



Full wwPDB X-ray Structure Validation Report

Aug 29, 2014 – 12:18 PM EDT

PDB ID : 4UUJ
Title : POTASSIUM CHANNEL KCSA-FAB WITH TETRAHEXYLAMMONIUM
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Deposited on : 2014-07-29
Resolution : 2.40 Å(reported)

This is a full wwPDB validation 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>

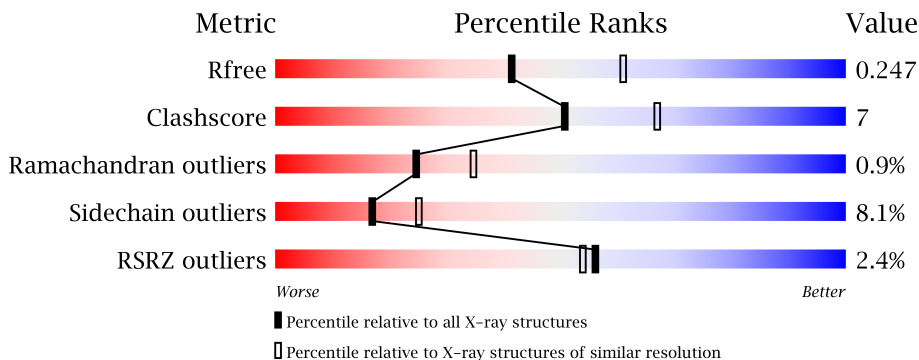
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable23489
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) : stable23489

1 Overall quality at a glance

The reported resolution of this entry is 2.40 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	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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	A	219	
2	B	212	
3	C	111	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
7	DGA	C	1129	-	X
9	XA7	C	1131[A]	-	X
9	XA7	C	1131[B]	-	X
9	XA7	C	1132[A]	-	X
9	XA7	C	1132[B]	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 4392 atoms, of which 0 are hydrogen 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 ANTIBODY FAB FRAGMENT LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1625	1030	271	318	6			

- Molecule 2 is a protein called ANTIBODY FAB FRAGMENT HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	212	Total	C	N	O	S	0	4	0
			1682	1041	292	344	5			

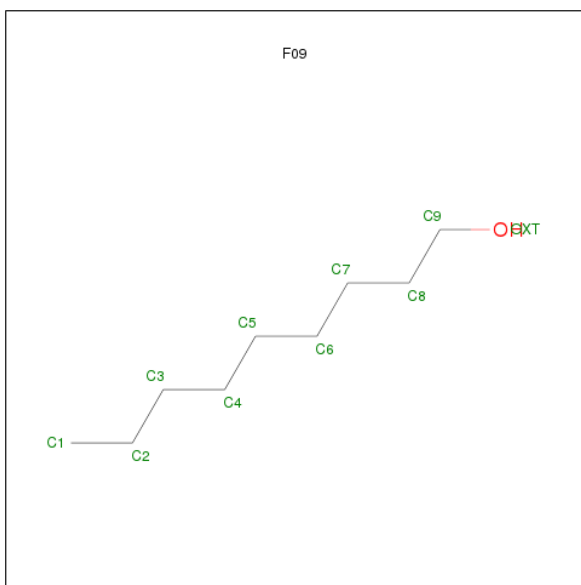
- Molecule 3 is a protein called VOLTAGE-GATED POTASSIUM CHANNEL KCSA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	111	Total	C	N	O	S	0	0	0
			820	538	140	140	2			

There are 9 discrepancies between the modelled and reference sequences:

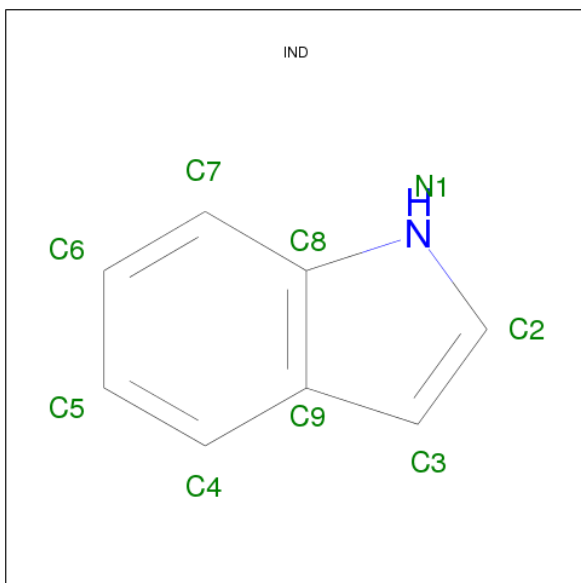
Chain	Residue	Modelled	Actual	Comment	Reference
C	11	ALA	-	EXPRESSION TAG	UNP P0A334
C	12	ALA	-	EXPRESSION TAG	UNP P0A334
C	13	VAL	-	EXPRESSION TAG	UNP P0A334
C	14	ALA	-	EXPRESSION TAG	UNP P0A334
C	15	LEU	-	EXPRESSION TAG	UNP P0A334
C	16	LEU	-	EXPRESSION TAG	UNP P0A334
C	17	LEU	-	EXPRESSION TAG	UNP P0A334
C	21	GLY	-	EXPRESSION TAG	UNP P0A334
C	90	CYS	LEU	CONFLICT	UNP P0A334

- Molecule 4 is NONAN-1-OL (three-letter code: F09) (formula: C₉H₂₀O).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 10 9 1	0	0
4	C	1	Total C 7 7	0	0
4	C	1	Total C 7 7	0	0
4	C	1	Total C 4 4	0	0

- Molecule 5 is INDOLE (three-letter code: IND) (formula: C_8H_7N).

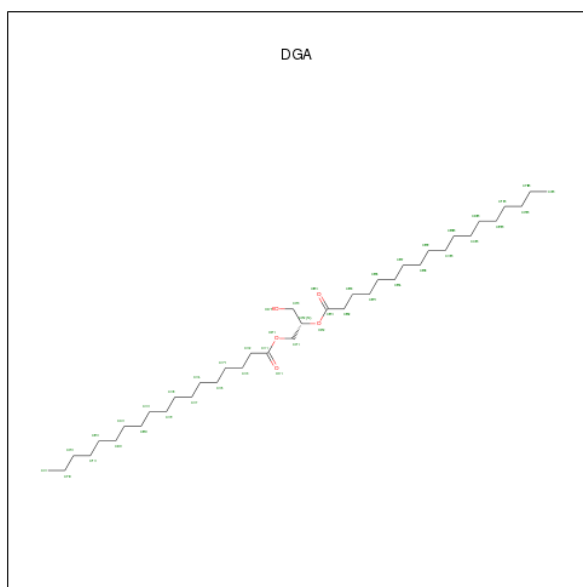


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	N	0	0
			9	8	1		

- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	4	Total	K	0	0
			4	4		

- Molecule 7 is DIACYL GLYCEROL (three-letter code: DGA) (formula: C₃₉H₇₆O₅).

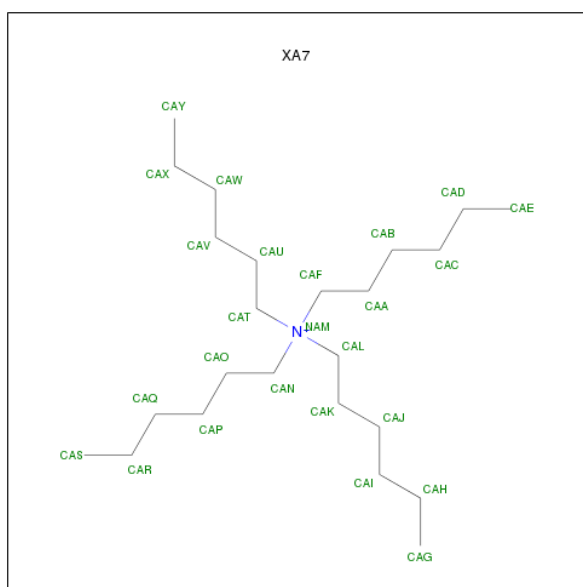


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			31	26	5		

- Molecule 8 is COBALT (II) ION (three-letter code: CO) (formula: Co).

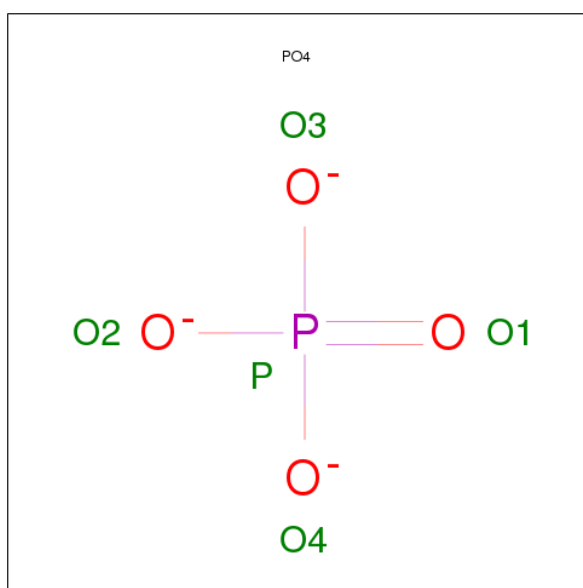
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	C	1	Total	Co	0	0
			1	1		

- Molecule 9 is TETRAHEXYL AMMONNIUM (three-letter code: XA7) (formula: C₂₄H₅₂N).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	C	1	Total	C	N	0	1
			50	48	2		
9	C	1	Total	C	N	0	1
			50	48	2		

- Molecule 10 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	C	1	Total	O	P	0	0
			5	4	1		

- Molecule 11 is water.

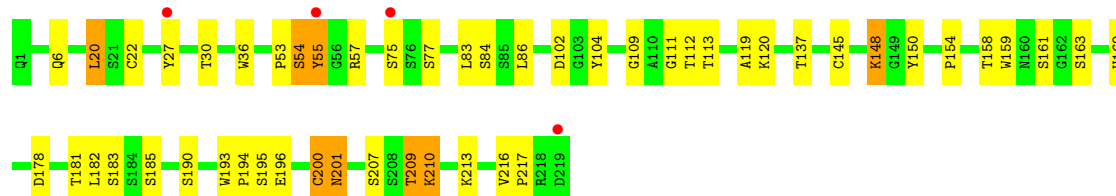
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	40	Total 40	O 40	0	0
11	B	35	Total 35	O 35	0	0
11	C	12	Total 12	O 12	0	0

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.

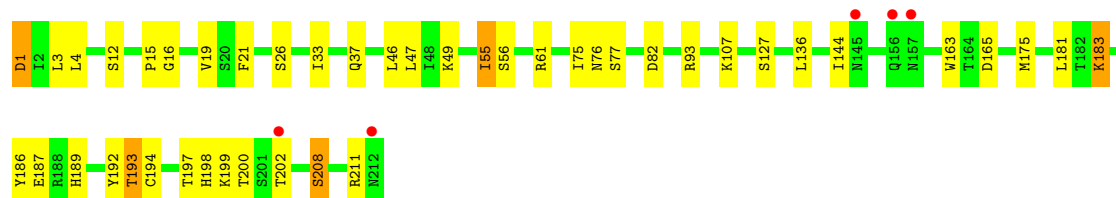
• Molecule 1: ANTIBODY FAB FRAGMENT LIGHT CHAIN

Chain A: 



• Molecule 2: ANTIBODY FAB FRAGMENT HEAVY CHAIN

Chain B: 



• Molecule 3: VOLTAGE-GATED POTASSIUM CHANNEL KCSA

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	154.62Å 154.62Å 75.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.64 – 2.40 28.64 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.2 (28.64-2.40) 98.3 (28.64-2.40)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.191 , 0.248 0.199 , 0.247	Depositor DCC
R_{free} test set	1732 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	55.8	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 50.2	EDS
Estimated twinning fraction	0.036 for -k,-h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 34584 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4392	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.13% 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: DGA, CO, K, XA7, IND, F09, PO4

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	0.66	0/1669	0.82	1/2287 (0.0%)
2	B	0.71	0/1719	0.81	0/2331
3	C	0.79	0/839	0.81	0/1152
All	All	0.71	0/4227	0.81	1/5770 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	169	HIS	CB-CA-C	-5.50	99.39	110.40

There are no chirality outliers.

There are no planarity outliers.

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	A	1625	0	1563	26	0
2	B	1682	0	1606	27	0
3	C	820	0	837	10	0
4	A	10	0	19	0	0
4	C	18	0	33	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	9	0	7	0	0
6	C	4	0	0	0	0
7	C	31	0	44	0	0
8	C	1	0	0	0	0
9	C	100	0	0	4	0
10	C	5	0	0	0	0
11	A	40	0	0	2	0
11	B	35	0	0	3	0
11	C	12	0	0	3	0
All	All	4392	0	4109	62	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 7.

All (62) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:C:1134:F09:H11	4:C:1135:F09:C7	2.06	0.85
2:B:189:HIS:O	2:B:211:ARG:NH2	2.12	0.82
9:C:1131[B]:XA7:CAT	9:C:1131[B]:XA7:CAP	2.61	0.78
1:A:6:GLN:HE21	1:A:109:GLY:HA3	1.56	0.71
9:C:1131[A]:XA7:CAP	9:C:1131[A]:XA7:CAT	2.67	0.71
9:C:1131[A]:XA7:CAO	9:C:1131[A]:XA7:CAU	2.72	0.68
2:B:93[A]:ARG:HG2	3:C:58:GLN:HG2	1.76	0.67
1:A:20:LEU:HD23	1:A:20:LEU:N	2.11	0.65
2:B:183:LYS:O	2:B:187:GLU:HG2	1.98	0.63
9:C:1131[B]:XA7:CAU	9:C:1131[B]:XA7:CAO	2.77	0.63
2:B:163:TRP:CD1	2:B:175:MET:HG3	2.34	0.63
1:A:30:THR:O	1:A:54:SER:OG	2.16	0.61
1:A:207:SER:OG	1:A:209:THR:HG23	2.01	0.61
4:C:1134:F09:C1	4:C:1135:F09:C7	2.78	0.58
2:B:93[B]:ARG:CG	3:C:56:GLY:HA2	2.34	0.57
1:A:193:TRP:CD1	1:A:194:PRO:HA	2.40	0.57
2:B:93[B]:ARG:HG2	3:C:56:GLY:HA2	1.87	0.56
1:A:27:TYR:HA	11:A:2008:HOH:O	2.05	0.55
2:B:198:HIS:O	2:B:200:THR:N	2.41	0.54
2:B:15:PRO:HD3	2:B:107:LYS:O	2.07	0.54
2:B:46:LEU:HD23	2:B:55:ILE:HD12	1.89	0.53
1:A:150:TYR:OH	1:A:182:LEU:HD23	2.09	0.53
3:C:58:GLN:HB2	11:C:2003:HOH:O	2.10	0.51
2:B:93[A]:ARG:NH1	3:C:58:GLN:NE2	2.60	0.50
2:B:46:LEU:CD2	2:B:55:ILE:HD12	2.42	0.50
1:A:182:LEU:HD12	1:A:182:LEU:C	2.32	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:193:THR:HG22	2:B:208:SER:HB3	1.93	0.49
2:B:61:ARG:NH1	2:B:82:ASP:OD2	2.45	0.49
2:B:93[A]:ARG:NH2	11:B:2027:HOH:O	2.31	0.48
1:A:20:LEU:HD13	1:A:112:THR:HG21	1.94	0.48
2:B:16:GLY:O	2:B:77:SER:HA	2.14	0.48
1:A:20:LEU:CD2	1:A:20:LEU:N	2.77	0.48
2:B:21:PHE:HB3	11:B:2006:HOH:O	2.13	0.47
1:A:53:PRO:O	1:A:55:TYR:N	2.43	0.47
1:A:83:LEU:HB3	1:A:86:LEU:HD21	1.96	0.47
2:B:93[A]:ARG:CG	3:C:58:GLN:HG2	2.44	0.47
1:A:216:VAL:HG23	1:A:217:PRO:O	2.16	0.46
1:A:159:TRP:CZ3	1:A:200:CYS:HB3	2.51	0.46
1:A:195:SER:OG	1:A:196:GLU:N	2.49	0.46
1:A:6:GLN:NE2	1:A:109:GLY:HA3	2.27	0.45
1:A:161:SER:HA	11:A:2037:HOH:O	2.17	0.45
1:A:104:TYR:CE2	2:B:49:LYS:HD2	2.52	0.45
1:A:161:SER:N	1:A:201:ASN:OD1	2.45	0.44
2:B:19:VAL:HG12	2:B:75:ILE:HB	2.00	0.44
1:A:6:GLN:NE2	1:A:111:GLY:H	2.15	0.44
1:A:148:LYS:HB3	1:A:181:THR:HG23	2.00	0.44
1:A:22:CYS:HB2	1:A:36:TRP:CH2	2.53	0.43
2:B:1[A]:ASP:HA	11:B:2002:HOH:O	2.18	0.43
2:B:3:LEU:HB3	2:B:26:SER:HB3	2.01	0.43
2:B:46:LEU:CD2	2:B:55:ILE:CD1	2.96	0.43
1:A:182:LEU:HD12	1:A:183:SER:N	2.34	0.43
3:C:71:GLU:OE2	11:C:2007:HOH:O	2.21	0.42
1:A:158:THR:HG1	1:A:201:ASN:HB2	1.85	0.42
2:B:186:TYR:HD1	2:B:192:TYR:HH	1.66	0.42
3:C:81:LEU:HB2	11:C:2007:HOH:O	2.18	0.42
1:A:113:THR:HB	1:A:154:PRO:HD3	2.02	0.42
2:B:187:GLU:O	2:B:211:ARG:NH2	2.53	0.42
2:B:37:GLN:HB2	2:B:47:LEU:HD11	2.01	0.42
2:B:93[B]:ARG:CD	3:C:56:GLY:HA2	2.50	0.41
3:C:24:LEU:O	3:C:25:HIS:C	2.59	0.41
1:A:102:ASP:N	1:A:102:ASP:OD1	2.52	0.40
2:B:144:ILE:HG23	2:B:175:MET:HE1	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	217/219 (99%)	206 (95%)	7 (3%)	4 (2%)	13	15
2	B	213/212 (100%)	202 (95%)	10 (5%)	1 (0%)	38	53
3	C	107/111 (96%)	105 (98%)	2 (2%)	0	100	100
All	All	537/542 (99%)	513 (96%)	19 (4%)	5 (1%)	25	35

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	199	LYS
1	A	55	TYR
1	A	54	SER
1	A	119	ALA
1	A	210	LYS

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	176/185 (95%)	158 (90%)	18 (10%)	11	15
2	B	193/190 (102%)	175 (91%)	18 (9%)	13	19
3	C	78/79 (99%)	77 (99%)	1 (1%)	80	93
All	All	447/454 (98%)	410 (92%)	37 (8%)	17	24

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	LEU
1	A	57	ARG
1	A	75	SER
1	A	77	SER
1	A	84	SER
1	A	120	LYS
1	A	137	THR
1	A	145	CYS
1	A	148	LYS
1	A	163	SER
1	A	178	ASP
1	A	185	SER
1	A	190	SER
1	A	200	CYS
1	A	201	ASN
1	A	209	THR
1	A	210	LYS
1	A	213	LYS
2	B	1[A]	ASP
2	B	1[B]	ASP
2	B	4	LEU
2	B	12	SER
2	B	33	ILE
2	B	55	ILE
2	B	56	SER
2	B	76	ASN
2	B	127	SER
2	B	136	LEU
2	B	165	ASP
2	B	181	LEU
2	B	183	LYS
2	B	193	THR
2	B	194	CYS
2	B	197	THR
2	B	202	THR
2	B	208	SER
3	C	49	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	39	GLN

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Mol	Chain	Res	Type
1	A	65	GLN
2	B	27	GLN
2	B	38	GLN
2	B	85	ASN
2	B	92	ASN
2	B	137	ASN
2	B	138	ASN
3	C	25	HIS
3	C	58	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 16 ligands modelled in this entry, 5 are monoatomic - leaving 11 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	F09	A	1220	-	9,9,9	1.20	1 (11%)	8,8,8	0.64	0
5	IND	B	1213	-	10,10,10	0.99	1 (10%)	13,13,13	0.62	0
7	DGA	C	1129	-	30,30,43	2.25	6 (20%)	32,32,45	1.82	8 (25%)
9	XA7	C	1131[A]	-	24,24,24	0.77	0	26,26,26	0.69	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	XA7	C	1131[B]	-	24,24,24	0.76	0	26,26,26	0.69	0
9	XA7	C	1132[A]	-	24,24,24	0.68	0	26,26,26	0.76	0
9	XA7	C	1132[B]	-	24,24,24	0.68	0	26,26,26	0.71	0
10	PO4	C	1133	-	4,4,4	0.43	0	6,6,6	0.32	0
4	F09	C	1134	-	6,6,9	0.98	1 (16%)	5,5,8	0.26	0
4	F09	C	1135	-	6,6,9	1.87	1 (16%)	5,5,8	0.32	0
4	F09	C	1136	-	3,3,9	1.76	1 (33%)	2,2,8	0.36	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	F09	A	1220	-	-	0/7/7/7	0/0/0/0
5	IND	B	1213	-	-	0/0/0/0	0/2/2/2
7	DGA	C	1129	-	-	0/32/32/45	0/0/0/0
9	XA7	C	1131[A]	-	-	0/28/28/28	0/0/0/0
9	XA7	C	1131[B]	-	-	0/28/28/28	0/0/0/0
9	XA7	C	1132[A]	-	-	0/28/28/28	0/0/0/0
9	XA7	C	1132[B]	-	-	0/28/28/28	0/0/0/0
10	PO4	C	1133	-	-	0/0/0/0	0/0/0/0
4	F09	C	1134	-	-	0/4/4/7	0/0/0/0
4	F09	C	1135	-	-	0/4/4/7	0/0/0/0
4	F09	C	1136	-	-	0/1/1/7	0/0/0/0

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	C	1129	DGA	CEB-CDB	-9.33	1.51	1.55
7	C	1129	DGA	OG1-CA1	4.67	1.47	1.33
4	C	1135	F09	C7-C6	-4.52	1.53	1.55
7	C	1129	DGA	OG2-CB1	3.70	1.45	1.34
4	A	1220	F09	OXT-C9	-3.26	1.24	1.42
4	C	1136	F09	C4-C3	-2.99	1.54	1.55
7	C	1129	DGA	CB5-CB4	-2.75	1.35	1.51
7	C	1129	DGA	CA9-CA8	-2.70	1.54	1.55
7	C	1129	DGA	CG3-CG2	2.42	1.55	1.50
5	B	1213	IND	C5-C4	2.33	1.42	1.36
4	C	1134	F09	C7-C6	-2.19	1.54	1.55

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
7	C	1129	DGA	OG1-CA1-CA2	5.51	128.76	111.90
7	C	1129	DGA	OG2-CB1-CB2	4.10	120.28	111.54
7	C	1129	DGA	OG1-CG1-CG2	3.20	117.22	108.80
7	C	1129	DGA	OG1-CA1-OA1	-3.02	115.58	123.48
7	C	1129	DGA	CG2-OG2-CB1	-2.51	111.95	117.86
7	C	1129	DGA	CA9-CA8-CA7	2.49	120.05	112.94
7	C	1129	DGA	OG2-CB1-OB1	-2.34	117.42	123.66
7	C	1129	DGA	OA1-CA1-CA2	-2.00	115.66	123.78

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	A	219/219 (100%)	-0.26	4 (1%) 65 63	45, 81, 111, 128	0
2	B	212/212 (100%)	-0.28	5 (2%) 56 54	36, 74, 113, 158	0
3	C	111/111 (100%)	-0.09	4 (3%) 41 39	36, 51, 104, 124	0
All	All	542/542 (100%)	-0.23	13 (2%) 56 54	36, 73, 111, 158	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	55	TYR	4.1
1	A	27	TYR	3.9
2	B	212	ASN	3.3
3	C	17	LEU	3.1
2	B	157	ASN	3.1
3	C	15	LEU	2.8
2	B	202	THR	2.7
3	C	13	VAL	2.2
2	B	156	GLN	2.2
1	A	75	SER	2.1
1	A	219	ASP	2.1
2	B	145	ASN	2.1
3	C	11	ALA	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
9	XA7	C	1131[B]	25/25	0.27	13.05	92,96,99,100	25
9	XA7	C	1131[A]	25/25	0.27	13.05	73,77,82,83	25
9	XA7	C	1132[A]	25/25	0.26	5.22	11,11,12,12	25
9	XA7	C	1132[B]	25/25	0.26	5.22	36,36,37,37	25
7	DGA	C	1129	31/44	0.22	2.95	51,90,98,104	0
4	F09	A	1220	10/10	0.30	1.75	70,79,84,86	0
4	F09	C	1136	4/10	0.17	1.37	72,74,74,79	0
4	F09	C	1134	7/10	0.20	0.59	62,66,77,86	0
6	K	C	1128	1/1	0.14	-0.24	44,44,44,44	1
4	F09	C	1135	7/10	0.13	-0.48	83,101,118,125	0
10	PO4	C	1133	5/5	0.10	-0.63	69,70,102,114	0
6	K	C	1125	1/1	0.10	-1.07	39,39,39,39	1
6	K	C	1126	1/1	0.07	-4.49	35,35,35,35	1
6	K	C	1127	1/1	0.08	-8.51	36,36,36,36	1
5	IND	B	1213	9/9	0.17	-	100,112,124,127	0
8	CO	C	1130	1/1	0.09	-	51,51,51,51	1

6.5 Other polymers ⓘ

There are no such residues in this entry.