Full wwPDB X-ray Structure Validation Report ⓘ

Feb 25, 2024 – 05:31 AM EST

PDB ID	:	5C4I
Title	:	Structure of an Oxalate Oxidoreductase
Authors	:	Gibson, M.I.; Brignole, E.J.; Pierce, E.; Can, M.; Ragsdale, S.W.; Drennan, C.L.
Deposited on	:	2015-06-18
Resolution	:	2.27 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

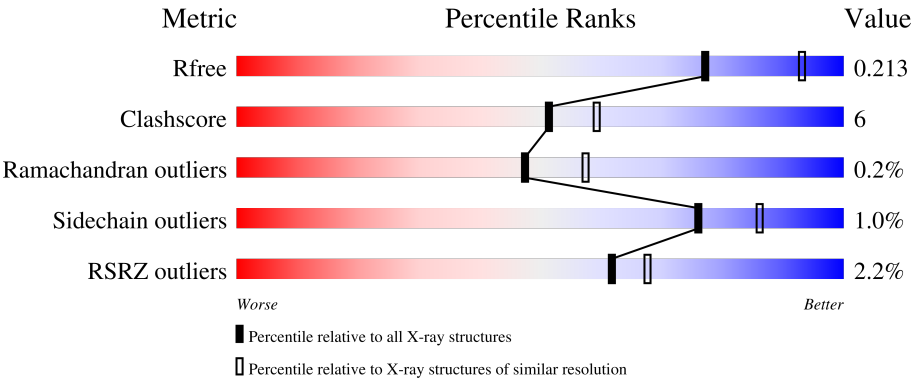
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 2.27 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	6980 (2.30-2.26)
Clashscore	141614	7711 (2.30-2.26)
Ramachandran outliers	138981	7597 (2.30-2.26)
Sidechain outliers	138945	7598 (2.30-2.26)
RSRZ outliers	127900	6849 (2.30-2.26)

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	395	2% 85% 14%
1	D	395	1% 89% 10%
2	B	315	5% 83% 14%
2	E	315	2% 87% 12%
3	C	314	3% 88% 11%

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Mol	Chain	Length	Quality of chain
3	F	314	

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
4	SF4	C	401	-	-	X	-

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 17286 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 Oxalate oxidoreductase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	394	Total	C	N	O	S	0	0	0
			3062	1948	524	576	14			
1	D	393	Total	C	N	O	S	0	0	0
			3054	1943	522	575	14			

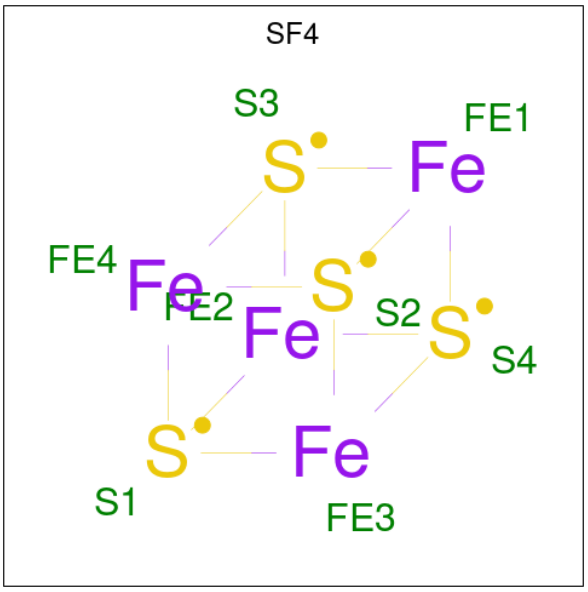
- Molecule 2 is a protein called Oxalate oxidoreductase subunit delta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	308	Total	C	N	O	S	0	0	0
			2320	1461	392	451	16			
2	E	312	Total	C	N	O	S	0	0	0
			2324	1462	395	451	16			

- Molecule 3 is a protein called Oxalate oxidoreductase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	312	Total	C	N	O	S	0	0	0
			2393	1535	409	432	17			
3	F	312	Total	C	N	O	S	0	0	0
			2393	1535	409	432	17			

- Molecule 4 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).

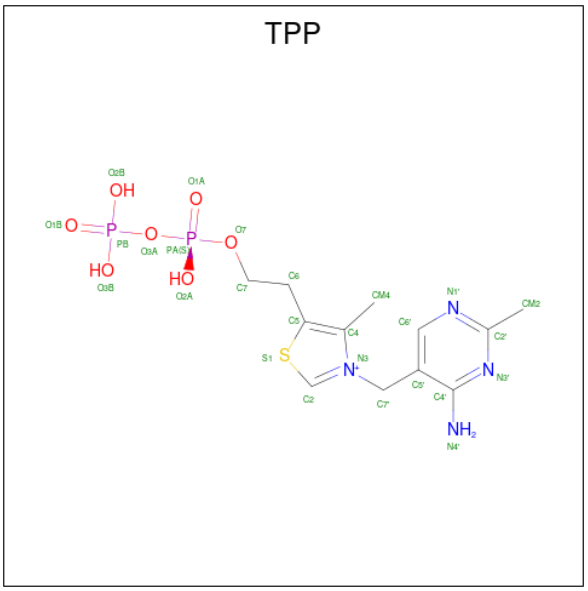


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Fe S 8 4 4	0	0
4	B	1	Total Fe S 8 4 4	0	0
4	C	1	Total Fe S 8 4 4	0	0
4	E	1	Total Fe S 8 4 4	0	0
4	E	1	Total Fe S 8 4 4	0	0
4	F	1	Total Fe S 8 4 4	0	0

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Na 1 1	0	0
5	F	1	Total Na 1 1	0	0

- Molecule 6 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: $C_{12}H_{19}N_4O_7P_2S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	C	1	Total C N O P S 26 12 4 7 2 1	0	0
6	F	1	Total C N O P S 26 12 4 7 2 1	0	0

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	1	Total Mg 1 1	0	0
7	F	1	Total Mg 1 1	0	0

- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	240	Total O 240 240	0	0
8	B	273	Total O 273 273	0	0
8	C	245	Total O 245 245	0	0
8	D	268	Total O 268 268	0	0
8	E	333	Total O 333 333	0	0

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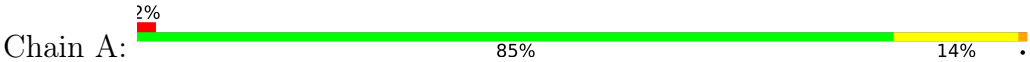
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	F	277	Total O 277 277	0	0

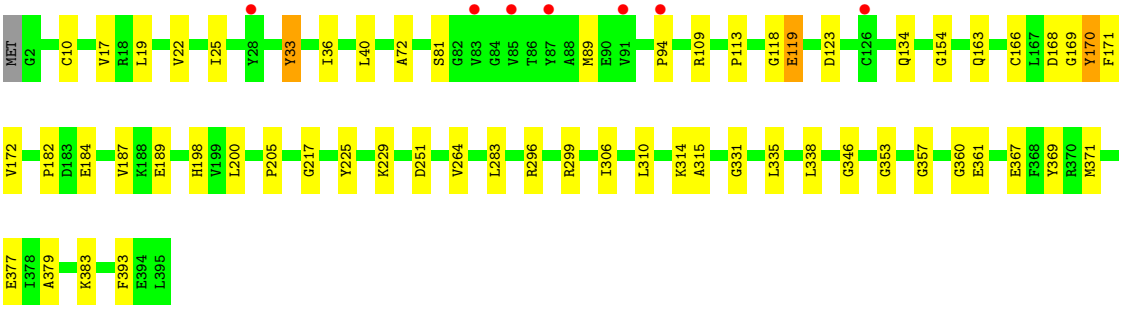
3 Residue-property plots (i)

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: Oxalate oxidoreductase subunit alpha

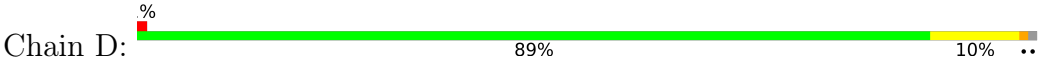
Chain A:

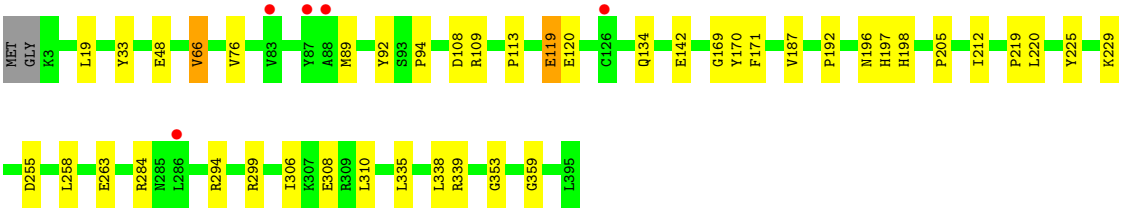




• Molecule 1: Oxalate oxidoreductase subunit alpha

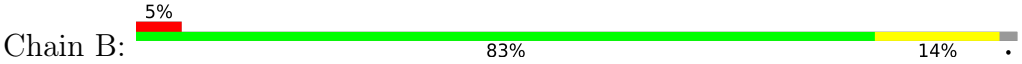
Chain D:

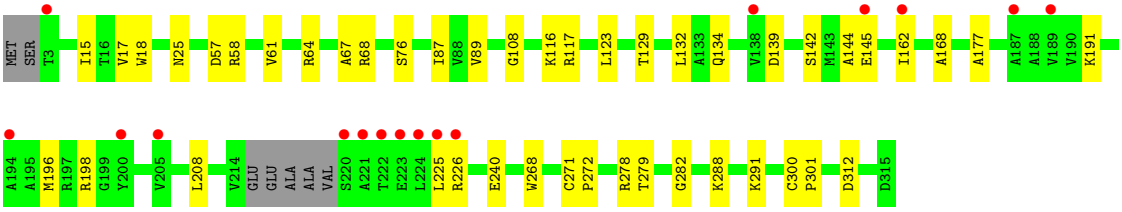




• Molecule 2: Oxalate oxidoreductase subunit delta

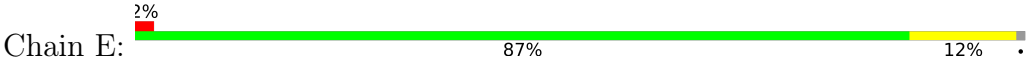
Chain B:

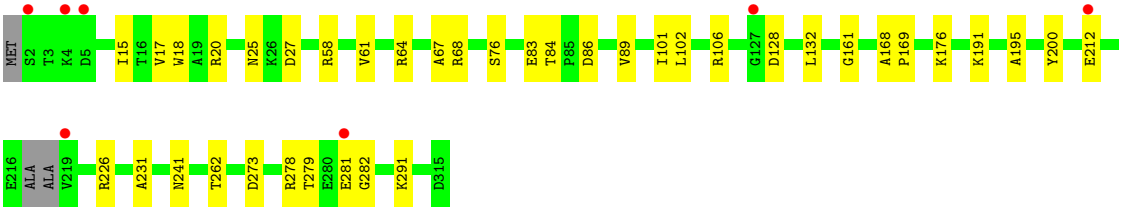




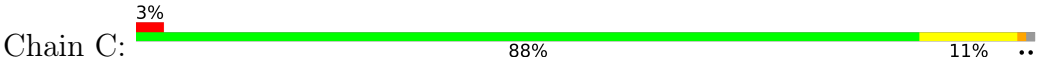
• Molecule 2: Oxalate oxidoreductase subunit delta

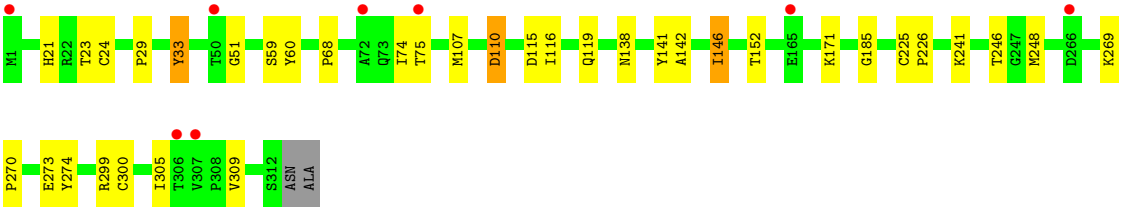
Chain E:



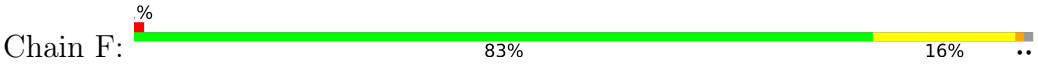


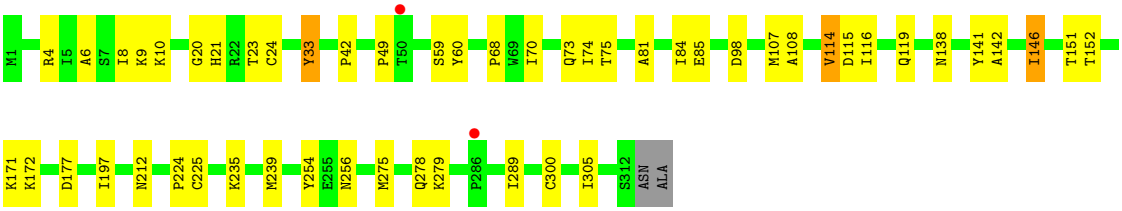
• Molecule 3: Oxalate oxidoreductase subunit beta





• Molecule 3: Oxalate oxidoreductase subunit beta





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	84.35Å 152.20Å 171.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.66 – 2.27 48.66 – 2.27	Depositor EDS
% Data completeness (in resolution range)	80.5 (48.66-2.27) 80.5 (48.66-2.27)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.11 (at 2.27Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.174 , 0.216 0.173 , 0.213	Depositor DCC
R_{free} test set	4131 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	24.3	Xtriage
Anisotropy	1.464	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 47.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	17286	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, NA, MG, TPP

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	0.22	0/3134	0.40	0/4251
1	D	0.22	0/3126	0.39	0/4242
2	B	0.21	0/2361	0.41	0/3219
2	E	0.21	0/2365	0.41	0/3227
3	C	0.21	0/2458	0.39	0/3339
3	F	0.21	0/2458	0.40	0/3339
All	All	0.21	0/15902	0.40	0/21617

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3062	0	2992	40	0
1	D	3054	0	2978	27	0
2	B	2320	0	2311	32	0
2	E	2324	0	2280	26	0
3	C	2393	0	2394	27	0
3	F	2393	0	2394	38	0
4	B	16	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	8	0	0	2	0
4	E	16	0	0	0	0
4	F	8	0	0	1	0
5	B	1	0	0	0	0
5	F	1	0	0	0	0
6	C	26	0	16	3	0
6	F	26	0	16	0	0
7	C	1	0	0	0	0
7	F	1	0	0	0	0
8	A	240	0	0	7	0
8	B	273	0	0	9	1
8	C	245	0	0	6	0
8	D	268	0	0	7	0
8	E	333	0	0	9	1
8	F	277	0	0	14	0
All	All	17286	0	15381	174	1

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 (174) 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:346:GLY:O	8:A:401:HOH:O	1.81	0.98
1:A:331:GLY:O	8:A:402:HOH:O	1.84	0.94
1:D:212:ILE:O	8:D:401:HOH:O	1.89	0.89
3:F:254:TYR:O	8:F:501:HOH:O	1.98	0.80
3:F:172:LYS:NZ	8:F:505:HOH:O	2.10	0.80
3:F:42:PRO:O	8:F:502:HOH:O	2.00	0.79
3:C:119:GLN:HB2	3:F:119:GLN:HB2	1.66	0.78
3:C:115:ASP:OD2	8:C:501:HOH:O	2.02	0.77
2:E:132:LEU:O	8:E:502:HOH:O	2.05	0.74
2:B:145:GLU:OE1	8:B:501:HOH:O	2.07	0.72
2:B:279:THR:OG1	2:B:282:GLY:O	2.08	0.71
2:E:262:THR:OG1	8:E:501:HOH:O	1.93	0.69
1:A:377:GLU:OE2	8:A:404:HOH:O	2.12	0.68
3:F:4:ARG:NH1	8:F:504:HOH:O	2.09	0.68
2:B:108:GLY:O	8:B:502:HOH:O	2.13	0.67
2:B:177:ALA:O	8:B:503:HOH:O	2.13	0.67
2:E:128:ASP:OD2	8:E:503:HOH:O	2.12	0.67
1:D:48:GLU:OE2	8:D:402:HOH:O	2.12	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:278:GLN:O	8:F:506:HOH:O	2.14	0.66
1:A:166:CYS:O	8:A:406:HOH:O	2.14	0.65
1:A:189:GLU:OE2	8:A:405:HOH:O	2.13	0.65
1:D:258:LEU:HD13	1:D:284:ARG:HG3	1.79	0.65
2:B:117:ARG:NH2	2:B:312:ASP:OD1	2.31	0.64
3:C:241:LYS:NZ	8:C:504:HOH:O	2.19	0.63
2:E:278:ARG:NH2	3:F:8:ILE:O	2.33	0.61
1:D:225:TYR:CZ	1:D:229:LYS:HD2	2.35	0.61
2:E:68:ARG:NH1	2:E:76:SER:OG	2.34	0.61
2:E:212:GLU:OE1	8:E:505:HOH:O	2.16	0.61
1:A:19:LEU:HB3	1:A:187:VAL:HG21	1.82	0.60
1:A:383:LYS:O	8:A:407:HOH:O	2.17	0.59
2:B:68:ARG:NH1	2:B:76:SER:OG	2.35	0.59
2:E:84:THR:HB	2:E:106:ARG:HG3	1.85	0.59
3:F:152:THR:O	3:F:171:LYS:NZ	2.34	0.58
3:F:115:ASP:OD2	3:F:141:TYR:OH	2.22	0.58
3:F:73:GLN:OE1	8:F:507:HOH:O	2.17	0.58
1:A:225:TYR:CZ	1:A:229:LYS:HD2	2.39	0.58
1:A:314:LYS:HE3	1:A:379:ALA:HB1	1.86	0.57
1:D:192:PRO:O	8:D:404:HOH:O	2.18	0.57
2:E:273:ASP:OD1	8:E:506:HOH:O	2.17	0.56
2:B:240:GLU:OE1	8:B:504:HOH:O	2.17	0.56
3:C:300:CYS:HB3	3:C:305:ILE:HB	1.88	0.56
2:E:231:ALA:O	8:E:507:HOH:O	2.18	0.55
1:D:66:VAL:HG22	1:D:76:VAL:HB	1.88	0.55
3:C:141:TYR:HD1	6:C:402:TPP:H61	1.72	0.54
3:C:142:ALA:HA	3:C:146:ILE:HD13	1.90	0.54
1:A:184:GLU:OE1	1:A:184:GLU:N	2.39	0.54
2:B:225:LEU:HA	1:D:219:PRO:HB3	1.89	0.54
1:A:264:VAL:HG12	1:A:315:ALA:HB3	1.88	0.53
1:D:255:ASP:HB3	1:D:294:ARG:HB3	1.90	0.53
1:D:308:GLU:O	8:D:405:HOH:O	2.18	0.53
2:E:27:ASP:OD2	8:E:508:HOH:O	2.19	0.53
2:B:15:ILE:HG12	2:B:87:ILE:HB	1.89	0.53
1:A:134:GLN:HB3	1:A:299:ARG:HB2	1.91	0.53
3:F:212:ASN:ND2	8:F:511:HOH:O	2.35	0.53
2:E:279:THR:OG1	2:E:282:GLY:O	2.21	0.53
1:A:217:GLY:HA3	1:D:359:GLY:HA3	1.90	0.52
1:D:109:ARG:HA	1:D:119:GLU:HA	1.90	0.52
2:B:240:GLU:OE2	2:B:288:LYS:NZ	2.37	0.52
1:D:212:ILE:HD13	1:D:220:LEU:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:335:LEU:HD22	1:D:353:GLY:HA3	1.92	0.51
1:D:196:ASN:OD1	1:D:197:HIS:N	2.43	0.51
2:E:17:VAL:HG22	2:E:89:VAL:HB	1.91	0.51
2:E:291:LYS:NZ	3:F:23:THR:O	2.32	0.51
2:B:162:ILE:O	2:B:191:LYS:N	2.41	0.51
3:F:142:ALA:HA	3:F:146:ILE:HD13	1.93	0.50
1:A:113:PRO:HB3	8:C:561:HOH:O	2.11	0.50
3:F:279:LYS:HE2	8:F:641:HOH:O	2.12	0.50
3:F:75:THR:HG22	3:F:116:ILE:HG12	1.94	0.50
1:A:306:ILE:HG23	1:A:310:LEU:HD12	1.93	0.50
2:B:18:TRP:CH2	2:B:64:ARG:HD3	2.47	0.50
2:B:198:ARG:NH1	8:B:517:HOH:O	2.40	0.50
2:B:58:ARG:O	2:B:61:VAL:HG12	2.12	0.49
1:D:339:ARG:NH2	8:D:422:HOH:O	2.42	0.49
1:A:335:LEU:HD22	1:A:353:GLY:HA3	1.95	0.49
2:B:17:VAL:HG22	2:B:89:VAL:HB	1.94	0.49
2:B:291:LYS:NZ	3:C:23:THR:O	2.36	0.48
2:E:25:ASN:ND2	8:E:528:HOH:O	2.44	0.48
2:E:18:TRP:CH2	2:E:64:ARG:HD3	2.47	0.48
3:C:309:VAL:O	8:C:503:HOH:O	2.19	0.48
3:C:75:THR:HG22	3:C:116:ILE:HG12	1.95	0.48
3:F:114:VAL:HG21	3:F:151:THR:HG23	1.96	0.48
3:F:59:SER:HA	3:F:60:TYR:HA	1.61	0.48
1:D:263:GLU:OE2	8:D:406:HOH:O	2.20	0.48
3:F:85:GLU:N	8:F:508:HOH:O	2.25	0.47
2:B:68:ARG:NH2	8:B:505:HOH:O	2.23	0.47
2:B:226:ARG:HG3	8:B:575:HOH:O	2.13	0.47
3:F:275:MET:HE1	3:F:289:ILE:HG23	1.96	0.47
2:E:58:ARG:O	2:E:61:VAL:HG12	2.15	0.47
2:B:116:LYS:NZ	2:B:139:ASP:OD2	2.47	0.47
3:C:74:ILE:HD12	6:C:402:TPP:H72	1.97	0.46
2:B:116:LYS:HZ1	2:B:142:SER:HG	1.61	0.46
2:B:144:ALA:HA	8:B:535:HOH:O	2.15	0.46
2:B:168:ALA:HB1	2:B:196:MET:HB2	1.98	0.46
3:C:152:THR:HB	3:C:171:LYS:HE3	1.97	0.46
3:F:21:HIS:HA	8:F:569:HOH:O	2.14	0.46
1:A:25:ILE:HD13	1:A:40:LEU:HD13	1.97	0.46
2:E:176:LYS:HG2	2:E:200:TYR:CZ	2.51	0.46
3:C:110:ASP:OD1	3:C:110:ASP:N	2.43	0.46
1:A:200:LEU:HD21	3:F:70:ILE:HB	1.97	0.46
1:A:10:CYS:HA	1:A:36:ILE:HG12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:142:GLU:HB2	8:D:437:HOH:O	2.16	0.45
3:C:21:HIS:HA	8:C:565:HOH:O	2.16	0.45
1:A:251:ASP:O	1:A:296:ARG:HD3	2.16	0.45
2:E:169:PRO:HG3	2:E:195:ALA:HB1	1.99	0.45
3:F:33:TYR:CE2	3:F:107:MET:HG3	2.52	0.45
3:C:51:GLY:HA2	6:C:402:TPP:H71	1.99	0.45
2:E:15:ILE:HB	2:E:67:ALA:HB3	1.98	0.45
2:B:271:CYS:HA	2:B:272:PRO:HD3	1.86	0.44
3:F:256:ASN:ND2	8:F:527:HOH:O	2.50	0.44
1:A:283:LEU:HD21	1:A:369:TYR:CD1	2.52	0.44
1:A:283:LEU:HD21	1:A:369:TYR:HD1	1.83	0.44
3:C:68:PRO:HD3	1:D:205:PRO:HB3	1.99	0.44
3:C:185:GLY:HA2	3:F:177:ASP:HB3	1.98	0.44
2:E:161:GLY:HA3	2:E:191:LYS:HD2	1.99	0.44
1:D:134:GLN:HB3	1:D:299:ARG:HB2	2.00	0.44
1:A:94:PRO:HA	1:D:113:PRO:HD3	1.99	0.44
2:E:168:ALA:HB3	2:E:169:PRO:HD3	1.99	0.44
1:A:72:ALA:HB2	3:F:84:ILE:HG23	2.00	0.44
3:F:9:LYS:NZ	8:F:514:HOH:O	2.37	0.44
3:F:138:ASN:HB2	3:F:225:CYS:HB2	2.00	0.44
2:B:116:LYS:NZ	2:B:142:SER:HG	2.16	0.43
2:B:134:GLN:OE1	8:B:503:HOH:O	2.21	0.43
2:B:25:ASN:ND2	2:B:57:ASP:OD1	2.51	0.43
3:C:270:PRO:HG2	3:C:273:GLU:HG3	2.00	0.43
3:C:59:SER:HA	3:C:60:TYR:HA	1.62	0.43
3:F:74:ILE:HG22	8:F:545:HOH:O	2.17	0.43
3:F:300:CYS:HB3	3:F:305:ILE:HB	1.99	0.43
3:F:49:PRO:HG2	3:F:108:ALA:HB2	2.00	0.43
3:F:197:ILE:HD11	3:F:224:PRO:HD2	2.00	0.43
1:A:154:GLY:HA3	1:A:163:GLN:NE2	2.34	0.43
1:A:109:ARG:HA	1:A:119:GLU:HA	2.00	0.43
1:A:113:PRO:HD3	1:D:94:PRO:HA	2.01	0.43
1:A:393:PHE:CE1	2:B:225:LEU:HB2	2.54	0.43
3:F:6:ALA:HB3	3:F:10:LYS:HD3	2.01	0.43
1:A:205:PRO:HA	3:F:68:PRO:HG3	2.01	0.42
2:B:226:ARG:HE	2:B:226:ARG:HB2	1.72	0.42
3:C:24:CYS:HB2	4:C:401:SF4:S3	2.58	0.42
2:E:20:ARG:NH2	8:E:525:HOH:O	2.42	0.42
2:E:86:ASP:OD2	2:E:106:ARG:NH2	2.51	0.42
3:F:24:CYS:HB2	4:F:401:SF4:S3	2.59	0.42
3:C:29:PRO:HG2	4:C:401:SF4:S4	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:248:MET:HG3	3:C:274:TYR:CD2	2.55	0.42
2:E:241:ASN:ND2	3:F:20:GLY:O	2.48	0.42
3:F:235:LYS:O	3:F:239:MET:HG2	2.20	0.42
1:D:108:ASP:HB3	1:D:120:GLU:O	2.20	0.42
2:E:83:GLU:HG2	2:E:84:THR:HG23	2.01	0.42
1:A:357:GLY:HA2	1:A:361:GLU:O	2.20	0.42
1:D:306:ILE:HG23	1:D:310:LEU:HD12	2.02	0.42
1:A:367:GLU:O	1:A:371:MET:HG3	2.20	0.42
3:C:33:TYR:CE2	3:C:107:MET:HG3	2.55	0.42
1:A:17:VAL:HG13	1:A:22:VAL:HG21	2.02	0.42
2:B:300:CYS:HA	2:B:301:PRO:HD3	1.83	0.41
1:A:33:TYR:HB3	1:A:81:SER:OG	2.20	0.41
3:C:299:ARG:NH2	8:C:502:HOH:O	2.10	0.41
1:A:89:MET:HG2	1:D:89:MET:HE3	2.03	0.41
2:E:101:ILE:HG13	2:E:102:LEU:HG	2.01	0.41
1:A:168:ASP:HB2	1:A:172:VAL:HG23	2.02	0.41
2:B:15:ILE:HB	2:B:67:ALA:HB3	2.01	0.41
1:A:169:GLY:O	1:A:171:PHE:N	2.52	0.41
2:B:268:TRP:CD2	2:B:278:ARG:HD2	2.56	0.41
3:C:246:THR:HG22	3:C:269:LYS:HB2	2.03	0.41
1:D:19:LEU:HB3	1:D:187:VAL:HG21	2.02	0.41
1:D:169:GLY:O	1:D:171:PHE:N	2.48	0.41
3:F:98:ASP:OD1	3:F:98:ASP:N	2.52	0.41
1:A:19:LEU:HD13	1:A:182:PRO:HG2	2.03	0.41
1:A:123:ASP:OD1	1:A:123:ASP:N	2.53	0.41
2:B:129:THR:HB	2:B:132:LEU:HB3	2.02	0.41
3:C:246:THR:HG21	3:C:274:TYR:HB2	2.02	0.40
1:A:118:GLY:HA3	1:A:360:GLY:HA3	2.03	0.40
1:A:170:TYR:HB3	8:A:452:HOH:O	2.21	0.40
3:C:225:CYS:HA	3:C:226:PRO:HD2	1.94	0.40
3:F:81:ALA:O	8:F:508:HOH:O	2.22	0.40
1:D:89:MET:HA	1:D:92:TYR:CD2	2.56	0.40
3:C:138:ASN:HB2	3:C:225:CYS:HB2	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:713:HOH:O	8:E:672:HOH:O[3_644]	2.16	0.04

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	392/395 (99%)	381 (97%)	10 (3%)	1 (0%)	41	49
1	D	391/395 (99%)	382 (98%)	8 (2%)	1 (0%)	41	49
2	B	304/315 (96%)	296 (97%)	8 (3%)	0	100	100
2	E	308/315 (98%)	300 (97%)	8 (3%)	0	100	100
3	C	310/314 (99%)	300 (97%)	9 (3%)	1 (0%)	41	49
3	F	310/314 (99%)	301 (97%)	8 (3%)	1 (0%)	41	49
All	All	2015/2048 (98%)	1960 (97%)	51 (2%)	4 (0%)	47	57

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	170	TYR
1	A	170	TYR
3	C	146	ILE
3	F	146	ILE

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	319/322 (99%)	315 (99%)	4 (1%)	69	80
1	D	318/322 (99%)	313 (98%)	5 (2%)	62	76
2	B	249/256 (97%)	247 (99%)	2 (1%)	81	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	E	243/256 (95%)	241 (99%)	2 (1%)	81 90
3	C	249/250 (100%)	247 (99%)	2 (1%)	81 90
3	F	249/250 (100%)	247 (99%)	2 (1%)	81 90
All	All	1627/1656 (98%)	1610 (99%)	17 (1%)	76 86

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	TYR
1	A	119	GLU
1	A	198	HIS
1	A	338	LEU
2	B	123	LEU
2	B	208	LEU
3	C	33	TYR
3	C	110	ASP
1	D	33	TYR
1	D	66	VAL
1	D	119	GLU
1	D	198	HIS
1	D	338	LEU
2	E	226	ARG
2	E	281	GLU
3	F	33	TYR
3	F	114	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	227	GLN
3	F	73	GLN
3	F	256	ASN

5.3.3 RNA

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 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	SF4	B	402	2	0,12,12	-	-	-		
4	SF4	E	401	2	0,12,12	-	-	-		
4	SF4	F	401	3	0,12,12	-	-	-		
6	TPP	C	402	7	22,27,27	2.04	6 (27%)	29,40,40	1.68	10 (34%)
4	SF4	E	402	2	0,12,12	-	-	-		
4	SF4	B	401	2	0,12,12	-	-	-		
4	SF4	C	401	3	0,12,12	-	-	-		
6	TPP	F	402	7	22,27,27	2.07	6 (27%)	29,40,40	1.59	8 (27%)

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	SF4	B	402	2	-	-	0/6/5/5
4	SF4	E	401	2	-	-	0/6/5/5
4	SF4	F	401	3	-	-	0/6/5/5
6	TPP	C	402	7	-	1/16/17/17	0/2/2/2
4	SF4	E	402	2	-	-	0/6/5/5
4	SF4	B	401	2	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SF4	C	401	3	-	-	0/6/5/5
6	TPP	F	402	7	-	1/16/17/17	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	402	TPP	C4-N3	-4.74	1.35	1.39
6	C	402	TPP	C4-N3	-4.31	1.36	1.39
6	C	402	TPP	C6-C5	4.04	1.52	1.50
6	F	402	TPP	C6-C5	3.92	1.52	1.50
6	F	402	TPP	C4'-N4'	3.80	1.43	1.34
6	C	402	TPP	C4'-N4'	3.71	1.43	1.34
6	C	402	TPP	C7'-C5'	3.34	1.58	1.51
6	F	402	TPP	C7'-N3	-3.26	1.42	1.48
6	F	402	TPP	C7'-C5'	3.23	1.57	1.51
6	C	402	TPP	C7'-N3	-3.11	1.42	1.48
6	C	402	TPP	C6'-C5'	2.33	1.42	1.37
6	F	402	TPP	C6'-C5'	2.28	1.42	1.37

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	F	402	TPP	C5'-C7'-N3	3.36	118.88	113.28
6	C	402	TPP	C6-C5-C4	-3.35	124.74	127.43
6	C	402	TPP	C5'-C7'-N3	3.04	118.34	113.28
6	F	402	TPP	C6'-N1'-C2'	2.95	120.98	115.96
6	C	402	TPP	C6'-N1'-C2'	2.94	120.96	115.96
6	F	402	TPP	PA-O3A-PB	-2.80	123.22	132.83
6	C	402	TPP	PA-O3A-PB	-2.73	123.45	132.83
6	F	402	TPP	C5'-C6'-N1'	-2.57	119.54	123.82
6	C	402	TPP	C5'-C6'-N1'	-2.45	119.74	123.82
6	F	402	TPP	N4'-C4'-N3'	2.37	120.38	117.03
6	C	402	TPP	C2'-N3'-C4'	2.34	121.73	118.08
6	C	402	TPP	N1'-C2'-N3'	-2.32	121.55	125.54
6	C	402	TPP	N4'-C4'-N3'	2.21	120.15	117.03
6	F	402	TPP	C6-C5-C4	-2.19	125.67	127.43
6	C	402	TPP	CM4-C4-N3	2.17	125.30	122.53
6	F	402	TPP	N1'-C2'-N3'	-2.13	121.87	125.54
6	F	402	TPP	C2'-N3'-C4'	2.06	121.29	118.08
6	C	402	TPP	CM2-C2'-N1'	2.02	119.36	117.14

There are no chirality outliers.

All (2) torsion outliers are listed below:

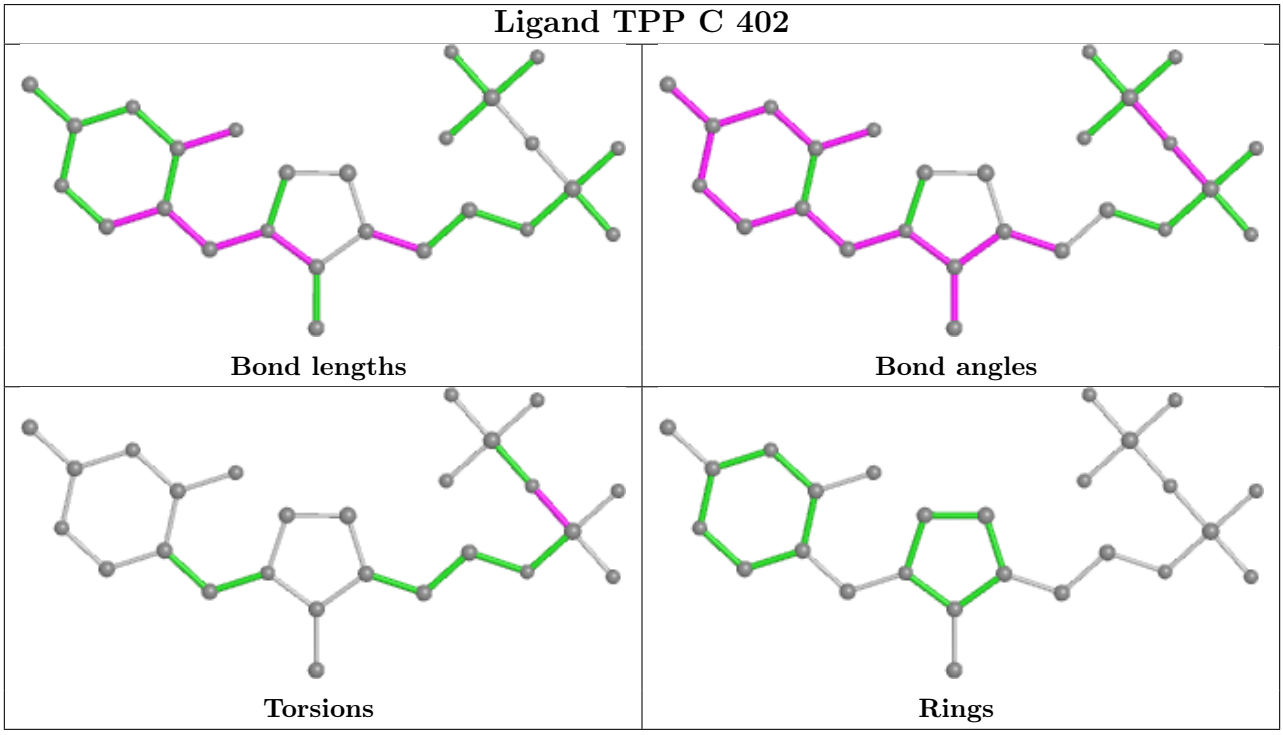
Mol	Chain	Res	Type	Atoms
6	C	402	TPP	PB-O3A-PA-O7
6	F	402	TPP	PB-O3A-PA-O7

There are no ring outliers.

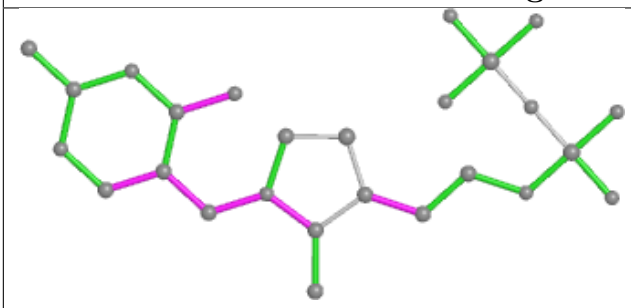
3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	401	SF4	1	0
6	C	402	TPP	3	0
4	C	401	SF4	2	0

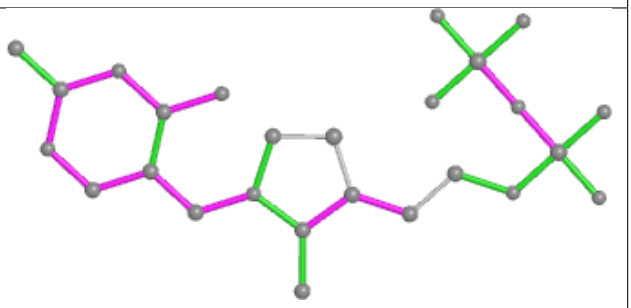
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



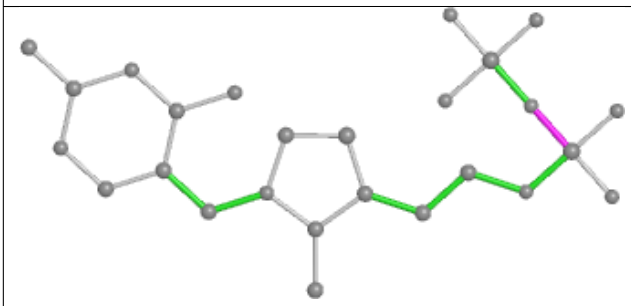
Ligand TPP F 402



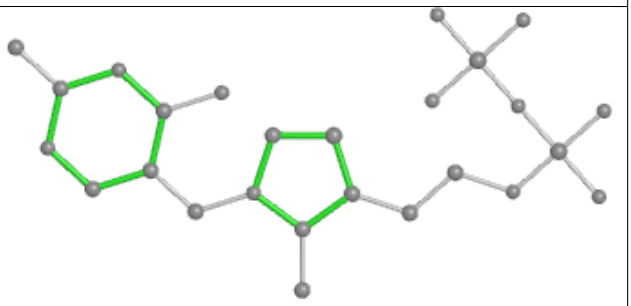
Bond lengths



Bond angles



Torsions



Rings

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, 95^{th} 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	394/395 (99%)	-0.23	7 (1%)	68	74	9, 20, 36, 48	0
1	D	393/395 (99%)	-0.12	5 (1%)	77	81	9, 19, 33, 42	0
2	B	308/315 (97%)	-0.02	16 (5%)	27	32	9, 25, 48, 84	0
2	E	312/315 (99%)	-0.35	7 (2%)	62	68	11, 22, 46, 83	0
3	C	312/314 (99%)	-0.13	8 (2%)	56	62	8, 18, 38, 60	0
3	F	312/314 (99%)	-0.14	2 (0%)	89	91	8, 19, 38, 55	0
All	All	2031/2048 (99%)	-0.17	45 (2%)	62	68	8, 20, 38, 84	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	219	VAL	8.2
2	B	3	THR	6.4
2	B	220	SER	4.6
2	B	226	ARG	4.5
2	B	225	LEU	4.5
2	E	2	SER	4.4
2	B	222	THR	4.3
3	C	1	MET	4.2
3	C	307	VAL	3.4
2	B	221	ALA	3.3
1	A	83	VAL	3.1
1	D	88	ALA	3.1
2	B	223	GLU	2.9
2	B	162	ILE	2.8
1	A	126	CYS	2.7
3	C	266	ASP	2.6
2	B	224	LEU	2.5
1	A	85	VAL	2.5
2	B	200	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	91	VAL	2.4
3	C	75	THR	2.4
3	C	165	GLU	2.4
1	D	126	CYS	2.4
1	A	28	TYR	2.4
1	D	83	VAL	2.3
2	E	281	GLU	2.3
2	B	194	ALA	2.3
3	C	306	THR	2.3
1	D	87	TYR	2.2
1	D	286	LEU	2.2
2	B	205	VAL	2.2
1	A	94	PRO	2.2
2	B	189	VAL	2.2
2	E	5	ASP	2.2
1	A	87	TYR	2.1
2	E	4	LYS	2.1
2	B	187	ALA	2.1
3	F	286	PRO	2.1
3	C	50	THR	2.1
3	F	50	THR	2.1
3	C	72	ALA	2.1
2	B	138	VAL	2.1
2	B	145	GLU	2.0
2	E	212	GLU	2.0
2	E	127	GLY	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)

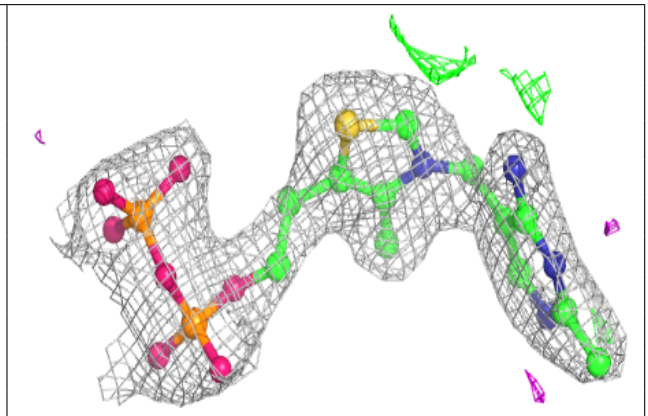
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

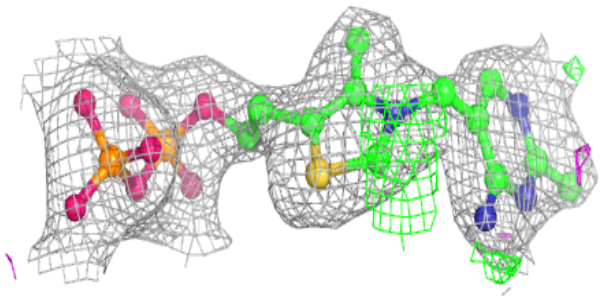
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	NA	F	404	1/1	0.79	0.09	22,22,22,22	1
5	NA	B	403	1/1	0.96	0.04	24,24,24,24	1
6	TPP	F	402	26/26	0.97	0.15	12,20,29,30	0
7	MG	C	403	1/1	0.97	0.04	15,15,15,15	0
4	SF4	C	401	8/8	0.98	0.12	6,7,9,12	0
6	TPP	C	402	26/26	0.98	0.12	12,21,33,38	0
4	SF4	F	401	8/8	0.98	0.10	5,9,10,11	0
4	SF4	B	401	8/8	0.98	0.10	7,9,11,12	0
7	MG	F	403	1/1	0.98	0.15	12,12,12,12	0
4	SF4	E	401	8/8	0.99	0.08	7,10,13,13	0
4	SF4	E	402	8/8	0.99	0.06	8,10,13,16	0
4	SF4	B	402	8/8	0.99	0.09	8,9,12,14	0

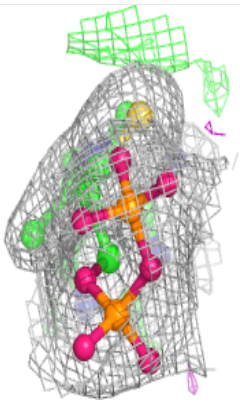
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around TPP F 402:

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

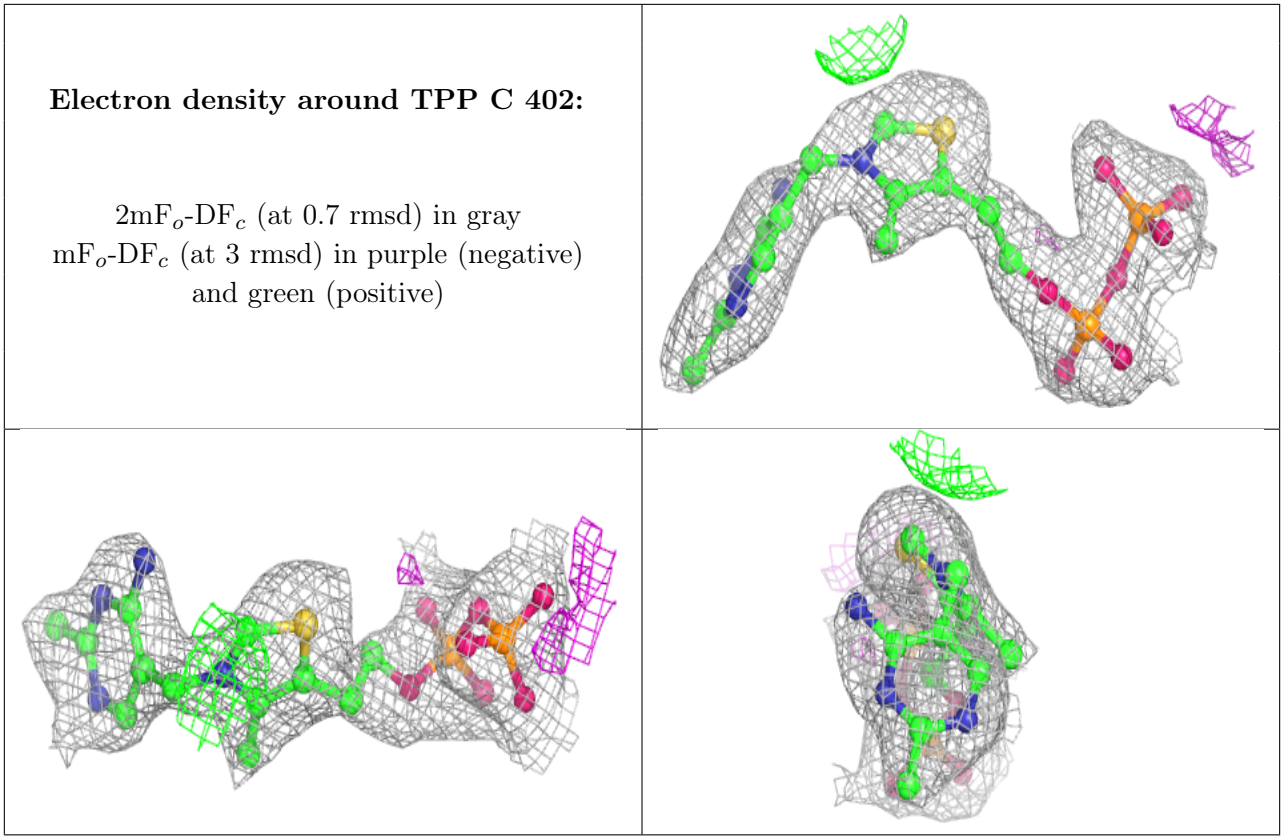






Electron density around TPP C 402:

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



6.5 Other polymers (i)

There are no such residues in this entry.