Full wwPDB X-ray Structure Validation Report (i)

Nov 14, 2023 – 10:05 PM JST

PDB ID	:	6AFV
Title	:	Proton pyrophosphatase-L555K mutant
Authors	:	Tsai, J.-Y.; Li, K.-M.; Sun, Y.-J.
Deposited on	:	2018-08-08
Resolution	:	2.70 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 (i) 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 (i)) were used in the production of this report:

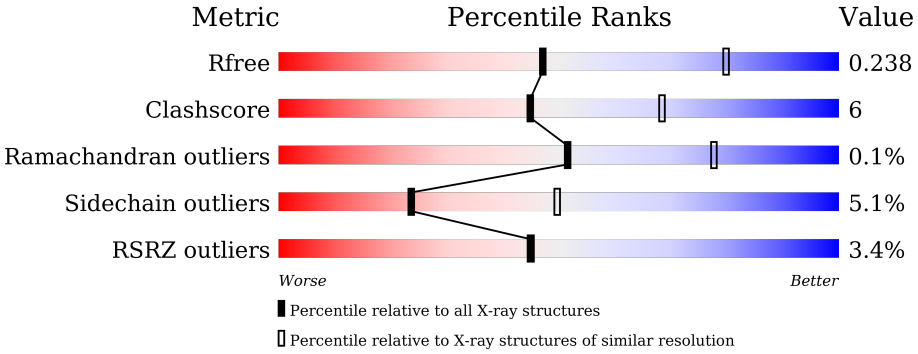
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 <=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	766	2% 79% 16% • •
1	B	766	5% 82% 13% • •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	1PG	A	1011	-	-	-	X
5	1PG	B	1011	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 11215 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.

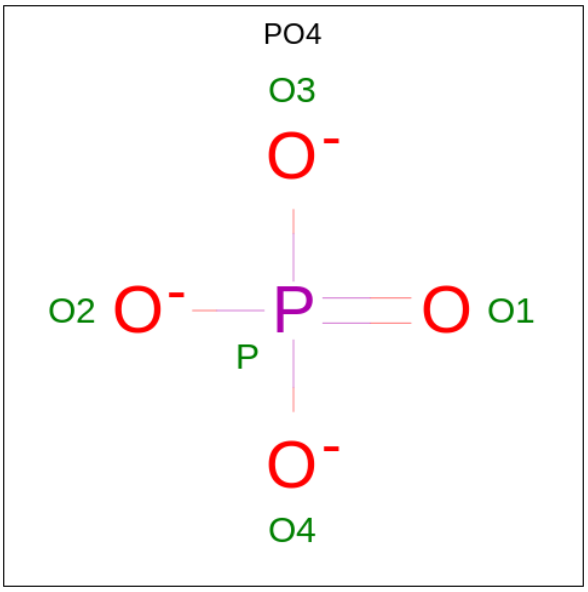
- Molecule 1 is a protein called Pyrophosphate-energized vacuolar membrane proton pump.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	740	5432	3540	863	1000	29	0	0	0
1	B	740	5432	3540	863	1000	29	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	555	LYS	LEU	engineered mutation	UNP P21616
B	555	LYS	LEU	engineered mutation	UNP P21616

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	A	1	5	4	1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0

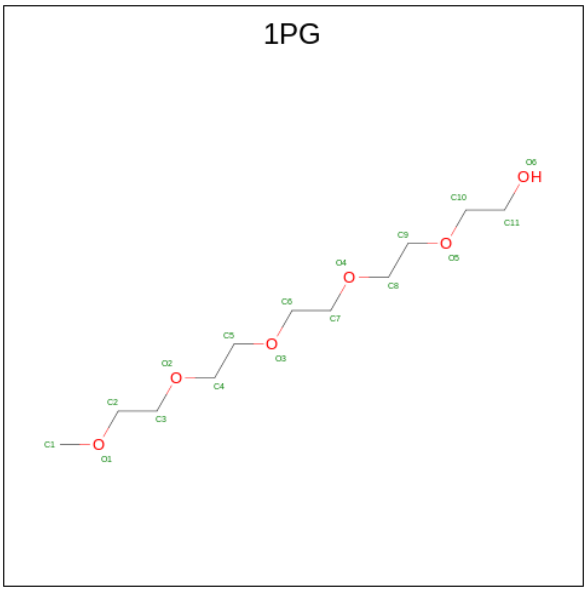
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	5	Total Mg 5 5	0	0
3	B	5	Total Mg 5 5	0	0

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total K 1 1	0	0
4	B	1	Total K 1 1	0	0

- Molecule 5 is 2-(2-{2-[2-(2-METHOXY-ETHOXY)-ETHOXY]-ETHOXY}-ETHOXY)-ETHANOL (three-letter code: 1PG) (formula: $C_{11}H_{24}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	17	11	6	0	0
5	A	1	17	11	6	0	0
5	A	1	17	11	6	0	0
5	B	1	17	11	6	0	0
5	B	1	17	11	6	0	0
5	B	1	17	11	6	0	0

- Molecule 6 is water.

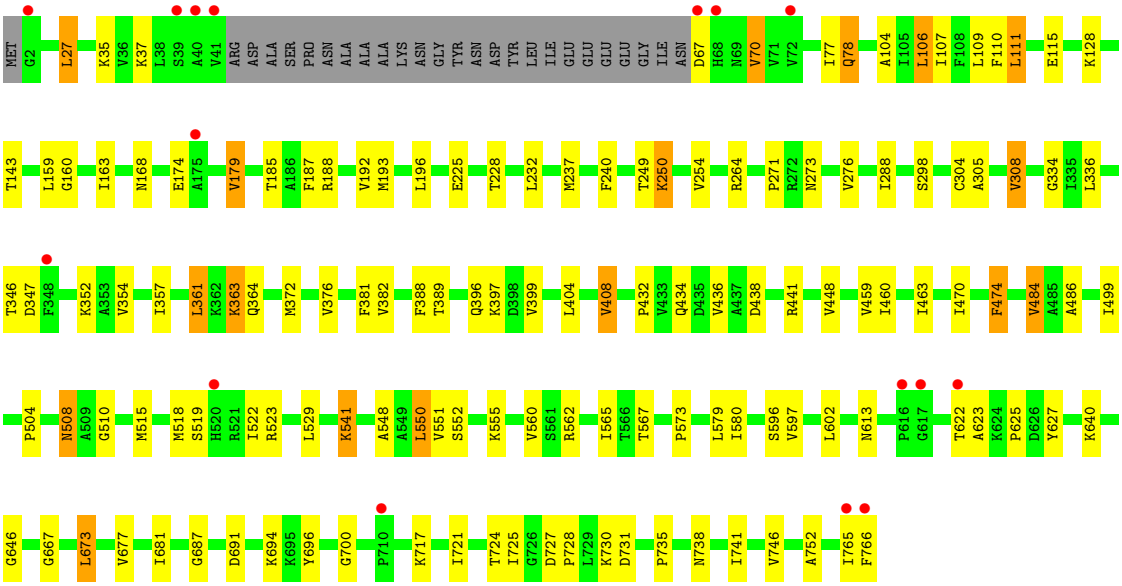
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	130	130	130	0	0
6	B	87	87	87	0	0

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.

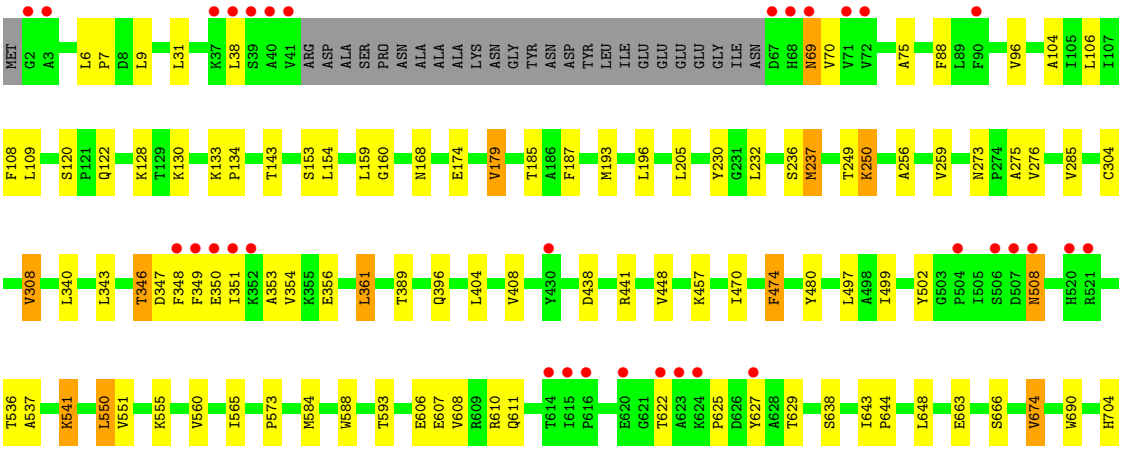
• Molecule 1: Pyrophosphate-energized vacuolar membrane proton pump

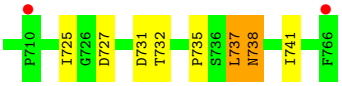
Chain A:



• Molecule 1: Pyrophosphate-energized vacuolar membrane proton pump

Chain B:




P710
I725
G726
D727
D731
T732
P735
S736
L737
N738
I741
F766

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	221.35Å 88.62Å 160.96Å 90.00° 126.05° 90.00°	Depositor
Resolution (Å)	28.06 – 2.70 28.06 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.8 (28.06-2.70) 87.7 (28.06-2.70)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.13 (at 2.72Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.197 , 0.238 0.198 , 0.238	Depositor DCC
R_{free} test set	2000 reflections (2.92%)	wwPDB-VP
Wilson B-factor (Å^2)	55.8	Xtriage
Anisotropy	0.656	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 53.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	11215	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.44% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: 1PG, K, PO4, MG

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	0.43	0/5538	0.57	0/7524
1	B	0.41	0/5538	0.53	0/7524
All	All	0.42	0/11076	0.55	0/15048

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	A	5432	0	5578	83	0
1	B	5432	0	5578	66	0
2	A	10	0	0	0	0
2	B	10	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	51	0	72	2	0
5	B	51	0	72	5	0
6	A	130	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	87	0	0	3	0
All	All	11215	0	11300	144	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 6.

All (144) 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)
1:A:271:PRO:HG3	1:A:515:MET:HA	1.61	0.81
1:A:249:THR:HG23	1:A:250:LYS:HD2	1.70	0.74
1:B:735:PRO:O	1:B:738:ASN:ND2	2.24	0.70
1:A:441:ARG:NH2	1:B:606:GLU:OE1	2.25	0.68
1:B:187:PHE:HE1	1:B:499:ILE:HG22	1.58	0.68
1:B:273:ASN:HB3	1:B:276:VAL:HG23	1.77	0.67
1:B:130:LYS:NZ	6:B:1101:HOH:O	2.28	0.65
1:A:273:ASN:HB3	1:A:276:VAL:HG23	1.80	0.64
1:B:250:LYS:HG3	1:B:727:ASP:HB3	1.81	0.63
1:B:457:LYS:HE2	5:B:1011:1PG:H32	1.82	0.62
1:A:187:PHE:HE1	1:A:499:ILE:HG22	1.65	0.62
1:A:357:ILE:HD13	1:A:529:LEU:HD23	1.80	0.62
1:B:343:LEU:HA	1:B:346:THR:HG22	1.81	0.61
1:B:351:ILE:HG23	1:B:356:GLU:HB2	1.83	0.61
1:A:560:VAL:HG13	1:A:565:ILE:HB	1.82	0.60
1:B:179:VAL:HG11	1:B:354:VAL:HG12	1.83	0.60
1:B:249:THR:HG23	1:B:250:LYS:HD2	1.85	0.59
1:A:78:GLN:NE2	1:A:168:ASN:OD1	2.34	0.59
1:A:174:GLU:HG3	1:A:185:THR:HG21	1.85	0.59
1:B:259:VAL:HG21	1:B:608:VAL:HB	1.84	0.59
1:A:580:ILE:HA	1:B:674:VAL:HG22	1.84	0.59
1:A:305:ALA:HB2	1:A:555:LYS:HE2	1.85	0.58
1:A:250:LYS:NZ	6:A:1110:HOH:O	2.36	0.58
1:A:106:LEU:HD13	1:A:110:PHE:CE2	2.39	0.58
1:A:179:VAL:HG11	1:A:354:VAL:HG12	1.86	0.57
1:B:174:GLU:HG3	1:B:185:THR:HG21	1.86	0.57
1:B:560:VAL:HG13	1:B:565:ILE:HB	1.87	0.57
1:B:470:ILE:O	1:B:474:PHE:HB2	2.04	0.56
1:A:250:LYS:HG3	1:A:727:ASP:HB3	1.88	0.55
1:B:499:ILE:O	1:B:536:THR:HG21	2.06	0.55
1:A:518:MET:HE1	1:A:522:ILE:HG21	1.90	0.54
1:B:122:GLN:NE2	1:B:133:LYS:O	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:648:LEU:HA	5:B:1009:1PG:H82	1.89	0.53
1:B:69:ASN:N	1:B:69:ASN:OD1	2.42	0.53
1:A:727:ASP:O	1:A:731:ASP:HB2	2.09	0.53
1:B:448:VAL:HA	1:B:690:TRP:CZ2	2.43	0.53
1:A:725:ILE:O	1:A:728:PRO:HD2	2.10	0.52
1:B:38:LEU:HD12	1:B:75:ALA:HB2	1.92	0.51
1:A:250:LYS:HD3	1:A:731:ASP:HB3	1.92	0.51
1:A:510:GLY:O	1:A:523:ARG:NH1	2.43	0.50
1:B:438:ASP:OD1	1:B:704:HIS:NE2	2.41	0.50
1:B:389:THR:HB	1:B:396:GLN:HB3	1.94	0.50
1:B:438:ASP:OD2	1:B:441:ARG:NH1	2.45	0.50
1:A:486:ALA:HB2	1:A:550:LEU:HB3	1.93	0.50
1:B:160:GLY:HA2	1:B:193:MET:HG3	1.94	0.49
1:A:254:VAL:HG13	1:A:724:THR:HB	1.94	0.49
1:B:108:PHE:HD2	1:B:109:LEU:HD12	1.77	0.49
1:A:438:ASP:OD2	1:A:441:ARG:NH1	2.44	0.49
1:B:159:LEU:HD13	1:B:196:LEU:HD13	1.93	0.49
1:A:548:ALA:HA	1:A:551:VAL:HG12	1.95	0.49
1:B:499:ILE:HG13	1:B:536:THR:HG23	1.95	0.48
1:A:334:GLY:HA2	1:A:372:MET:SD	2.53	0.48
1:A:640:LYS:HB2	5:A:1011:1PG:H101	1.95	0.48
1:A:463:ILE:HG13	1:B:584:MET:HB2	1.95	0.48
1:B:625:PRO:HG2	1:B:627:TYR:CE1	2.50	0.47
1:A:363:LYS:HA	1:A:363:LYS:HD2	1.66	0.47
1:A:765:ILE:HG13	1:A:766:PHE:CE1	2.49	0.47
1:A:225:GLU:O	1:A:228:THR:OG1	2.32	0.47
1:A:361:LEU:O	1:A:364:GLN:HB2	2.14	0.47
1:B:250:LYS:NZ	6:B:1118:HOH:O	2.46	0.47
1:A:573:PRO:HG3	1:B:474:PHE:CG	2.50	0.47
1:A:107:ILE:O	1:A:111:LEU:HB2	2.16	0.46
1:A:555:LYS:NZ	6:A:1115:HOH:O	2.40	0.46
1:A:104:ALA:HB1	1:A:143:THR:HG23	1.98	0.46
1:A:264:ARG:NH2	1:A:613:ASN:OD1	2.48	0.46
1:B:663:GLU:O	1:B:666:SER:HB2	2.15	0.46
1:A:687:GLY:HA3	1:A:730:LYS:HB3	1.96	0.46
1:B:537:ALA:O	1:B:541:LYS:HD3	2.16	0.46
1:A:160:GLY:HA2	1:A:193:MET:HG3	1.98	0.45
1:A:163:ILE:HG12	1:A:192:VAL:HB	1.98	0.45
1:B:96:VAL:HG11	1:B:154:LEU:HD21	1.98	0.45
1:B:610:ARG:HH21	1:B:611:GLN:HG2	1.82	0.45
1:A:434:GLN:HG2	1:A:696:TYR:CZ	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:LYS:O	1:A:37:LYS:HG2	2.17	0.45
1:A:597:VAL:HG11	1:A:728:PRO:HB3	1.99	0.45
5:B:1009:1PG:H42	5:B:1009:1PG:H22	1.55	0.45
1:A:623:ALA:O	6:A:1101:HOH:O	2.20	0.45
1:A:432:PRO:O	1:A:436:VAL:HG23	2.16	0.45
1:A:159:LEU:HD13	1:A:196:LEU:HD13	1.99	0.44
1:A:168:ASN:HB2	1:A:508:ASN:HB3	1.98	0.44
1:A:724:THR:HA	1:A:727:ASP:OD2	2.18	0.44
1:B:31:LEU:HD12	1:B:31:LEU:HA	1.85	0.44
1:B:643:ILE:HB	1:B:644:PRO:HD3	1.99	0.44
1:A:470:ILE:O	1:A:474:PHE:HB2	2.16	0.44
1:B:6:LEU:HD12	1:B:7:PRO:HD2	1.99	0.44
1:B:104:ALA:HB1	1:B:143:THR:HG23	1.99	0.44
1:A:27:LEU:HD12	1:A:27:LEU:HA	1.81	0.44
1:B:404:LEU:HD11	1:B:480:TYR:HE2	1.82	0.44
1:A:389:THR:HB	1:A:396:GLN:HB3	2.00	0.44
5:B:1009:1PG:H72	5:B:1009:1PG:H52	1.61	0.44
1:A:273:ASN:HB3	1:A:276:VAL:CG2	2.46	0.43
1:B:555:LYS:NZ	6:B:1122:HOH:O	2.51	0.43
1:B:96:VAL:CG1	1:B:237:MET:HG3	2.49	0.43
1:A:188:ARG:O	1:A:192:VAL:HG23	2.18	0.43
5:B:1010:1PG:H21	5:B:1010:1PG:H41	1.67	0.43
1:A:388:PHE:CE1	1:A:399:VAL:HB	2.54	0.43
1:A:691:ASP:O	1:A:694:LYS:HB3	2.18	0.43
1:B:6:LEU:HA	1:B:7:PRO:HD3	1.87	0.43
1:B:737:LEU:O	1:B:741:ILE:HG13	2.18	0.43
1:A:159:LEU:HD23	1:A:159:LEU:HA	1.87	0.43
1:B:256:ALA:HB2	1:B:275:ALA:HB3	1.99	0.43
1:A:67:ASP:HB3	1:A:70:VAL:HB	1.99	0.43
1:A:240:PHE:CE1	1:A:646:GLY:HA3	2.54	0.43
1:A:448:VAL:HG11	1:B:725:ILE:HD13	1.99	0.43
1:B:168:ASN:HB2	1:B:508:ASN:HB3	2.01	0.43
1:A:346:THR:HG22	1:A:347:ASP:CG	2.39	0.43
1:A:404:LEU:HD23	1:A:404:LEU:HA	1.79	0.43
1:B:497:LEU:HD23	1:B:497:LEU:HA	1.90	0.43
1:A:717:LYS:O	1:A:721:ILE:HG12	2.18	0.42
1:A:389:THR:HA	1:A:397:LYS:O	2.19	0.42
1:A:552:SER:OG	1:A:741:ILE:HG22	2.19	0.42
1:B:106:LEU:HD23	1:B:106:LEU:HA	1.83	0.42
1:B:205:LEU:HD13	1:B:230:TYR:CD2	2.53	0.42
1:B:353:ALA:HB3	1:B:356:GLU:HG3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:593:THR:HB	1:B:732:THR:HG22	2.01	0.42
1:B:250:LYS:HD3	1:B:731:ASP:HB2	2.02	0.42
1:A:474:PHE:CG	1:B:573:PRO:HG3	2.55	0.42
1:A:128:LYS:HE2	1:A:128:LYS:HB3	1.89	0.42
1:A:579:LEU:HA	1:A:667:GLY:O	2.19	0.42
1:B:350:GLU:HG2	1:B:351:ILE:N	2.34	0.42
1:A:765:ILE:HG13	1:A:766:PHE:CD1	2.55	0.42
1:A:625:PRO:HG2	1:A:627:TYR:CE1	2.55	0.41
1:B:361:LEU:HD21	1:B:502:TYR:CE2	2.55	0.41
1:A:562:ARG:HG3	1:A:752:ALA:HB3	2.02	0.41
1:B:304:CYS:O	1:B:308:VAL:HG13	2.20	0.41
1:B:88:PHE:HE1	1:B:638:SER:HG	1.64	0.41
1:B:120:SER:O	1:B:134:PRO:HB3	2.20	0.41
1:A:288:ILE:HG12	1:A:504:PRO:HG2	2.02	0.41
1:A:376:VAL:HG11	1:A:408:VAL:HG22	2.02	0.41
1:A:460:ILE:HD11	1:B:588:TRP:CD1	2.56	0.41
1:A:304:CYS:O	1:A:308:VAL:HG22	2.21	0.41
1:A:352:LYS:HB2	1:A:352:LYS:NZ	2.35	0.41
1:A:381:PHE:HD2	1:A:382:VAL:HG12	1.86	0.41
1:A:725:ILE:HD13	1:B:448:VAL:HG11	2.02	0.41
1:B:550:LEU:HD12	1:B:550:LEU:HA	1.90	0.41
1:A:694:LYS:HB3	1:A:694:LYS:HE2	1.91	0.40
1:A:459:VAL:HA	1:A:681:ILE:HG21	2.04	0.40
1:A:552:SER:HB3	1:A:673:LEU:HD22	2.03	0.40
1:B:607:GLU:OE2	1:B:629:THR:HG21	2.21	0.40
1:A:541:LYS:HD2	1:A:735:PRO:HB3	2.02	0.40
1:A:77:ILE:HD13	1:A:515:MET:HB3	2.03	0.40
1:A:408:VAL:HG12	1:A:484:VAL:HG13	2.03	0.40
1:A:640:LYS:HG3	5:A:1011:1PG:H82	2.03	0.40
1:B:122:GLN:HE22	1:B:134:PRO:HA	1.87	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	736/766 (96%)	717 (97%)	18 (2%)	1 (0%)	51	78
1	B	736/766 (96%)	703 (96%)	32 (4%)	1 (0%)	51	78
All	All	1472/1532 (96%)	1420 (96%)	50 (3%)	2 (0%)	51	78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	700	GLY
1	B	348	PHE

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	A	568/588 (97%)	537 (94%)	31 (6%)	21	46
1	B	568/588 (97%)	541 (95%)	27 (5%)	25	53
All	All	1136/1176 (97%)	1078 (95%)	58 (5%)	24	50

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	LEU
1	A	70	VAL
1	A	78	GLN
1	A	106	LEU
1	A	109	LEU
1	A	111	LEU
1	A	115	GLU
1	A	179	VAL
1	A	232	LEU
1	A	237	MET
1	A	250	LYS

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Mol	Chain	Res	Type
1	A	298	SER
1	A	308	VAL
1	A	336	LEU
1	A	361	LEU
1	A	363	LYS
1	A	408	VAL
1	A	474	PHE
1	A	484	VAL
1	A	508	ASN
1	A	519	SER
1	A	541	LYS
1	A	550	LEU
1	A	567	THR
1	A	596	SER
1	A	602	LEU
1	A	622	THR
1	A	673	LEU
1	A	677	VAL
1	A	738	ASN
1	A	746	VAL
1	B	9	LEU
1	B	69	ASN
1	B	70	VAL
1	B	128	LYS
1	B	153	SER
1	B	179	VAL
1	B	232	LEU
1	B	236	SER
1	B	237	MET
1	B	250	LYS
1	B	285	VAL
1	B	308	VAL
1	B	340	LEU
1	B	346	THR
1	B	347	ASP
1	B	349	PHE
1	B	361	LEU
1	B	408	VAL
1	B	474	PHE
1	B	508	ASN
1	B	541	LYS
1	B	550	LEU

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Mol	Chain	Res	Type
1	B	551	VAL
1	B	622	THR
1	B	674	VAL
1	B	737	LEU
1	B	738	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	284	ASN
1	B	78	GLN

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)

Of 22 ligands modelled in this entry, 12 are monoatomic - leaving 10 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	$\#\|Z\| > 2$
2	PO4	A	1001	3	4,4,4	0.80	0	6,6,6	0.94	0
2	PO4	B	1001	3	4,4,4	0.81	0	6,6,6	0.77	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	1PG	A	1011	-	16,16,16	0.79	0	15,15,15	0.26	0
5	1PG	B	1010	-	16,16,16	0.77	0	15,15,15	0.37	0
5	1PG	A	1009	-	16,16,16	0.76	0	15,15,15	0.54	0
2	PO4	A	1002	3	4,4,4	0.90	0	6,6,6	0.73	0
5	1PG	B	1009	-	16,16,16	0.86	0	15,15,15	0.48	0
2	PO4	B	1002	3	4,4,4	1.01	0	6,6,6	0.54	0
5	1PG	B	1011	-	16,16,16	0.91	0	15,15,15	0.59	0
5	1PG	A	1010	-	16,16,16	0.82	0	15,15,15	0.30	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
5	1PG	A	1011	-	-	9/14/14/14	-
5	1PG	B	1010	-	-	9/14/14/14	-
5	1PG	A	1009	-	-	7/14/14/14	-
5	1PG	B	1009	-	-	7/14/14/14	-
5	1PG	B	1011	-	-	7/14/14/14	-
5	1PG	A	1010	-	-	8/14/14/14	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (47) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1009	1PG	C7-C6-O3-C5
5	B	1009	1PG	C2-C3-O2-C4
5	B	1009	1PG	O3-C6-C7-O4
5	B	1010	1PG	O3-C6-C7-O4
5	A	1009	1PG	O4-C8-C9-O5
5	B	1010	1PG	O1-C2-C3-O2
5	B	1010	1PG	O4-C8-C9-O5
5	B	1011	1PG	O3-C6-C7-O4
5	A	1010	1PG	O3-C6-C7-O4
5	A	1011	1PG	O4-C8-C9-O5
5	B	1010	1PG	C2-C3-O2-C4

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Mol	Chain	Res	Type	Atoms
5	A	1009	1PG	O3-C6-C7-O4
5	B	1011	1PG	O1-C2-C3-O2
5	A	1009	1PG	O5-C10-C11-O6
5	A	1010	1PG	O5-C10-C11-O6
5	A	1010	1PG	O1-C2-C3-O2
5	A	1010	1PG	O4-C8-C9-O5
5	B	1009	1PG	O4-C8-C9-O5
5	B	1011	1PG	O2-C4-C5-O3
5	B	1010	1PG	C6-C7-O4-C8
5	B	1009	1PG	O2-C4-C5-O3
5	A	1011	1PG	O5-C10-C11-O6
5	A	1011	1PG	C7-C6-O3-C5
5	B	1011	1PG	O4-C8-C9-O5
5	B	1010	1PG	C3-C2-O1-C1
5	A	1010	1PG	O2-C4-C5-O3
5	B	1009	1PG	C5-C4-O2-C3
5	A	1011	1PG	C8-C9-O5-C10
5	A	1011	1PG	C6-C7-O4-C8
5	A	1009	1PG	C3-C2-O1-C1
5	A	1010	1PG	C5-C4-O2-C3
5	A	1011	1PG	C4-C5-O3-C6
5	B	1011	1PG	C4-C5-O3-C6
5	A	1010	1PG	C9-C8-O4-C7
5	A	1009	1PG	O1-C2-C3-O2
5	B	1010	1PG	C4-C5-O3-C6
5	B	1011	1PG	C2-C3-O2-C4
5	A	1009	1PG	C9-C8-O4-C7
5	A	1010	1PG	C4-C5-O3-C6
5	A	1011	1PG	C11-C10-O5-C9
5	A	1009	1PG	O2-C4-C5-O3
5	A	1011	1PG	O3-C6-C7-O4
5	A	1011	1PG	O2-C4-C5-O3
5	B	1009	1PG	C11-C10-O5-C9
5	B	1010	1PG	O2-C4-C5-O3
5	B	1011	1PG	C9-C8-O4-C7
5	B	1010	1PG	C8-C9-O5-C10

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1011	1PG	2	0

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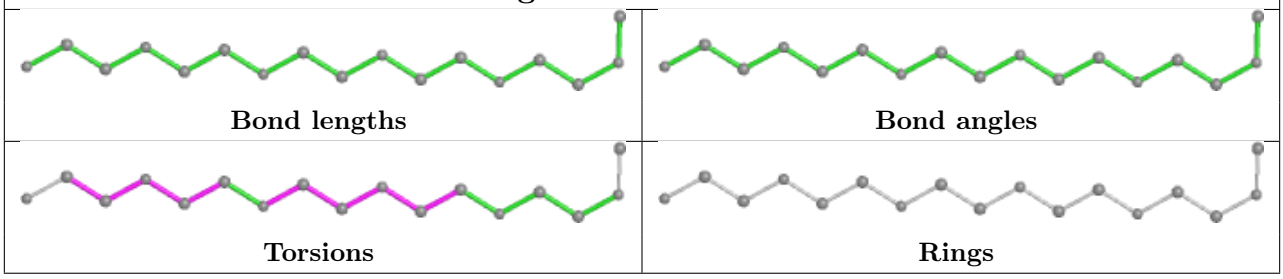
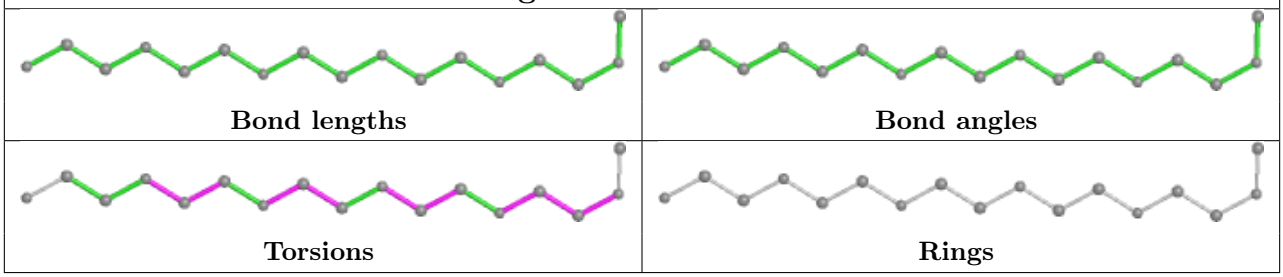
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1010	1PG	1	0
5	B	1009	1PG	3	0
5	B	1011	1PG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

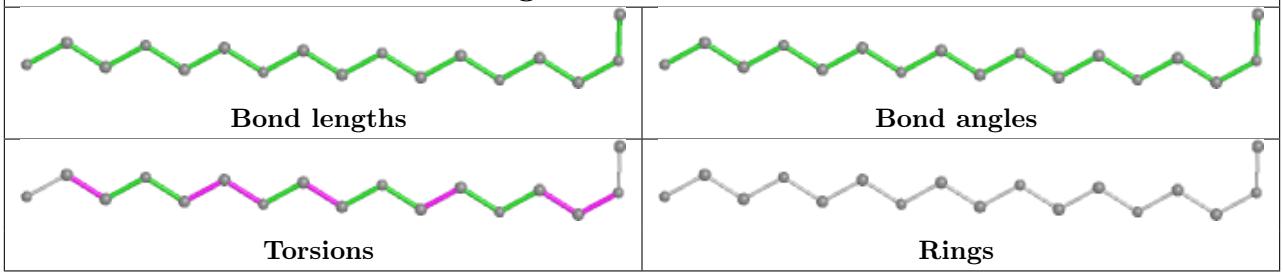
Ligand 1PG A 1011

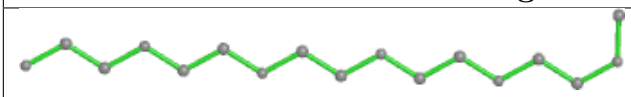
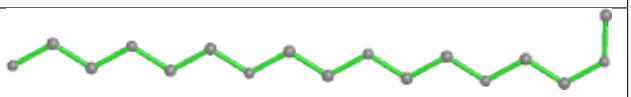
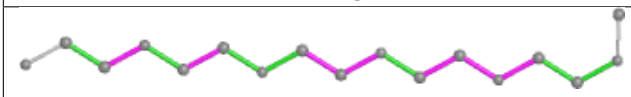
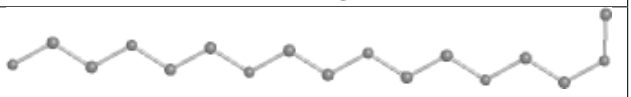


Ligand 1PG B 1010



Ligand 1PG A 1009



Ligand 1PG B 1009	
 Bond lengths	 Bond angles
 Torsions	 Rings

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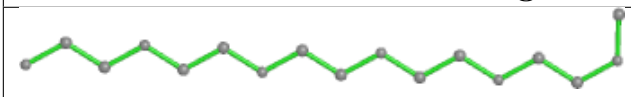
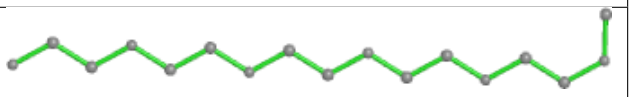
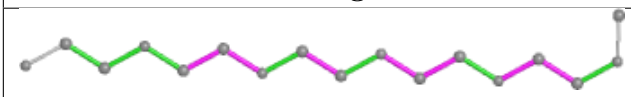
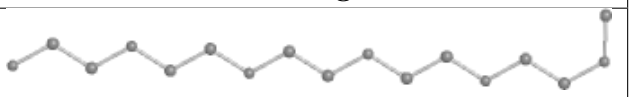
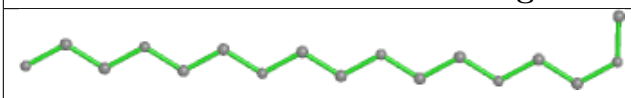
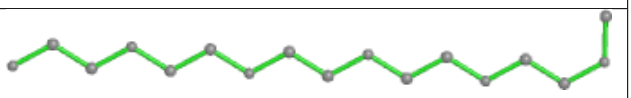
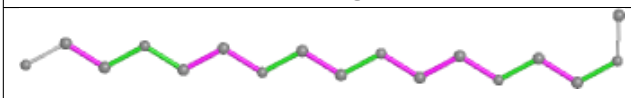
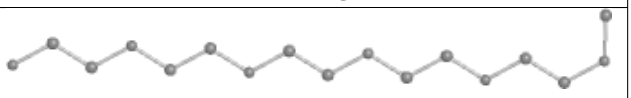
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand 1PG A 1010	
 Bond lengths	 Bond angles
 Torsions	 Rings

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 (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, 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	740/766 (96%)	-0.33	16 (2%)	62	63	34, 47, 67, 101	0
1	B	740/766 (96%)	-0.09	35 (4%)	31	30	32, 55, 85, 111	0
All	All	1480/1532 (96%)	-0.21	51 (3%)	45	45	32, 50, 79, 111	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	41	VAL	8.2
1	A	41	VAL	6.9
1	B	2	GLY	6.3
1	B	38	LEU	6.2
1	A	40	ALA	6.2
1	B	39	SER	5.5
1	B	40	ALA	5.0
1	B	352	LYS	4.4
1	B	623	ALA	4.3
1	A	39	SER	4.3
1	B	348	PHE	4.2
1	A	766	PHE	3.8
1	A	616	PRO	3.8
1	B	520	HIS	3.7
1	B	67	ASP	3.6
1	B	72	VAL	3.6
1	B	69	ASN	3.6
1	B	614	THR	3.5
1	A	68	HIS	3.4
1	B	68	HIS	3.3
1	B	624	LYS	3.3
1	A	175	ALA	3.2
1	A	348	PHE	3.1
1	B	71	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	2	GLY	3.1
1	B	90	PHE	3.1
1	A	67	ASP	3.0
1	B	350	GLU	2.9
1	A	765	ILE	2.9
1	B	766	PHE	2.8
1	A	520	HIS	2.8
1	B	37	LYS	2.7
1	B	615	ILE	2.6
1	B	620	GLU	2.6
1	A	617	GLY	2.5
1	B	622	THR	2.5
1	B	349	PHE	2.4
1	B	430	TYR	2.4
1	B	504	PRO	2.4
1	B	627	TYR	2.4
1	B	616	PRO	2.4
1	B	506	SER	2.3
1	B	508	ASN	2.2
1	B	507	ASP	2.2
1	A	710	PRO	2.2
1	B	521	ARG	2.2
1	B	710	PRO	2.2
1	A	622	THR	2.2
1	B	351	ILE	2.1
1	B	3	ALA	2.1
1	A	72	VAL	2.0

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

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

6.3 Carbohydrates (i)

There are no 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,

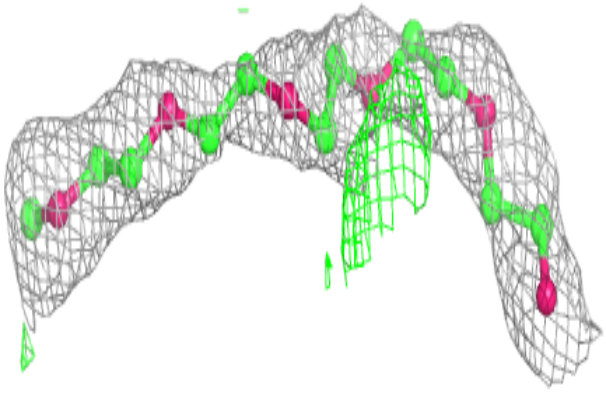
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

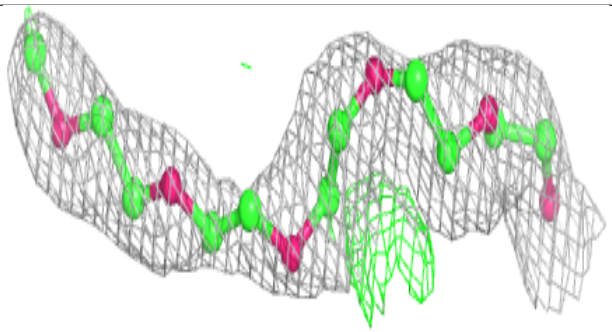
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	1PG	A	1011	17/17	0.75	0.43	59,74,84,84	0
5	1PG	B	1011	17/17	0.76	0.45	55,66,80,87	0
5	1PG	B	1010	17/17	0.79	0.39	61,67,81,91	0
5	1PG	B	1009	17/17	0.79	0.36	49,65,87,95	0
5	1PG	A	1009	17/17	0.87	0.29	51,57,75,83	0
4	K	A	1008	1/1	0.88	0.11	64,64,64,64	0
5	1PG	A	1010	17/17	0.88	0.27	49,65,90,91	0
3	MG	B	1005	1/1	0.89	0.26	52,52,52,52	0
3	MG	B	1003	1/1	0.90	0.24	56,56,56,56	0
3	MG	A	1007	1/1	0.91	0.21	49,49,49,49	0
3	MG	A	1004	1/1	0.94	0.19	53,53,53,53	0
4	K	B	1008	1/1	0.94	0.20	87,87,87,87	0
3	MG	A	1003	1/1	0.94	0.21	51,51,51,51	0
3	MG	B	1007	1/1	0.94	0.10	67,67,67,67	0
2	PO4	B	1001	5/5	0.95	0.25	57,58,72,74	0
2	PO4	A	1001	5/5	0.96	0.23	45,47,61,62	0
3	MG	B	1004	1/1	0.98	0.23	58,58,58,58	0
2	PO4	A	1002	5/5	0.98	0.25	43,49,53,53	0
3	MG	B	1006	1/1	0.98	0.29	54,54,54,54	0
2	PO4	B	1002	5/5	0.98	0.23	53,53,64,64	0
3	MG	A	1005	1/1	0.99	0.26	47,47,47,47	0
3	MG	A	1006	1/1	0.99	0.34	52,52,52,52	0

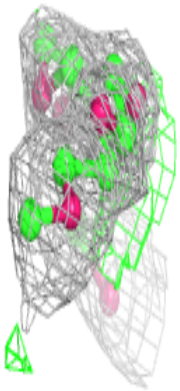
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around 1PG A 1011:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

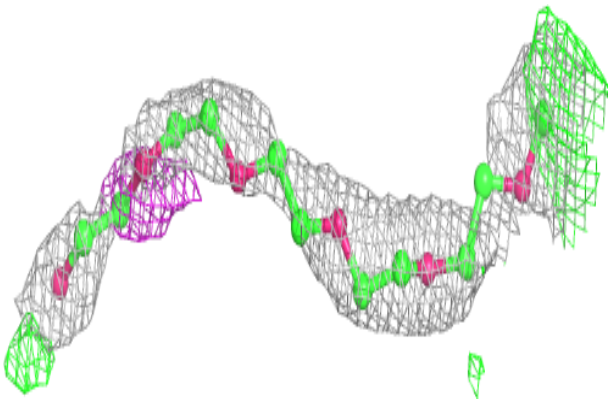


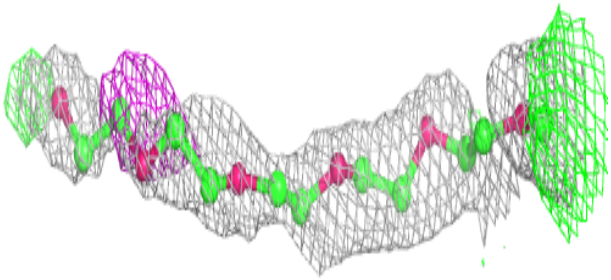


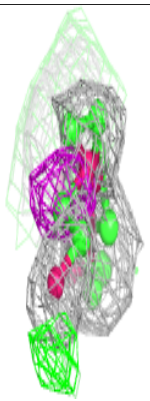


Electron density around 1PG B 1011:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

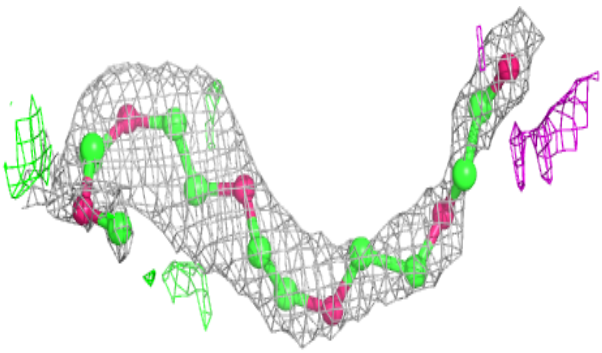


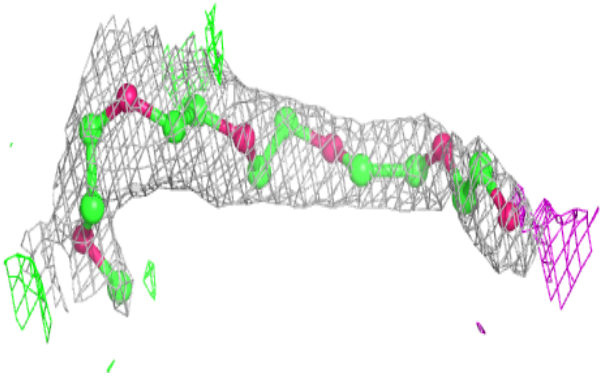


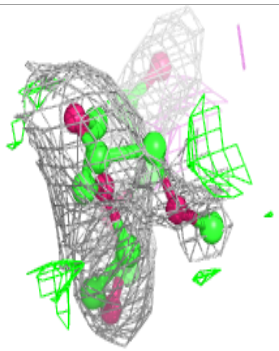


Electron density around 1PG B 1010:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

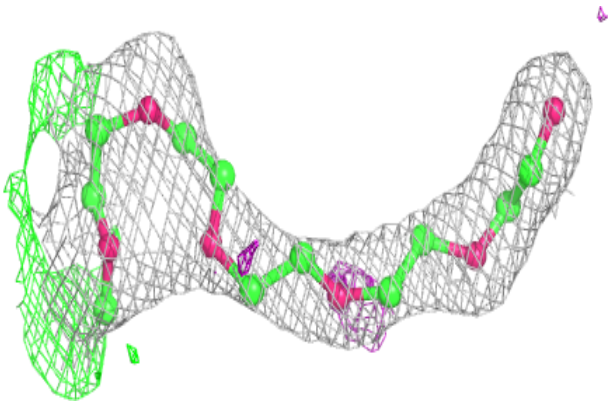


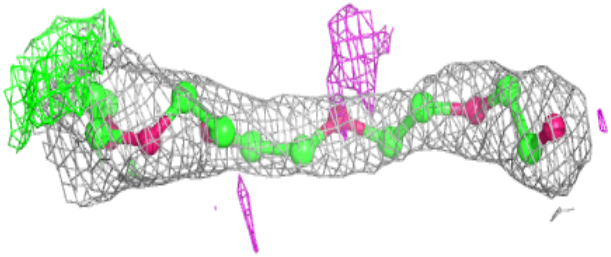


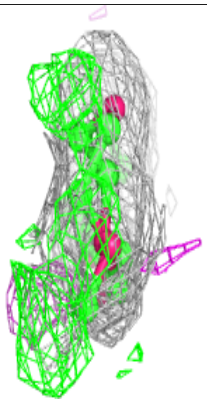


Electron density around 1PG B 1009:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

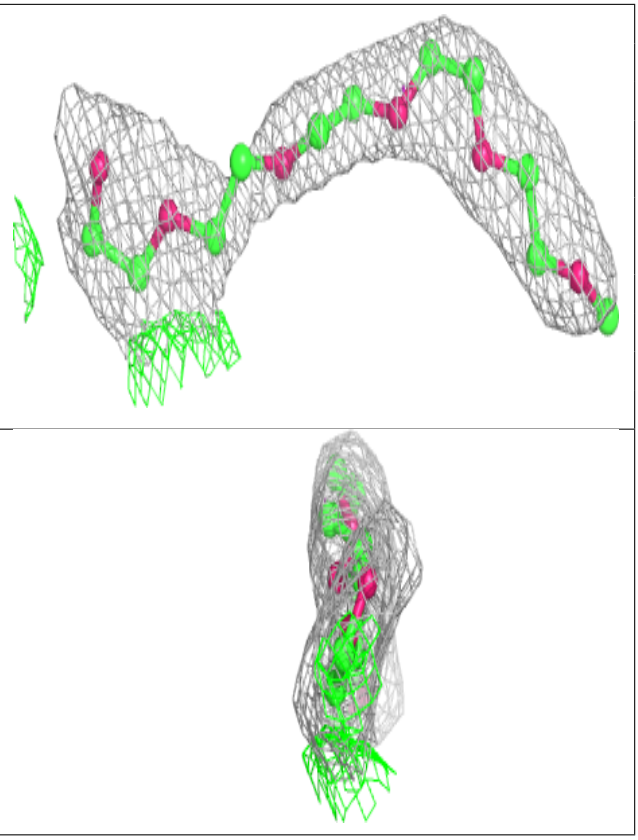






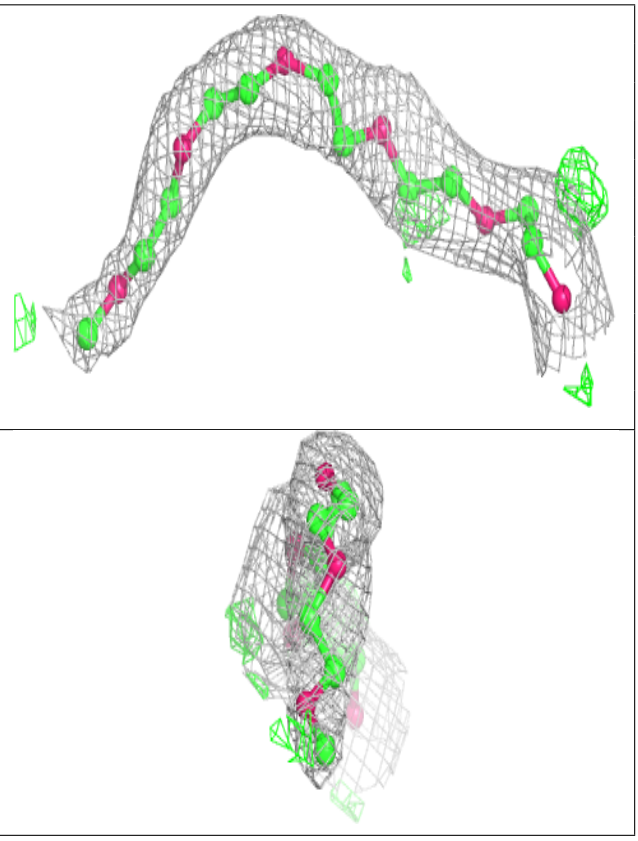
Electron density around 1PG A 1009:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 1PG A 1010:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.