6	6.98	114.31	106.98
5	G	656	NAG	O5-C5-C6	6.49	113.79	106.98
4	G	561	NAG	O5-C5-C6	6.01	113.28	106.98
4	G	560	NAG	O5-C5-C6	5.97	113.25	106.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.6 Ligand geometry

12 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	B	213	-	4,4,4	0.21	0	6,6,6	0.07	0
6	SO4	B	214	-	4,4,4	0.17	0	6,6,6	0.11	0
6	SO4	B	215	-	4,4,4	0.18	0	6,6,6	0.09	0
6	SO4	B	216	-	4,4,4	0.18	0	6,6,6	0.13	0
6	SO4	G	15	-	4,4,4	0.16	0	6,6,6	0.06	0
6	SO4	L	12	-	4,4,4	0.17	0	6,6,6	0.10	0
6	SO4	L	213	-	4,4,4	0.17	0	6,6,6	0.07	0
6	SO4	L	214	-	4,4,4	0.13	0	6,6,6	0.11	0
6	SO4	L	215	-	4,4,4	0.22	0	6,6,6	0.07	0
6	SO4	L	216	-	4,4,4	0.21	0	6,6,6	0.14	0
6	SO4	L	217	-	4,4,4	0.13	0	6,6,6	0.11	0
6	SO4	L	218	-	4,4,4	0.18	0	6,6,6	0.16	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
6	SO4	B	213	-	-	0/0/0/0	0/0/0/0
6	SO4	B	214	-	-	0/0/0/0	0/0/0/0
6	SO4	B	215	-	-	0/0/0/0	0/0/0/0
6	SO4	B	216	-	-	0/0/0/0	0/0/0/0
6	SO4	G	15	-	-	0/0/0/0	0/0/0/0
6	SO4	L	12	-	-	0/0/0/0	0/0/0/0
6	SO4	L	213	-	-	0/0/0/0	0/0/0/0
6	SO4	L	214	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	SO4	L	215	-	-	0/0/0/0	0/0/0/0
6	SO4	L	216	-	-	0/0/0/0	0/0/0/0
6	SO4	L	217	-	-	0/0/0/0	0/0/0/0
6	SO4	L	218	-	-	0/0/0/0	0/0/0/0

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.

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 ⓘ

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	G	108/124 (87%)	0.54	13 (12%) 5 5	29, 49, 96, 124	0
1	J	109/124 (87%)	0.65	15 (13%) 4 4	31, 61, 103, 120	0
2	A	230/248 (92%)	0.13	5 (2%) 59 60	21, 42, 85, 122	0
2	H	239/248 (96%)	-0.03	1 (0%) 90 92	21, 34, 68, 106	0
3	B	212/216 (98%)	0.15	7 (3%) 44 46	24, 46, 81, 102	0
3	L	214/216 (99%)	-0.08	1 (0%) 88 90	19, 34, 55, 109	0
All	All	1112/1176 (94%)	0.15	42 (3%) 39 40	19, 41, 84, 124	0

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	136	ILE	5.6
2	A	191	THR	5.5
3	B	155	VAL	5.1
1	G	151	THR	4.8
1	J	136	ILE	4.2

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	TYS	A	100(G)	16/17	0.10	-	28,38,92,103	0
2	PCA	A	2	8/9	0.11	-	31,45,55,60	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	TYS	H	100(H)	16/17	0.13	-	25,35,102,112	0
2	TYS	H	100(G)	16/17	0.13	-	27,35,105,119	0
2	TYS	A	100(H)	16/17	0.10	-	21,33,94,107	0
2	PCA	H	2	8/9	0.09	-	27,35,48,61	0

6.3 Carbohydrates

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	MAN	G	565	11/12	0.09	-	27,37,49,53	0
4	BMA	G	562	11/12	0.15	-	41,67,96,100	0
7	NAG	J	1657	14/15	0.12	-	48,63,77,82	0
7	NAG	J	1656	14/15	0.09	-	38,47,62,66	0
4	MAN	G	566	11/12	0.11	-	23,37,50,50	0
8	BMA	A	1658	11/12	0.12	-	136,144,171,173	0
5	NAG	G	656	14/15	0.08	-	32,51,61,69	0
5	NAG	G	657	14/15	0.11	-	49,68,88,100	0
4	MAN	G	563	11/12	0.36	-	93,110,131,132	0
5	BMA	G	658	11/12	0.12	-	116,141,169,171	0
4	MAN	J	1564	11/12	0.07	-	32,39,46,54	0
4	NAG	G	560	14/15	0.10	-	27,40,50,58	0
8	MAN	A	1659	11/12	0.29	-	118,143,167,174	0
4	NAG	G	561	14/15	0.11	-	33,47,84,101	0
4	MAN	J	1563	11/12	0.31	-	108,114,138,138	0
4	NAG	J	1561	14/15	0.10	-	22,46,74,85	0
5	MAN	G	660	11/12	0.46	-	130,148,176,178	0
4	MAN	J	1566	11/12	0.08	-	24,38,58,58	0
4	MAN	J	1565	11/12	0.09	-	32,42,52,60	0
5	MAN	G	662	11/12	0.41	-	112,142,167,171	0
5	MAN	G	659	11/12	0.29	-	111,144,176,190	0
4	BMA	J	1562	11/12	0.11	-	45,61,91,96	0
4	NAG	J	1560	14/15	0.08	-	27,41,55,58	0
4	MAN	G	564	11/12	0.08	-	29,37,47,48	0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
6	SO4	B	214	5/5	0.13	-	85,93,99,103	0
6	SO4	L	217	5/5	0.08	-	40,50,55,65	0
6	SO4	L	218	5/5	0.22	-	115,120,123,129	0
6	SO4	B	213	5/5	0.09	-	70,83,90,92	0
6	SO4	L	216	5/5	0.07	-	35,38,45,53	0
6	SO4	G	15	5/5	0.23	-	116,116,122,132	0
6	SO4	L	215	5/5	0.12	-	68,72,79,83	0
6	SO4	B	215	5/5	0.17	-	94,98,103,108	0
6	SO4	L	214	5/5	0.11	-	44,52,82,91	0
6	SO4	L	12	5/5	0.15	-	85,89,96,100	0
6	SO4	B	216	5/5	0.21	-	107,121,125,126	0
6	SO4	L	213	5/5	0.12	-	80,89,94,99	0

6.5 Other polymers

There are no such residues in this entry.