



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 05:47 am BST

PDB ID : 3BNX
Title : Crystal structure of Aristolochene synthase complexed with farnesyl diphosphate
Authors : Shishova, E.Y.; Christianson, D.W.
Deposited on : 2007-12-14
Resolution : 2.10 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 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 : 2.11
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) : 2.11

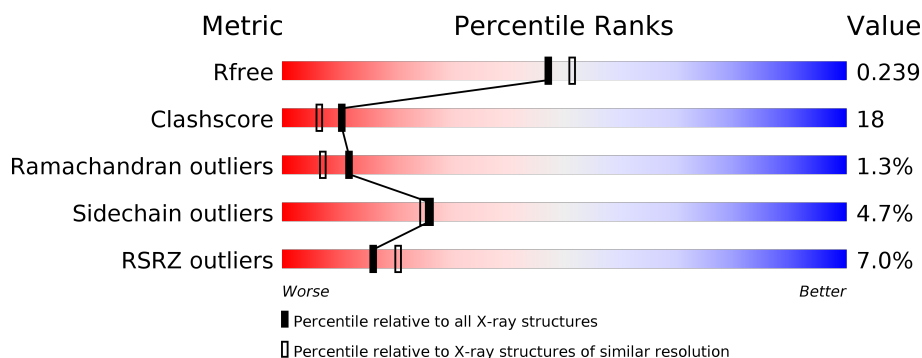
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 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	320	<div> <div>3%</div> <div> <div></div> <div>69%</div> <div>22%</div> <div>•</div> <div>8%</div> </div> </div>
1	B	320	<div> <div>4%</div> <div> <div></div> <div>60%</div> <div>32%</div> <div>•</div> <div>7%</div> </div> </div>
1	C	320	<div> <div>7%</div> <div> <div></div> <div>61%</div> <div>28%</div> <div>•</div> <div>8%</div> </div> </div>
1	D	320	<div> <div>11%</div> <div> <div></div> <div>54%</div> <div>33%</div> <div>•</div> <div>9%</div> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	BME	A	1273	-	-	-	X
2	BME	B	1271	-	-	X	-
2	BME	C	1270	-	-	X	-

2 Entry composition [i](#)

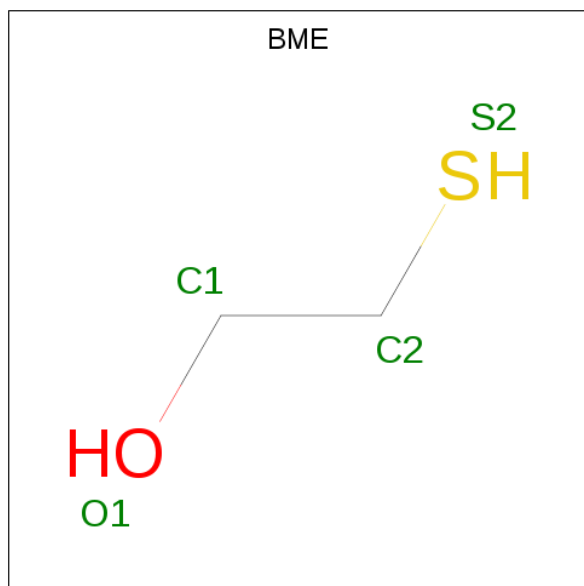
There are 7 unique types of molecules in this entry. The entry contains 9964 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Aristolochene synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	S	0	0	0
			2398	1532	404	447	15			
1	B	298	Total	C	N	O	S	0	0	0
			2415	1544	407	449	15			
1	C	295	Total	C	N	O	S	0	0	0
			2392	1529	403	445	15			
1	D	290	Total	C	N	O	S	0	0	0
			2349	1501	395	438	15			

- Molecule 2 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C₂H₆OS).



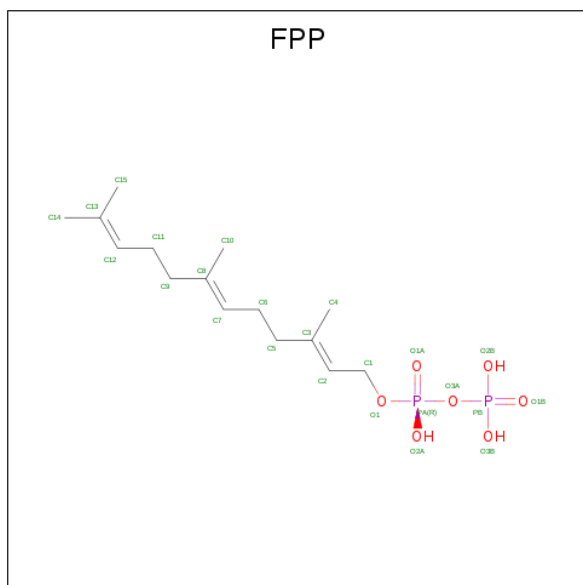
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			4	2	1	1		
2	B	1	Total	C	O	S	0	0
			4	2	1	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	O	S	0	0
			4	2	1	1		
2	D	1	Total	C	O	S	0	0
			4	2	1	1		
2	D	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 3 is FARNESYL DIPHOSPHATE (three-letter code: FPP) (formula: $C_{15}H_{28}O_7P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			24	15	7	2		
3	B	1	Total	C	O	P	0	0
			24	15	7	2		
3	C	1	Total	C	O	P	0	0
			24	15	7	2		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

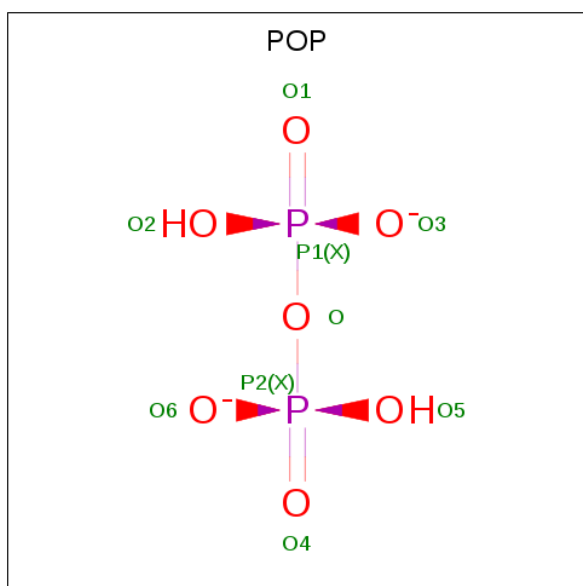


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	1	Total	Mg	0	0
			1	1		

- Molecule 6 is PYROPHOSPHATE 2- (three-letter code: POP) (formula: H₂O₇P₂).



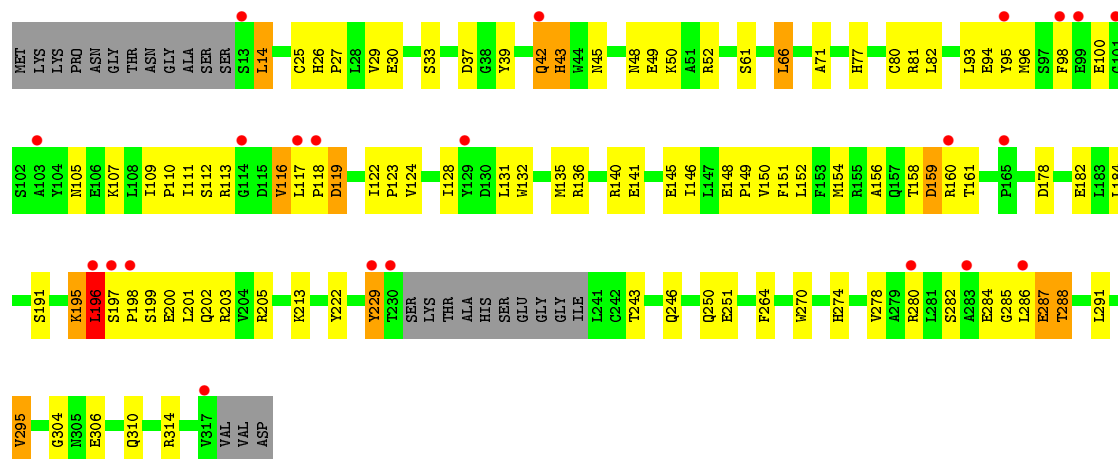
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	O	P	0	0
			9	7	2		

- Molecule 7 is water.

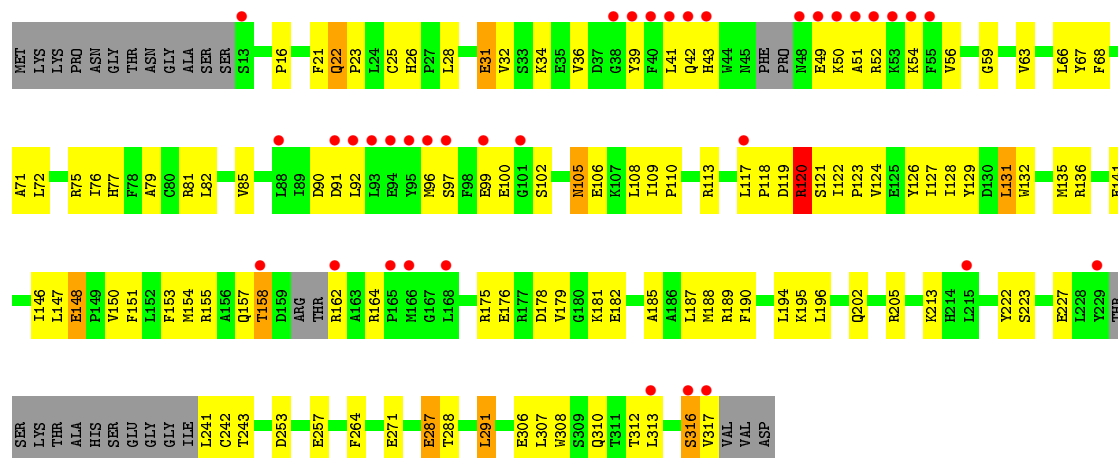
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	78	Total	O	0	0
			78	78		
7	B	85	Total	O	0	0
			85	85		
7	C	71	Total	O	0	0
			71	71		
7	D	68	Total	O	0	0
			68	68		

- Molecule 1: Aristolochene synthase





• Molecule 1: Aristolochene synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.89Å 147.37Å 84.21Å 90.00° 97.72° 90.00°	Depositor
Resolution (Å)	50.00 – 2.10 46.53 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.10) 91.9 (46.53-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.06 (at 2.10Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.240 , 0.278 0.241 , 0.239	Depositor DCC
R_{free} test set	4063 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	37.5	Xtriage
Anisotropy	0.287	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 56.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9964	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MG, FPP, POP, BME

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	0.37	0/2451	0.54	0/3317
1	B	0.37	0/2468	0.53	0/3339
1	C	0.37	0/2445	0.56	1/3309 (0.0%)
1	D	0.34	0/2398	0.53	0/3241
All	All	0.36	0/9762	0.54	1/13206 (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	C	201	LEU	N-CA-C	-5.04	97.39	111.00

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	2398	0	2370	65	0
1	B	2415	0	2394	76	0
1	C	2392	0	2365	104	0
1	D	2349	0	2319	111	0
2	A	4	0	6	1	0
2	B	4	0	6	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	4	0	6	7	0
2	D	8	0	12	3	0
3	A	24	0	25	2	0
3	B	24	0	25	1	0
3	C	24	0	25	2	0
4	C	6	0	8	1	0
5	D	1	0	0	0	0
6	D	9	0	0	0	0
7	A	78	0	0	1	0
7	B	85	0	0	1	0
7	C	71	0	0	2	0
7	D	68	0	0	1	0
All	All	9964	0	9561	355	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 18.

All (355) 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:C:66:LEU:HG	2:C:1270:BME:H12	1.26	1.13
1:C:200:GLU:HB3	1:C:291:LEU:HD11	1.40	1.04
1:C:284:GLU:HG3	1:C:286:LEU:HD23	1.47	0.96
1:B:77:HIS:HD2	1:B:81:ARG:HE	1.09	0.96
1:A:50:LYS:HD2	1:A:53:LYS:HD2	1.52	0.91
1:C:200:GLU:HA	1:C:203:ARG:HB3	1.53	0.90
1:D:123:PRO:O	1:D:127:ILE:HG12	1.71	0.90
1:B:181:LYS:HE3	1:B:215:LEU:HB3	1.53	0.89
1:C:25:CYS:HG	2:C:1270:BME:HS2	0.88	0.84
1:A:54:LYS:HE3	1:A:54:LYS:HA	1.59	0.83
1:B:242:CYS:HG	2:B:1271:BME:HS2	0.96	0.82
1:C:141:GLU:O	1:C:145:GLU:HG2	1.80	0.82
1:D:242:CYS:HG	2:D:1272:BME:HS2	1.21	0.82
1:C:116:VAL:HG12	1:C:117:LEU:H	1.45	0.82
1:C:96:MET:HE2	1:C:100:GLU:HB3	1.63	0.81
1:D:77:HIS:HD2	1:D:81:ARG:HE	1.29	0.79
1:A:229:TYR:H	1:A:229:TYR:HD2	1.28	0.78
1:D:313:LEU:HD12	1:D:316:SER:HA	1.64	0.78
1:C:200:GLU:HA	1:C:203:ARG:CB	2.13	0.77
1:A:203:ARG:HD3	1:A:286:LEU:HB3	1.66	0.77
3:B:401:FPP:O1B	3:B:401:FPP:O1A	2.03	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:203:ARG:HH22	1:C:280:ARG:HH12	1.34	0.76
1:C:25:CYS:SG	2:C:1270:BME:S2	2.67	0.76
1:D:146:ILE:HD11	1:D:190:PHE:CB	2.16	0.76
1:A:142:MET:HE1	1:A:193:GLY:HA2	1.68	0.75
1:C:199:SER:O	1:C:200:GLU:HB2	1.85	0.75
1:A:132:TRP:HB3	1:A:136:ARG:HH12	1.51	0.75
1:D:25:CYS:SG	2:D:1274:BME:S2	2.50	0.74
1:B:77:HIS:CD2	1:B:81:ARG:HE	2.01	0.73
1:C:66:LEU:HG	2:C:1270:BME:C1	2.12	0.72
1:C:282:SER:HA	1:C:287:GLU:OE1	1.90	0.72
1:D:306:GLU:O	1:D:310:GLN:HG3	1.90	0.72
1:C:136:ARG:HD3	1:C:140:ARG:HH11	1.54	0.72
1:C:136:ARG:HD3	1:C:140:ARG:NH1	2.06	0.70
1:C:25:CYS:HB2	2:C:1270:BME:H11	1.72	0.70
1:A:120:ARG:HG3	7:A:1331:HOH:O	1.91	0.69
1:C:77:HIS:HD2	1:C:81:ARG:HE	1.40	0.69
1:D:185:ALA:O	1:D:189:ARG:HG3	1.92	0.69
1:D:21:PHE:CE2	1:D:271:GLU:HG2	2.27	0.69
1:C:146:ILE:C	1:C:149:PRO:HD2	2.13	0.69
1:B:96:MET:HB2	1:B:100:GLU:HG3	1.73	0.69
1:C:222:TYR:CZ	1:C:310:GLN:HG2	2.28	0.68
1:D:146:ILE:HD11	1:D:190:PHE:HB2	1.76	0.68
1:B:163:ALA:HA	2:B:1271:BME:O1	1.93	0.68
1:B:242:CYS:SG	2:B:1271:BME:S2	2.68	0.68
1:B:96:MET:HB2	1:B:100:GLU:CD	2.14	0.68
1:A:96:MET:CE	1:A:100:GLU:HG2	2.23	0.68
1:C:314:ARG:HB2	4:C:2647:GOL:H12	1.76	0.67
1:B:197:SER:OG	1:B:200:GLU:HG3	1.95	0.67
1:C:203:ARG:HH22	1:C:280:ARG:NH1	1.93	0.67
1:D:202:GLN:O	1:D:205:ARG:HG3	1.93	0.67
1:D:26:HIS:HD2	1:D:28:LEU:H	1.43	0.67
1:A:30:GLU:O	1:A:34:LYS:HD3	1.95	0.67
1:A:168:LEU:HD22	1:A:172:LEU:HD11	1.76	0.66
1:B:205:ARG:HG2	1:B:205:ARG:HH11	1.59	0.66
1:B:219:ASN:HD21	1:B:305:ASN:HD21	1.43	0.66
1:C:306:GLU:O	1:C:310:GLN:HG3	1.95	0.66
1:D:242:CYS:SG	2:D:1272:BME:S2	2.88	0.65
1:B:96:MET:HB2	1:B:100:GLU:CG	2.26	0.65
1:A:48:ASN:ND2	1:A:50:LYS:HB2	2.12	0.65
1:C:116:VAL:HG12	1:C:117:LEU:N	2.11	0.65
1:B:72:LEU:HD12	1:B:75:ARG:HD3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:ARG:HB2	1:C:52:ARG:HH11	1.63	0.64
1:C:274:HIS:O	1:C:278:VAL:HG23	1.97	0.64
1:A:132:TRP:HB3	1:A:136:ARG:NH1	2.12	0.64
1:D:50:LYS:O	1:D:54:LYS:HG3	1.98	0.64
1:C:66:LEU:HD22	1:C:304:GLY:HA2	1.80	0.63
1:D:82:LEU:O	1:D:85:VAL:HG12	1.98	0.63
3:A:400:FPP:O1A	3:A:400:FPP:O1B	2.16	0.63
1:C:200:GLU:OE2	1:C:286:LEU:HD12	1.99	0.62
1:A:168:LEU:HD22	1:A:172:LEU:CD1	2.29	0.62
1:C:203:ARG:NH2	1:C:280:ARG:HH12	1.97	0.62
1:C:96:MET:CE	1:C:100:GLU:HB3	2.30	0.62
1:D:187:LEU:HD23	1:D:187:LEU:O	2.00	0.62
1:B:38:GLY:O	1:B:42:GLN:HG2	2.00	0.61
1:D:102:SER:HA	1:D:158:THR:HG22	1.82	0.61
1:D:194:LEU:HD22	1:D:196:LEU:HD11	1.80	0.61
1:D:307:LEU:HD23	1:D:307:LEU:C	2.20	0.61
1:B:181:LYS:HG3	1:B:215:LEU:HD23	1.82	0.61
1:C:116:VAL:CG1	1:C:117:LEU:H	2.08	0.61
3:C:402:FPP:O1B	3:C:402:FPP:O1A	2.17	0.61
1:B:176:GLU:OE1	1:B:213:LYS:HD2	2.01	0.61
1:B:26:HIS:CD2	1:B:28:LEU:H	2.19	0.60
1:D:178:ASP:OD2	1:D:181:LYS:HG2	2.00	0.60
1:C:150:VAL:HG12	1:C:154:MET:HE2	1.82	0.60
1:C:197:SER:O	1:C:199:SER:N	2.35	0.60
1:C:52:ARG:NH1	1:C:52:ARG:HB2	2.17	0.59
1:A:96:MET:HE3	1:A:100:GLU:HG2	1.83	0.59
1:C:200:GLU:CA	1:C:203:ARG:HB3	2.29	0.59
1:A:48:ASN:HD21	1:A:50:LYS:HB2	1.67	0.59
1:A:25:CYS:SG	2:A:1273:BME:S2	3.01	0.59
1:C:52:ARG:CB	1:C:52:ARG:HH11	2.16	0.58
1:B:282:SER:HB2	1:B:287:GLU:OE2	2.04	0.58
1:B:142:MET:HG3	1:B:195:LYS:HE2	1.86	0.57
1:B:306:GLU:O	1:B:310:GLN:HG3	2.04	0.57
1:D:122:ILE:HG22	1:D:124:VAL:HG12	1.85	0.57
1:D:154:MET:HA	1:D:157:GLN:HE21	1.70	0.57
1:C:184:LEU:HD11	3:C:402:FPP:H103	1.85	0.57
1:A:281:LEU:HD22	1:A:286:LEU:HB2	1.86	0.56
1:C:124:VAL:O	1:C:128:ILE:HG12	2.05	0.56
1:D:150:VAL:HG12	1:D:154:MET:HE2	1.86	0.56
1:A:46:PHE:HB2	1:A:52:ARG:NH1	2.20	0.56
1:B:230:THR:O	1:B:230:THR:HG22	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:109:ILE:HG23	1:D:151:PHE:CE1	2.41	0.56
1:C:203:ARG:NH2	1:C:280:ARG:NH1	2.53	0.56
1:A:229:TYR:CG	1:A:230:THR:N	2.71	0.56
1:A:96:MET:HE2	1:A:100:GLU:HG2	1.88	0.56
1:D:79:ALA:CB	1:D:187:LEU:HD21	2.36	0.56
1:B:172:LEU:O	1:B:176:GLU:HG3	2.06	0.55
1:D:308:TRP:O	1:D:312:THR:HG22	2.05	0.55
1:A:118:PRO:HD3	1:A:129:TYR:CD1	2.40	0.55
1:D:223:SER:O	1:D:227:GLU:HG3	2.06	0.55
1:C:112:SER:O	1:C:136:ARG:NH2	2.39	0.55
1:A:109:ILE:HB	1:A:110:PRO:HD3	1.89	0.55
1:A:139:ASP:OD2	1:A:142:MET:HE3	2.07	0.55
1:B:228:LEU:HD23	1:B:228:LEU:O	2.07	0.55
1:B:176:GLU:CG	1:B:213:LYS:HD2	2.37	0.55
1:C:131:LEU:O	1:C:135:MET:HG3	2.07	0.55
1:C:42:GLN:N	1:C:42:GLN:OE1	2.40	0.55
1:A:77:HIS:O	1:A:81:ARG:HG3	2.07	0.55
1:B:49:GLU:HA	1:B:52:ARG:HG3	1.88	0.55
1:C:66:LEU:CG	2:C:1270:BME:H12	2.18	0.54
1:D:162:ARG:HD2	1:D:164:ARG:CG	2.38	0.54
1:D:39:TYR:CE2	1:D:127:ILE:HD12	2.43	0.54
1:B:176:GLU:HG2	1:B:213:LYS:HD2	1.89	0.54
1:C:132:TRP:O	1:C:136:ARG:HG3	2.08	0.54
1:D:105:ASN:ND2	1:D:154:MET:HB3	2.22	0.54
1:A:229:TYR:CD2	1:A:230:THR:N	2.69	0.53
1:B:223:SER:O	1:B:227:GLU:HG2	2.09	0.53
1:B:26:HIS:HD2	1:B:28:LEU:H	1.55	0.53
1:B:241:LEU:HD23	1:B:246:GLN:NE2	2.24	0.53
1:C:25:CYS:HG	2:C:1270:BME:C2	2.20	0.53
1:D:96:MET:HB2	1:D:100:GLU:HB3	1.90	0.53
1:B:222:TYR:CZ	1:B:310:GLN:HG2	2.44	0.53
1:C:178:ASP:O	1:C:182:GLU:HG3	2.08	0.53
1:D:51:ALA:HA	1:D:54:LYS:CD	2.38	0.53
1:B:118:PRO:HD3	1:B:129:TYR:CG	2.44	0.53
1:D:63:VAL:HG12	1:D:67:TYR:CE2	2.43	0.53
1:A:213:LYS:NZ	1:D:253:ASP:HB3	2.24	0.53
1:A:229:TYR:HD2	1:A:229:TYR:N	2.00	0.52
1:B:112:SER:O	1:B:136:ARG:NH2	2.42	0.52
1:C:48:ASN:CG	1:C:49:GLU:N	2.63	0.52
1:D:118:PRO:HD3	1:D:129:TYR:CD1	2.44	0.52
1:D:118:PRO:HG2	1:D:120:ARG:HH11	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:31:GLU:HA	1:D:34:LYS:HE2	1.91	0.52
1:D:49:GLU:HG3	1:D:52:ARG:HD3	1.90	0.52
1:A:229:TYR:CD2	1:A:229:TYR:N	2.71	0.52
1:C:66:LEU:HD22	1:C:304:GLY:CA	2.39	0.52
1:B:136:ARG:HG2	1:B:140:ARG:HD2	1.92	0.52
1:C:195:LYS:O	1:C:196:LEU:C	2.49	0.52
1:D:141:GLU:CD	1:D:141:GLU:H	2.13	0.52
1:A:30:GLU:HB2	1:A:31:GLU:OE2	2.09	0.52
1:D:148:GLU:HA	1:D:148:GLU:OE1	2.10	0.52
1:B:150:VAL:O	1:B:154:MET:HG3	2.10	0.51
1:C:151:PHE:HD1	1:C:154:MET:CE	2.24	0.51
1:C:39:TYR:O	1:C:43:HIS:HB2	2.10	0.51
1:B:242:CYS:CB	2:B:1271:BME:HS2	2.23	0.51
1:A:28:LEU:O	1:A:32:VAL:HG23	2.10	0.51
1:D:155:ARG:HH11	1:D:155:ARG:HG3	1.74	0.51
1:A:184:LEU:HD11	3:A:400:FPP:H103	1.92	0.51
1:D:195:LYS:O	1:D:196:LEU:HD12	2.11	0.50
1:B:285:GLY:HA2	7:B:1338:HOH:O	2.11	0.50
1:A:90:ASP:OD2	1:A:314:ARG:NH2	2.44	0.50
1:B:181:LYS:CE	1:B:215:LEU:HB3	2.36	0.50
1:D:153:PHE:O	1:D:157:GLN:HG3	2.11	0.50
1:A:44:TRP:HB3	1:A:46:PHE:CE1	2.46	0.50
1:B:132:TRP:HB3	1:B:136:ARG:NH2	2.26	0.50
1:D:132:TRP:CE3	1:D:135:MET:HE3	2.47	0.50
1:D:79:ALA:HB2	1:D:187:LEU:HD21	1.93	0.50
1:D:51:ALA:HA	1:D:54:LYS:HD2	1.93	0.50
1:C:196:LEU:HD13	1:C:197:SER:N	2.27	0.49
1:A:203:ARG:CD	1:A:286:LEU:HB3	2.40	0.49
1:A:146:ILE:C	1:A:149:PRO:HD2	2.33	0.49
1:B:200:GLU:HB3	1:B:291:LEU:HD21	1.95	0.49
1:C:200:GLU:C	1:C:203:ARG:H	2.15	0.49
1:A:226:LYS:HD3	1:A:316:SER:O	2.12	0.49
1:D:151:PHE:HD1	1:D:154:MET:CE	2.26	0.49
1:B:148:GLU:HB2	1:B:149:PRO:HD3	1.94	0.49
1:B:205:ARG:NH1	1:B:205:ARG:HG2	2.25	0.49
1:D:222:TYR:CZ	1:D:310:GLN:HG2	2.48	0.49
1:D:43:HIS:HB3	1:D:126:TYR:OH	2.12	0.49
1:A:78:PHE:HB3	1:A:135:MET:CE	2.43	0.49
1:D:241:LEU:N	1:D:241:LEU:HD23	2.27	0.49
1:C:48:ASN:CG	1:C:49:GLU:H	2.15	0.49
1:B:72:LEU:HD12	1:B:75:ARG:CD	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:246:GLN:O	1:C:250:GLN:HG3	2.12	0.48
1:D:195:LYS:C	1:D:196:LEU:HD12	2.34	0.48
1:B:241:LEU:HD23	1:B:246:GLN:CD	2.34	0.48
1:B:29:VAL:HG13	1:B:30:GLU:N	2.28	0.48
1:C:107:LYS:CE	1:C:117:LEU:HD11	2.43	0.48
1:D:123:PRO:HA	1:D:126:TYR:CZ	2.48	0.48
1:D:51:ALA:HA	1:D:54:LYS:CG	2.43	0.48
1:D:118:PRO:HG2	1:D:120:ARG:NH1	2.29	0.48
1:C:160:ARG:HG3	1:C:161:THR:N	2.29	0.48
1:A:96:MET:HE1	1:A:101:GLY:HA2	1.94	0.48
1:A:106:GLU:OE2	1:A:109:ILE:HD12	2.14	0.48
1:A:281:LEU:HD13	1:A:287:GLU:HB2	1.94	0.48
1:D:162:ARG:HD2	1:D:164:ARG:HG3	1.95	0.48
1:D:32:VAL:O	1:D:36:VAL:HG23	2.14	0.48
1:B:313:LEU:HA	1:B:316:SER:OG	2.14	0.47
1:D:119:ASP:O	1:D:121:SER:N	2.47	0.47
1:A:52:ARG:O	1:A:56:VAL:HG23	2.14	0.47
1:C:107:LYS:O	1:C:110:PRO:HD2	2.14	0.47
1:A:204:VAL:O	1:A:204:VAL:HG22	2.14	0.47
1:C:109:ILE:HB	1:C:110:PRO:HD3	1.97	0.47
1:D:26:HIS:HE1	1:D:71:ALA:O	1.97	0.47
1:D:72:LEU:HD12	1:D:75:ARG:HD2	1.95	0.47
1:C:200:GLU:HB3	1:C:291:LEU:CD1	2.28	0.47
1:C:77:HIS:CD2	1:C:81:ARG:HE	2.27	0.47
1:D:178:ASP:HB3	1:D:181:LYS:HG2	1.95	0.47
1:D:63:VAL:HG22	1:D:308:TRP:NE1	2.30	0.47
1:A:50:LYS:HA	1:A:53:LYS:HD2	1.96	0.47
1:B:44:TRP:HB3	1:B:46:PHE:CE1	2.49	0.47
1:C:285:GLY:C	1:C:286:LEU:HD22	2.35	0.47
1:D:117:LEU:N	1:D:117:LEU:HD22	2.30	0.47
1:C:200:GLU:HA	1:C:203:ARG:HB2	1.96	0.47
1:C:29:VAL:HG13	1:C:30:GLU:N	2.29	0.47
1:C:42:GLN:HE22	1:C:52:ARG:HD2	1.79	0.47
1:C:49:GLU:CD	1:C:52:ARG:HH12	2.16	0.47
1:B:199:SER:O	1:B:203:ARG:HG3	2.14	0.47
1:B:203:ARG:HD3	1:B:286:LEU:HD13	1.96	0.47
1:C:49:GLU:HA	1:C:52:ARG:NH1	2.30	0.47
1:D:77:HIS:HD2	1:D:81:ARG:NE	2.07	0.47
1:B:140:ARG:NE	1:B:144:ASP:OD2	2.47	0.47
1:B:247:ILE:O	1:B:251:GLU:HG3	2.15	0.47
1:D:99:GLU:HG3	1:D:100:GLU:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:26:HIS:CD2	1:D:28:LEU:H	2.29	0.47
1:C:61:SER:OG	1:C:80:CYS:HB3	2.14	0.46
1:D:113:ARG:O	1:D:136:ARG:NH2	2.48	0.46
1:B:228:LEU:C	1:B:230:THR:H	2.18	0.46
1:C:33:SER:O	1:C:37:ASP:HB2	2.16	0.46
1:B:155:ARG:HD3	1:D:202:GLN:HG3	1.97	0.46
1:D:66:LEU:HD11	1:D:307:LEU:HD22	1.97	0.46
1:A:223:SER:O	1:A:227:GLU:HG3	2.16	0.46
1:A:75:ARG:HH12	1:A:142:MET:CE	2.29	0.46
1:D:106:GLU:OE2	1:D:109:ILE:HD12	2.15	0.46
1:D:131:LEU:HD13	1:D:135:MET:HE2	1.98	0.46
1:D:146:ILE:HD11	1:D:190:PHE:HB3	1.94	0.46
1:B:123:PRO:HA	1:B:126:TYR:CE2	2.51	0.46
1:C:49:GLU:HA	1:C:52:ARG:CZ	2.46	0.46
1:B:230:THR:C	1:B:232:LYS:N	2.68	0.46
1:C:291:LEU:O	1:C:295:VAL:HB	2.16	0.46
1:D:109:ILE:N	1:D:110:PRO:HD2	2.31	0.46
1:D:16:PRO:HG2	1:D:310:GLN:NE2	2.31	0.46
1:C:77:HIS:O	1:C:81:ARG:HG3	2.16	0.46
1:D:287:GLU:N	1:D:287:GLU:OE1	2.46	0.46
1:B:29:VAL:HG13	1:B:30:GLU:H	1.82	0.45
1:C:156:ALA:C	1:C:158:THR:H	2.19	0.45
1:D:90:ASP:C	1:D:92:LEU:H	2.20	0.45
1:D:97:SER:OG	1:D:99:GLU:HG2	2.16	0.45
1:B:131:LEU:O	1:B:135:MET:HG3	2.17	0.45
1:A:250:GLN:HE21	1:B:165:PRO:HD3	1.80	0.45
1:D:257:GLU:CD	1:D:257:GLU:H	2.19	0.45
1:B:124:VAL:O	1:B:128:ILE:HG12	2.17	0.45
1:B:148:GLU:OE2	1:B:148:GLU:HA	2.16	0.45
1:C:113:ARG:C	1:C:136:ARG:NH2	2.70	0.45
1:A:96:MET:CE	1:A:101:GLY:HA2	2.47	0.45
1:C:156:ALA:HA	1:C:159:ASP:OD1	2.16	0.45
1:D:102:SER:HA	1:D:158:THR:CG2	2.46	0.45
1:A:205:ARG:HG3	1:A:205:ARG:HH11	1.80	0.45
1:A:49:GLU:O	1:A:53:LYS:HE3	2.17	0.45
1:C:94:GLU:HG3	1:C:95:TYR:CD2	2.52	0.45
1:D:146:ILE:HG22	1:D:146:ILE:O	2.17	0.45
1:D:179:VAL:O	1:D:182:GLU:HB3	2.16	0.45
1:D:307:LEU:HD23	1:D:307:LEU:O	2.16	0.45
1:B:256:ALA:O	1:B:260:LYS:HG3	2.17	0.45
1:B:267:CYS:O	1:B:271:GLU:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:26:HIS:HA	1:C:27:PRO:HD3	1.84	0.45
1:C:131:LEU:C	1:C:131:LEU:HD13	2.36	0.45
1:C:61:SER:HB2	7:C:2662:HOH:O	2.17	0.45
1:D:151:PHE:O	1:D:155:ARG:HG2	2.17	0.44
1:D:119:ASP:C	1:D:121:SER:H	2.21	0.44
1:A:222:TYR:CZ	1:A:310:GLN:HG2	2.52	0.44
1:A:48:ASN:HD21	1:A:50:LYS:CB	2.31	0.44
1:B:271:GLU:O	1:B:274:HIS:HB3	2.17	0.44
1:D:131:LEU:HD13	1:D:132:TRP:N	2.33	0.44
1:D:150:VAL:HG12	1:D:154:MET:CE	2.48	0.44
1:C:213:LYS:HE3	1:C:270:TRP:CE2	2.53	0.44
1:A:75:ARG:HH22	1:A:142:MET:HE3	1.80	0.44
1:B:156:ALA:HA	1:B:159:ASP:OD2	2.17	0.44
1:D:32:VAL:HG21	1:D:76:ILE:HG23	1.99	0.44
1:B:109:ILE:HB	1:B:110:PRO:HD3	2.00	0.44
1:A:29:VAL:HG13	1:A:30:GLU:N	2.33	0.44
1:B:308:TRP:O	1:B:312:THR:HG22	2.18	0.44
1:B:169:GLY:HA3	1:C:251:GLU:HG2	2.00	0.44
1:C:280:ARG:HG2	1:C:280:ARG:HH11	1.83	0.44
1:A:26:HIS:ND1	1:A:27:PRO:HD2	2.33	0.44
1:C:117:LEU:H	1:C:117:LEU:HD23	1.83	0.44
1:C:45:ASN:ND2	1:C:123:PRO:HG2	2.33	0.44
1:C:111:ILE:HG12	1:C:117:LEU:O	2.18	0.43
1:D:146:ILE:HG22	1:D:150:VAL:HG23	2.00	0.43
1:C:229:TYR:C	1:C:229:TYR:CD2	2.90	0.43
1:D:72:LEU:HD12	1:D:75:ARG:CD	2.48	0.43
1:B:33:SER:O	1:B:37:ASP:HB2	2.17	0.43
1:C:71:ALA:HB1	1:C:191:SER:HB3	2.00	0.43
1:A:50:LYS:HD2	1:A:50:LYS:HA	1.86	0.43
1:C:29:VAL:HG13	1:C:30:GLU:H	1.84	0.43
1:D:39:TYR:O	1:D:42:GLN:HB3	2.18	0.43
1:B:181:LYS:HE3	1:B:215:LEU:CB	2.35	0.43
1:D:99:GLU:HG3	1:D:100:GLU:H	1.83	0.43
1:C:93:LEU:HD11	1:C:105:ASN:HD21	1.83	0.43
1:D:146:ILE:O	1:D:150:VAL:HG23	2.19	0.43
1:B:203:ARG:CD	1:B:286:LEU:HB3	2.49	0.43
1:C:280:ARG:O	1:C:284:GLU:HG2	2.18	0.43
1:A:75:ARG:HH12	1:A:142:MET:HE3	1.84	0.43
1:B:41:LEU:O	1:B:52:ARG:NH1	2.46	0.43
1:D:194:LEU:HD22	1:D:196:LEU:CD1	2.47	0.42
1:D:307:LEU:CD2	1:D:307:LEU:C	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:63:VAL:HG13	1:D:308:TRP:CG	2.54	0.42
1:B:32:VAL:HG21	1:B:76:ILE:HG23	2.01	0.42
1:D:59:GLY:O	1:D:63:VAL:HG23	2.19	0.42
1:D:22:GLN:NE2	1:D:23:PRO:O	2.51	0.42
1:D:26:HIS:CD2	1:D:28:LEU:HB2	2.55	0.42
1:D:41:LEU:HD11	1:D:56:VAL:CG2	2.49	0.42
1:A:148:GLU:OE1	1:A:148:GLU:HA	2.19	0.42
1:C:14:LEU:HA	7:C:2654:HOH:O	2.19	0.42
1:C:202:GLN:O	1:C:205:ARG:HG3	2.19	0.42
1:D:68:PHE:CE2	1:D:188:MET:HB2	2.54	0.42
1:A:31:GLU:CD	1:A:31:GLU:H	2.23	0.42
1:B:203:ARG:HH21	1:B:288:THR:HG23	1.85	0.42
1:C:119:ASP:OD1	1:C:122:ILE:HG13	2.20	0.42
1:C:42:GLN:OE1	1:C:52:ARG:HD3	2.19	0.42
1:C:42:GLN:CD	1:C:42:GLN:N	2.73	0.42
1:B:218:VAL:HG11	1:B:306:GLU:HA	2.02	0.42
1:C:118:PRO:O	1:C:119:ASP:C	2.57	0.42
1:D:288:THR:OG1	1:D:291:LEU:HB2	2.20	0.41
1:C:148:GLU:N	1:C:149:PRO:CD	2.83	0.41
1:A:160:ARG:HG3	1:A:160:ARG:HH11	1.85	0.41
1:C:107:LYS:HE3	1:C:117:LEU:HD11	2.02	0.41
1:D:132:TRP:CZ3	1:D:147:LEU:HD23	2.56	0.41
1:D:202:GLN:CD	1:D:205:ARG:HD2	2.40	0.41
1:A:223:SER:HB3	1:A:315:TYR:CE1	2.56	0.41
1:C:50:LYS:HE3	1:C:50:LYS:HB2	1.97	0.41
1:B:280:ARG:O	1:B:284:GLU:HG3	2.20	0.41
1:C:195:LYS:O	1:C:196:LEU:O	2.38	0.41
1:C:288:THR:HG23	1:C:291:LEU:H	1.86	0.41
1:C:49:GLU:OE2	1:C:52:ARG:NH1	2.48	0.41
1:C:98:PHE:HD1	1:C:98:PHE:H	1.69	0.41
1:B:55:PHE:O	1:B:58:ALA:HB3	2.20	0.41
1:D:119:ASP:C	1:D:121:SER:N	2.74	0.41
1:B:146:ILE:C	1:B:149:PRO:HD2	2.41	0.41
1:C:122:ILE:HG22	1:C:124:VAL:HG12	2.02	0.41
1:D:178:ASP:HB3	1:D:181:LYS:CG	2.51	0.41
1:D:51:ALA:HA	1:D:54:LYS:HG3	2.03	0.41
1:A:123:PRO:O	1:A:127:ILE:HG13	2.21	0.40
1:A:26:HIS:HB3	1:A:65:CYS:HB3	2.03	0.40
1:D:119:ASP:HB3	1:D:122:ILE:HG12	2.03	0.40
1:D:147:LEU:HB3	1:D:151:PHE:CE2	2.56	0.40
1:D:175:ARG:HA	1:D:175:ARG:HD3	1.71	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:176:GLU:HG2	1:D:213:LYS:HG3	2.04	0.40
1:A:78:PHE:HB3	1:A:135:MET:HE2	2.02	0.40
1:D:175:ARG:NH1	7:D:4321:HOH:O	2.53	0.40
1:A:174:TYR:HE1	1:A:175:ARG:NH1	2.19	0.40
1:A:96:MET:HB3	1:A:96:MET:HE2	1.99	0.40
1:D:108:LEU:HD22	1:D:128:ILE:HG13	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	292/320 (91%)	279 (96%)	12 (4%)	1 (0%)	41	41
1	B	294/320 (92%)	281 (96%)	8 (3%)	5 (2%)	9	4
1	C	291/320 (91%)	262 (90%)	23 (8%)	6 (2%)	7	3
1	D	282/320 (88%)	267 (95%)	12 (4%)	3 (1%)	14	9
All	All	1159/1280 (90%)	1089 (94%)	55 (5%)	15 (1%)	12	7

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	47	PRO
1	C	43	HIS
1	D	158	THR
1	C	14	LEU
1	C	119	ASP
1	C	196	LEU
1	D	120	ARG
1	B	14	LEU
1	B	120	ARG

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Mol	Chain	Res	Type
1	D	316	SER
1	A	47	PRO
1	B	229	TYR
1	C	116	VAL
1	C	198	PRO
1	B	15	GLU

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	261/279 (94%)	250 (96%)	11 (4%)	30	30
1	B	263/279 (94%)	250 (95%)	13 (5%)	25	23
1	C	260/279 (93%)	247 (95%)	13 (5%)	24	23
1	D	255/279 (91%)	243 (95%)	12 (5%)	26	25
All	All	1039/1116 (93%)	990 (95%)	49 (5%)	26	25

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	LYS
1	A	66	LEU
1	A	115	ASP
1	A	148	GLU
1	A	152	LEU
1	A	168	LEU
1	A	196	LEU
1	A	229	TYR
1	A	243	THR
1	A	264	PHE
1	A	281	LEU
1	B	14	LEU
1	B	66	LEU
1	B	94	GLU
1	B	117	LEU

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Mol	Chain	Res	Type
1	B	120	ARG
1	B	131	LEU
1	B	141	GLU
1	B	145	GLU
1	B	196	LEU
1	B	215	LEU
1	B	229	TYR
1	B	243	THR
1	B	264	PHE
1	C	42	GLN
1	C	66	LEU
1	C	82	LEU
1	C	152	LEU
1	C	159	ASP
1	C	195	LYS
1	C	196	LEU
1	C	229	TYR
1	C	243	THR
1	C	264	PHE
1	C	287	GLU
1	C	288	THR
1	C	295	VAL
1	D	22	GLN
1	D	31	GLU
1	D	91	ASP
1	D	105	ASN
1	D	120	ARG
1	D	131	LEU
1	D	148	GLU
1	D	243	THR
1	D	264	PHE
1	D	287	GLU
1	D	291	LEU
1	D	317	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	219	ASN
1	A	250	GLN
1	A	301	GLN

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Mol	Chain	Res	Type
1	A	305	ASN
1	B	26	HIS
1	B	77	HIS
1	B	305	ASN
1	C	45	ASN
1	C	157	GLN
1	D	22	GLN
1	D	26	HIS
1	D	77	HIS
1	D	105	ASN
1	D	157	GLN
1	D	246	GLN
1	D	250	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 1 is 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	$\# Z > 2$
3	FPP	B	401	-	21,23,23	1.07	3 (14%)	27,31,31	1.84	7 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BME	C	1270	-	3,3,3	0.24	0	1,2,2	0.06	0
3	FPP	A	400	-	21,23,23	0.86	0	27,31,31	1.83	6 (22%)
2	BME	D	1272	-	3,3,3	0.52	0	1,2,2	0.68	0
3	FPP	C	402	-	21,23,23	0.82	0	27,31,31	1.77	6 (22%)
2	BME	A	1273	-	3,3,3	0.26	0	1,2,2	0.68	0
2	BME	B	1271	-	3,3,3	0.41	0	1,2,2	1.40	0
4	GOL	C	2647	-	5,5,5	0.35	0	5,5,5	0.38	0
2	BME	D	1274	-	3,3,3	0.78	0	1,2,2	0.20	0
6	POP	D	4294	5	6,8,8	1.26	0	13,13,13	2.11	2 (15%)

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	FPP	B	401	-	-	6/25/25/25	-
2	BME	C	1270	-	-	0/1/1/1	-
3	FPP	A	400	-	-	5/25/25/25	-
2	BME	D	1272	-	-	0/1/1/1	-
3	FPP	C	402	-	-	6/25/25/25	-
2	BME	A	1273	-	-	0/1/1/1	-
2	BME	B	1271	-	-	0/1/1/1	-
4	GOL	C	2647	-	-	0/4/4/4	-
2	BME	D	1274	-	-	0/1/1/1	-
6	POP	D	4294	5	-	0/6/6/6	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	FPP	PB-O2B	2.37	1.64	1.54
3	B	401	FPP	PB-O3B	2.14	1.63	1.54
3	B	401	FPP	C1-C2	2.05	1.55	1.49

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	4294	POP	P2-O-P1	-6.92	109.07	132.83
3	B	401	FPP	PA-O3A-PB	-6.65	109.99	132.83
3	A	400	FPP	PA-O3A-PB	-6.29	111.24	132.83
3	C	402	FPP	PA-O3A-PB	-6.25	111.38	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	400	FPP	C1-C2-C3	-3.10	120.68	126.04
3	B	401	FPP	C10-C8-C9	3.02	120.35	115.27
3	A	400	FPP	C10-C8-C9	2.64	119.72	115.27
3	C	402	FPP	C1-C2-C3	-2.60	121.54	126.04
3	A	400	FPP	C6-C7-C8	-2.57	121.46	127.66
3	C	402	FPP	C10-C8-C9	2.53	119.53	115.27
6	D	4294	POP	O5-P2-O	2.51	113.07	104.64
3	B	401	FPP	C4-C3-C5	2.50	119.47	115.27
3	A	400	FPP	C4-C3-C5	2.45	119.40	115.27
3	C	402	FPP	C6-C7-C8	-2.43	121.81	127.66
3	C	402	FPP	C4-C3-C5	2.40	119.31	115.27
3	B	401	FPP	C1-C2-C3	-2.32	122.02	126.04
3	B	401	FPP	C6-C7-C8	-2.23	122.28	127.66
3	B	401	FPP	C15-C13-C14	2.18	119.42	114.60
3	C	402	FPP	C15-C13-C14	2.17	119.40	114.60
3	A	400	FPP	C15-C13-C14	2.15	119.35	114.60
3	B	401	FPP	C11-C12-C13	-2.13	120.46	127.75

There are no chirality outliers.

All (17) torsion outliers are listed below:

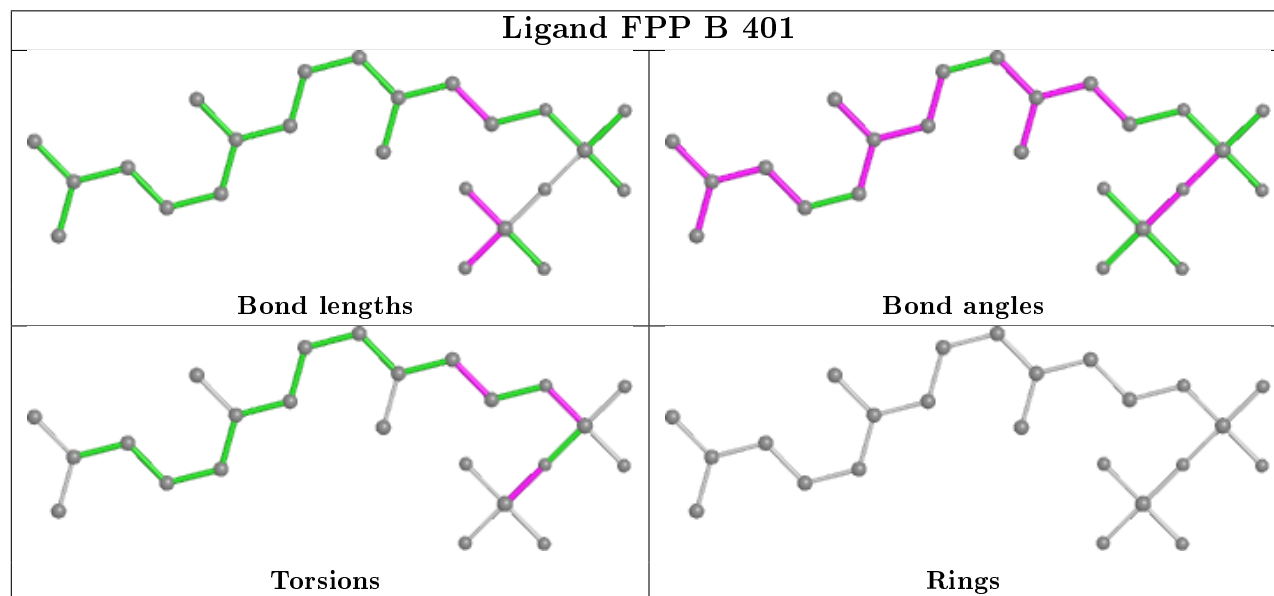
Mol	Chain	Res	Type	Atoms
3	A	400	FPP	C3-C5-C6-C7
3	C	402	FPP	C3-C5-C6-C7
3	C	402	FPP	C12-C11-C9-C8
3	A	400	FPP	C12-C11-C9-C8
3	B	401	FPP	C1-O1-PA-O3A
3	B	401	FPP	C1-O1-PA-O2A
3	A	400	FPP	PA-O3A-PB-O1B
3	B	401	FPP	PA-O3A-PB-O1B
3	C	402	FPP	PA-O3A-PB-O1B
3	B	401	FPP	PA-O3A-PB-O2B
3	B	401	FPP	PA-O3A-PB-O3B
3	A	400	FPP	PA-O3A-PB-O2B
3	A	400	FPP	PA-O3A-PB-O3B
3	C	402	FPP	PA-O3A-PB-O2B
3	C	402	FPP	PA-O3A-PB-O3B
3	C	402	FPP	C1-O1-PA-O3A
3	B	401	FPP	O1-C1-C2-C3

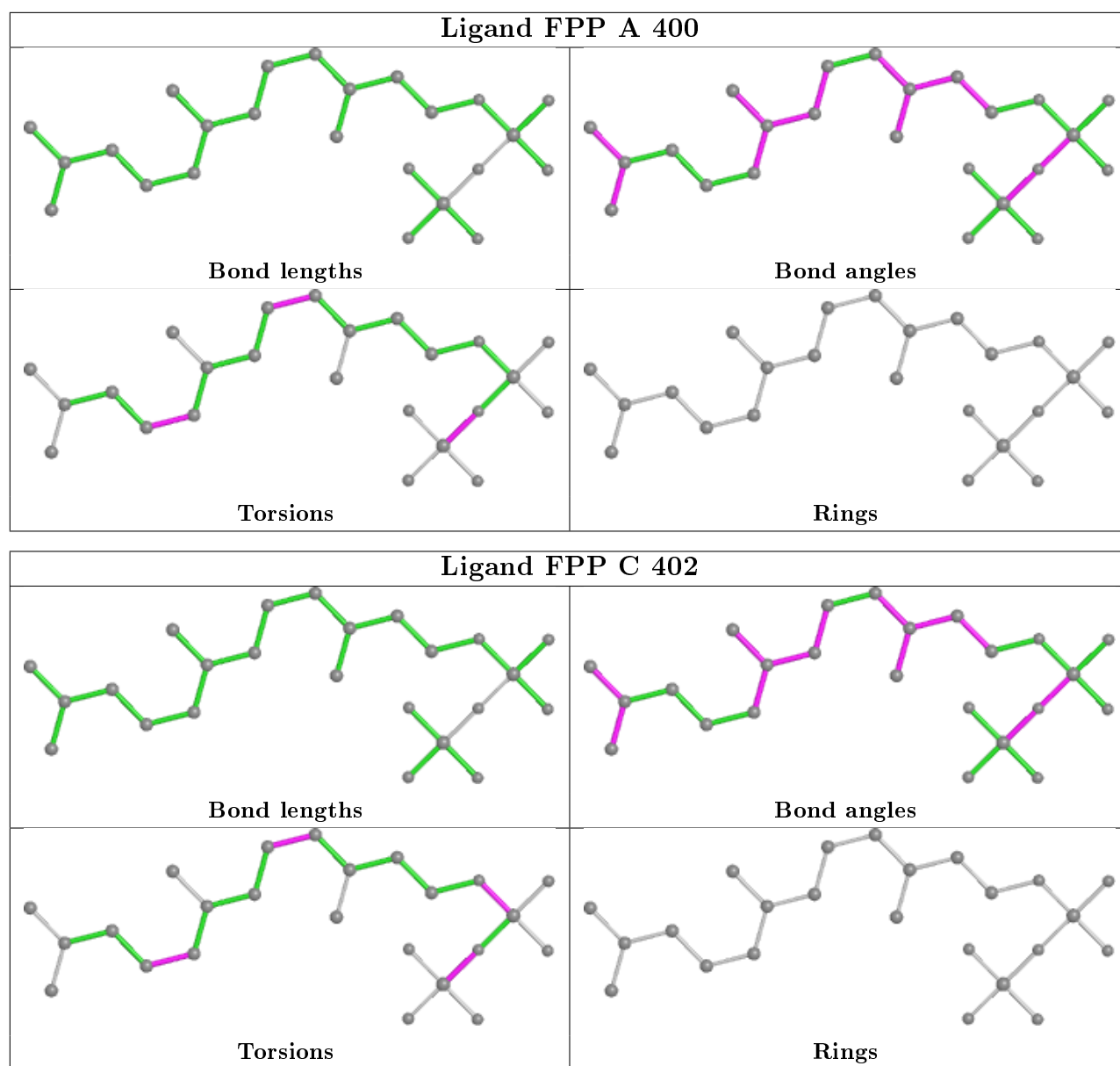
There are no ring outliers.

9 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	401	FPP	1	0
2	C	1270	BME	7	0
3	A	400	FPP	2	0
2	D	1272	BME	2	0
3	C	402	FPP	2	0
2	A	1273	BME	1	0
2	B	1271	BME	4	0
4	C	2647	GOL	1	0
2	D	1274	BME	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 than 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.





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	296/320 (92%)	0.52	10 (3%) 45 51	21, 42, 64, 78	0
1	B	298/320 (93%)	0.44	14 (4%) 31 37	25, 42, 65, 76	0
1	C	295/320 (92%)	0.64	22 (7%) 14 18	22, 46, 71, 75	0
1	D	290/320 (90%)	0.92	36 (12%) 4 5	23, 44, 74, 91	0
All	All	1179/1280 (92%)	0.63	82 (6%) 16 20	21, 44, 70, 91	0

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	117	LEU	9.7
1	D	95	TYR	7.8
1	B	240	ILE	6.8
1	A	230	THR	6.5
1	D	50	LYS	6.5
1	B	229	TYR	6.3
1	A	229	TYR	6.2
1	D	53	LYS	6.1
1	B	161	THR	5.7
1	D	48	ASN	5.4
1	C	230	THR	5.4
1	D	313	LEU	5.1
1	D	96	MET	5.1
1	A	231	SER	5.0
1	D	54	LYS	5.0
1	D	162	ARG	4.9
1	C	98	PHE	4.7
1	A	317	VAL	4.7
1	D	51	ALA	4.7
1	D	99	GLU	4.2
1	B	232	LYS	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	50	LYS	4.1
1	D	97	SER	4.0
1	B	160	ARG	4.0
1	C	13	SER	3.9
1	D	55	PHE	3.9
1	C	286	LEU	3.7
1	C	229	TYR	3.6
1	D	94	GLU	3.6
1	D	41	LEU	3.5
1	C	283	ALA	3.4
1	D	52	ARG	3.4
1	D	158	THR	3.4
1	C	196	LEU	3.3
1	B	98	PHE	3.2
1	D	92	LEU	3.2
1	D	42	GLN	3.1
1	C	99	GLU	3.1
1	D	91	ASP	3.1
1	B	317	VAL	3.0
1	C	103	ALA	3.0
1	D	229	TYR	3.0
1	D	49	GLU	3.0
1	D	101	GLY	2.9
1	A	47	PRO	2.9
1	D	316	SER	2.9
1	D	166	MET	2.8
1	D	117	LEU	2.8
1	D	13	SER	2.8
1	D	38	GLY	2.7
1	B	50	LYS	2.7
1	B	316	SER	2.6
1	D	215	LEU	2.6
1	B	14	LEU	2.6
1	C	118	PRO	2.6
1	A	141	GLU	2.6
1	B	51	ALA	2.6
1	A	204	VAL	2.5
1	C	317	VAL	2.5
1	C	114	GLY	2.5
1	D	39	TYR	2.5
1	C	42	GLN	2.5
1	D	93	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	231	SER	2.5
1	B	95	TYR	2.4
1	D	165	PRO	2.4
1	A	46	PHE	2.4
1	D	43	HIS	2.3
1	A	98	PHE	2.3
1	C	280	ARG	2.3
1	C	95	TYR	2.2
1	D	317	VAL	2.2
1	C	197	SER	2.2
1	D	40	PHE	2.2
1	C	129	TYR	2.1
1	C	160	ARG	2.1
1	C	198	PRO	2.0
1	D	88	LEU	2.0
1	C	101	GLY	2.0
1	C	165	PRO	2.0
1	D	168	LEU	2.0
1	B	25	CYS	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 carbohydrates 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
2	BME	A	1273	4/4	0.79	0.47	43,45,45,47	4
2	BME	B	1271	4/4	0.82	0.22	52,52,54,54	0
2	BME	C	1270	4/4	0.86	0.20	34,35,36,39	0
4	GOL	C	2647	6/6	0.87	0.14	47,50,50,51	0

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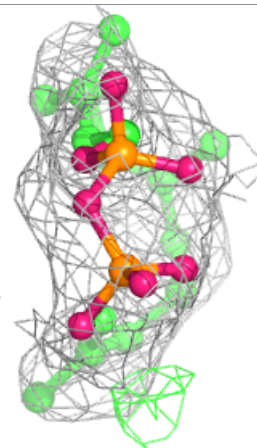
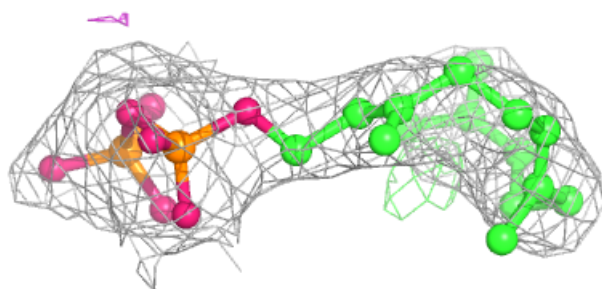
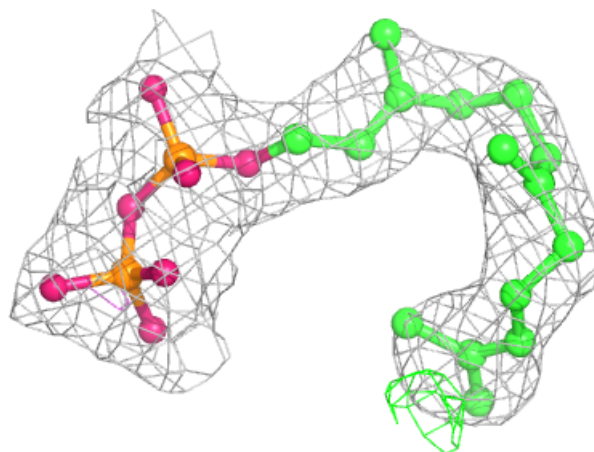
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	FPP	C	402	24/24	0.91	0.17	54,64,72,73	0
3	FPP	A	400	24/24	0.92	0.17	56,60,69,69	0
2	BME	D	1274	4/4	0.93	0.16	37,37,38,41	0
5	MG	D	701	1/1	0.93	0.12	54,54,54,54	0
3	FPP	B	401	24/24	0.94	0.14	40,51,59,59	0
2	BME	D	1272	4/4	0.94	0.19	56,57,57,57	0
6	POP	D	4294	9/9	0.96	0.10	41,43,46,47	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.

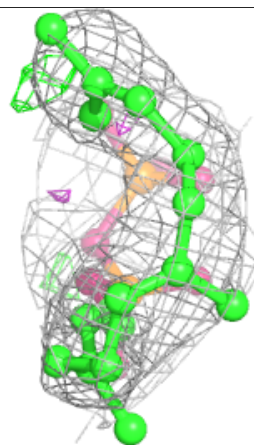
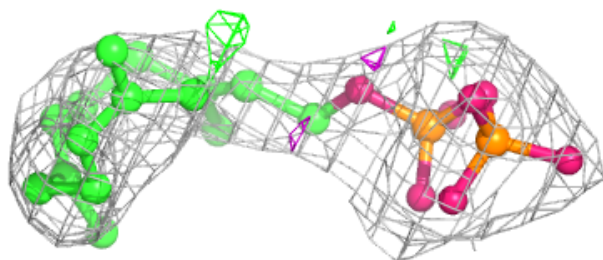
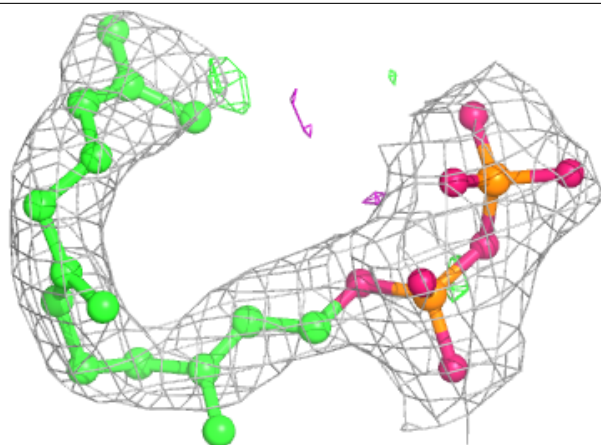
Electron density around FPP C 402:

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

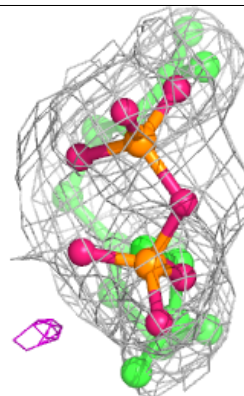
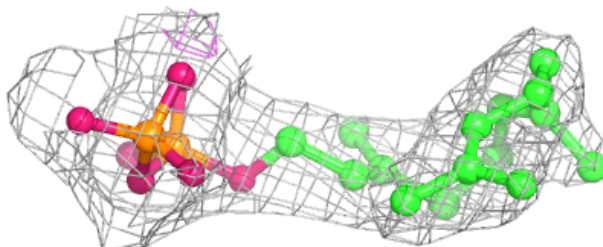
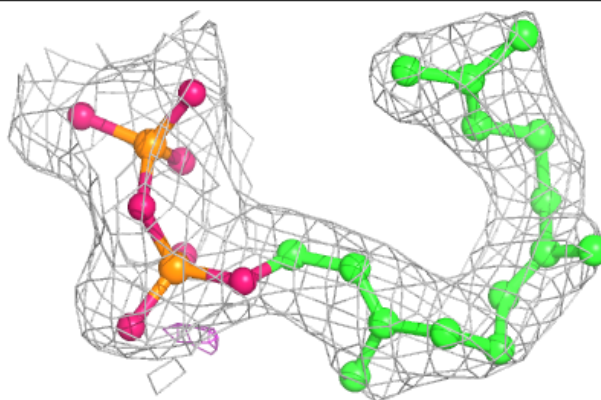


Electron density around FPP A 400:

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

**Electron density around FPP B 401:**

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



6.5 Other polymers

There are no such residues in this entry.