



Full wwPDB EM Validation Report ⓘ

Jul 9, 2025 – 12:23 PM JST

PDB ID : 8I6V / pdb_00008i6v
EMDB ID : EMD-35208
Title : Cryo-EM structure of the polyphosphate polymerase VTC complex(Vtc4/Vtc3/Vtc1)
Authors : Mayer, A.; Wu, S.; Ye, S.
Deposited on : 2023-01-29
Resolution : 3.06 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>
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:

EMDB validation analysis : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

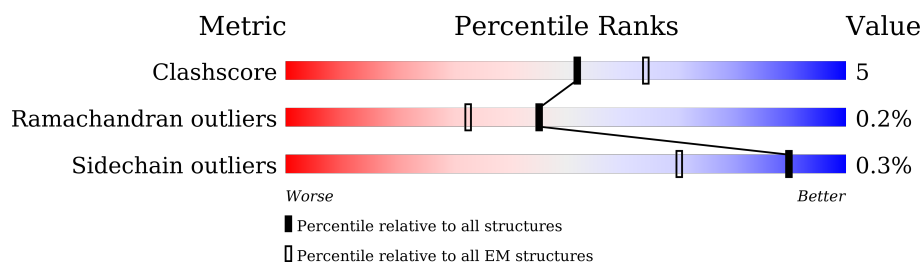
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.06 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)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	129	71% 8% 21%
1	B	129	71% 7% 22%
1	C	129	70% 9% 21%
2	D	835	70% 11% 19%
3	E	721	75% 10% 15%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 13172 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Vacuolar transporter chaperone complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	102	Total	C	N	O	S	0	0
			811	541	137	129	4		
1	B	101	Total	C	N	O	S	0	0
			804	536	136	128	4		
1	C	102	Total	C	N	O	S	0	0
			810	538	140	128	4		

- Molecule 2 is a protein called Vacuolar transporter chaperone 3 complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	678	Total	C	N	O	S	0	0
			5640	3625	955	1051	9		

- Molecule 3 is a protein called Vacuolar transporter chaperone complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	611	Total	C	N	O	S	0	0
			5022	3233	850	924	15		

- Molecule 4 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylammonio)ethyl phosphate (CCD ID: POV) (formula: C₄₂H₈₂NO₈P).



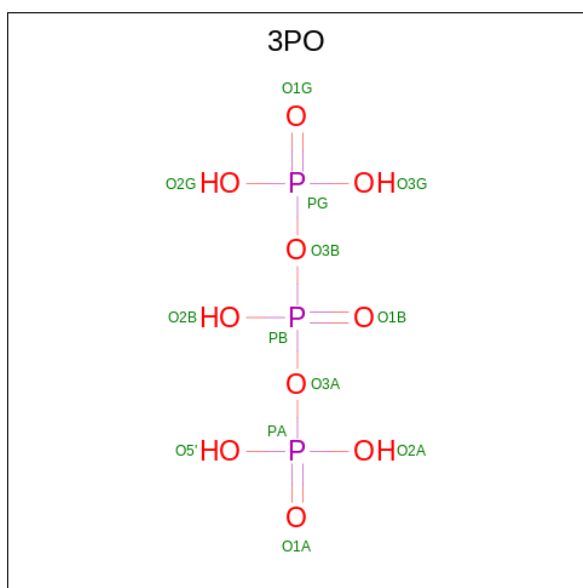
Mol	Chain	Residues	Atoms					AltConf
4	C	1	Total 52	C 42	N 1	O 8	P 1	0

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			AltConf
5	D	1	Total 5	O 4	P 1	0
5	D	1	Total 5	O 4	P 1	0
5	E	1	Total 5	O 4	P 1	0

- Molecule 6 is TRIPHOSPHATE (CCD ID: 3PO) (formula: $\text{H}_5\text{O}_{10}\text{P}_3$).



Mol	Chain	Residues	Atoms			AltConf
6	E	1	Total	O	P	0
			13	10	3	

- Molecule 7 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

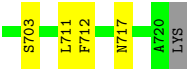
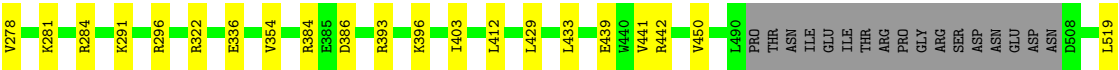
Mol	Chain	Residues	Atoms		AltConf
7	E	1	Total	Mn	0
			1	1	

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		AltConf
8	D	1	Total	O	0
			1	1	
8	E	3	Total	O	0
			3	3	



● Molecule 3: Vacuolar transporter chaperone complex subunit 4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1042873	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor

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: PO4, POV, MN, 3PO

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	0.11	0/832	0.25	0/1126
1	B	0.10	0/825	0.24	0/1116
1	C	0.14	0/830	0.35	1/1122 (0.1%)
2	D	0.23	0/5767	0.39	0/7798
3	E	0.12	0/5133	0.27	0/6939
All	All	0.17	0/13387	0.33	1/18101 (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	90	ARG	CB-CA-C	-5.63	110.06	116.54

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	811	0	838	9	0
1	B	804	0	829	8	0
1	C	810	0	842	8	0
2	D	5640	0	5624	75	0
3	E	5022	0	5050	54	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	52	0	82	3	0
5	D	10	0	0	0	0
5	E	5	0	0	0	0
6	E	13	0	0	1	0
7	E	1	0	0	0	0
8	D	1	0	0	0	0
8	E	3	0	0	0	0
All	All	13172	0	13265	138	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 5.

All (138) 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)
2:D:38:ARG:HG3	2:D:39:SER:H	1.53	0.73
2:D:83:GLU:HA	2:D:86:LYS:HE2	1.72	0.70
2:D:795:PHE:HE2	3:E:661:ILE:HG12	1.57	0.69
2:D:173:PHE:HE1	2:D:586:ARG:HA	1.58	0.68
2:D:81:LEU:HG	2:D:99:PHE:CD1	2.30	0.67
2:D:87:SER:C	2:D:89:GLU:H	2.05	0.64
1:C:37:LEU:HA	1:C:40:THR:HG22	1.82	0.62
2:D:77:LYS:HE3	2:D:106:CYS:SG	2.40	0.61
2:D:582:LEU:O	2:D:586:ARG:HB2	2.00	0.61
1:B:46:LEU:HB3	4:C:201:POV:H21C	1.83	0.61
2:D:84:ASN:HD22	2:D:99:PHE:HZ	1.48	0.61
3:E:403:ILE:HD13	3:E:412:LEU:HD11	1.81	0.61
1:C:45:GLY:HA2	4:C:201:POV:H21E	1.82	0.60
3:E:106:LEU:HD22	3:E:167:ILE:HG23	1.84	0.59
3:E:607:ALA:HB2	3:E:613:ILE:HG13	1.83	0.59
2:D:89:GLU:C	2:D:91:ILE:H	2.10	0.58
3:E:203:VAL:HG22	3:E:450:VAL:HG12	1.85	0.58
2:D:38:ARG:HG3	2:D:39:SER:N	2.18	0.58
3:E:687:LEU:HD22	3:E:689:ARG:HH22	1.69	0.57
3:E:1:MET:N	3:E:5:GLU:OE1	2.38	0.57
3:E:658:ILE:HD12	3:E:661:ILE:HD12	1.86	0.57
2:D:100:LYS:HE3	2:D:185:SER:HB2	1.87	0.56
2:D:784:ALA:HB1	3:E:671:LEU:HD21	1.87	0.56
3:E:322:ARG:NH2	3:E:336:GLU:OE1	2.37	0.56
2:D:83:GLU:C	2:D:85:THR:H	2.14	0.56
1:C:70:MET:O	1:C:74:ILE:HG13	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:436:ARG:NH2	3:E:228:LYS:O	2.39	0.55
2:D:807:ARG:NH1	2:D:835:GLU:OE2	2.40	0.55
2:D:747:LEU:HD21	2:D:786:VAL:HG11	1.90	0.53
3:E:138:THR:HG22	3:E:140:PHE:H	1.72	0.53
2:D:87:SER:O	2:D:91:ILE:HG13	2.07	0.53
2:D:341:ARG:HB3	2:D:354:PHE:HE1	1.74	0.53
1:B:50:LEU:HD22	1:B:62:ALA:HB2	1.90	0.53
1:A:52:ASN:OD1	3:E:717:ASN:ND2	2.42	0.53
3:E:243:ASP:HB3	3:E:354:VAL:HG21	1.90	0.53
2:D:87:SER:C	2:D:89:GLU:N	2.67	0.52
2:D:89:GLU:C	2:D:91:ILE:N	2.65	0.52
2:D:728:VAL:HG23	2:D:737:ALA:HB3	1.92	0.52
3:E:439:GLU:OE2	3:E:442:ARG:NH1	2.43	0.51
1:A:22:GLU:OE1	1:A:24:LYS:NZ	2.42	0.51
2:D:457:ILE:N	2:D:457:ILE:HD12	2.26	0.51
2:D:711:LEU:O	2:D:715:THR:HG23	2.10	0.51
2:D:34:ILE:HG13	2:D:134:LEU:HD13	1.91	0.51
2:D:196:HIS:O	2:D:586:ARG:NH2	2.44	0.50
3:E:658:ILE:HG13	3:E:712:PHE:HE2	1.77	0.50
1:B:50:LEU:HB2	4:C:201:POV:H211	1.93	0.50
3:E:41:THR:HB	3:E:44:LEU:HG	1.93	0.50
2:D:166:ARG:HA	2:D:169:TYR:CE1	2.49	0.48
1:C:33:PHE:O	1:C:37:LEU:HD23	2.13	0.48
3:E:284:ARG:HB2	3:E:291:LYS:O	2.13	0.48
1:C:36:TRP:HA	1:C:39:PHE:HD2	1.79	0.47
1:A:75:TYR:OH	1:A:97:ASP:OD2	2.32	0.47
2:D:13:PRO:HA	2:D:16:LYS:HD3	1.97	0.47
2:D:79:ASP:O	2:D:82:GLU:HB3	2.15	0.47
2:D:177:ASN:HD22	2:D:591:ILE:HG13	1.80	0.47
2:D:44:TRP:NE1	2:D:49:GLU:HG2	2.29	0.47
2:D:788:ILE:HD13	3:E:668:LEU:HD22	1.98	0.46
1:B:70:MET:HA	1:B:70:MET:HE2	1.96	0.46
2:D:88:ALA:HA	2:D:91:ILE:HD12	1.96	0.46
1:A:25:VAL:HG13	3:E:519:LEU:HD12	1.96	0.46
2:D:204:SER:N	2:D:498:ASN:O	2.48	0.46
2:D:457:ILE:HD12	2:D:457:ILE:H	1.79	0.46
3:E:266:ARG:NH1	6:E:801:3PO:O2A	2.45	0.46
2:D:302:ASP:OD2	2:D:528:TYR:OH	2.34	0.46
2:D:89:GLU:OE1	2:D:90:LYS:HD3	2.16	0.46
3:E:255:ARG:O	3:E:257:ASP:N	2.48	0.46
2:D:83:GLU:O	2:D:85:THR:N	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:5:GLU:HG2	3:E:9:LYS:NZ	2.30	0.46
2:D:724:ILE:HD11	3:E:646:THR:HG21	1.98	0.46
3:E:429:LEU:HD21	3:E:441:VAL:HG11	1.98	0.46
2:D:780:PRO:O	3:E:631:TYR:OH	2.27	0.45
3:E:671:LEU:O	3:E:675:VAL:HG23	2.17	0.45
2:D:7:LEU:O	2:D:11:VAL:HG23	2.17	0.45
2:D:173:PHE:CD2	2:D:585:MET:HE2	2.51	0.45
3:E:5:GLU:O	3:E:9:LYS:NZ	2.50	0.44
1:A:80:TYR:CE2	3:E:699:PRO:HG2	2.52	0.44
2:D:467:ASP:OD1	2:D:468:ILE:N	2.50	0.44
2:D:74:VAL:CG2	2:D:109:GLU:HG2	2.47	0.44
2:D:83:GLU:C	2:D:85:THR:N	2.76	0.44
2:D:189:ALA:O	2:D:192:SER:OG	2.24	0.44
2:D:315:LYS:HD3	2:D:524:LYS:HE2	1.99	0.44
2:D:780:PRO:HB3	3:E:631:TYR:CE2	2.53	0.44
2:D:54:GLU:O	2:D:58:LYS:HD2	2.18	0.44
2:D:81:LEU:HG	2:D:99:PHE:CE1	2.53	0.44
2:D:697:ALA:O	2:D:701:LEU:HG	2.17	0.44
1:A:94:PRO:HG3	1:B:23:PRO:HG3	1.99	0.44
1:B:101:PRO:HB3	1:C:33:PHE:CZ	2.52	0.44
2:D:730:LYS:N	2:D:730:LYS:HD3	2.33	0.44
1:A:73:MET:HE1	3:E:703:SER:OG	2.18	0.43
2:D:763:LEU:HD12	2:D:763:LEU:HA	1.86	0.43
3:E:673:ARG:HH22	3:E:698:GLY:HA3	1.83	0.43
2:D:78:LEU:HG	2:D:106:CYS:SG	2.58	0.43
3:E:5:GLU:O	3:E:8:SER:OG	2.36	0.43
2:D:130:LYS:HE3	2:D:130:LYS:HB2	1.79	0.43
2:D:76:ARG:HH11	2:D:76:ARG:HB3	1.83	0.43
3:E:88:LEU:HD21	3:E:99:PHE:HZ	1.83	0.43
1:A:25:VAL:HG22	3:E:519:LEU:HA	2.00	0.43
3:E:66:LYS:HD3	3:E:66:LYS:HA	1.86	0.43
2:D:584:ASN:O	2:D:588:LEU:HB2	2.19	0.43
2:D:80:ASP:C	2:D:82:GLU:N	2.73	0.43
2:D:747:LEU:HD21	2:D:786:VAL:CG1	2.49	0.43
2:D:809:LEU:HD23	2:D:809:LEU:H	1.84	0.42
3:E:193:ASN:N	3:E:433:LEU:HD12	2.34	0.42
2:D:704:GLU:OE2	2:D:759:TYR:OH	2.32	0.42
3:E:634:TRP:HB3	3:E:674:THR:HG21	2.01	0.42
2:D:581:LYS:O	2:D:585:MET:HG2	2.20	0.42
2:D:795:PHE:CE2	3:E:661:ILE:HG12	2.46	0.42
3:E:617:VAL:HG21	3:E:690:ALA:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:30:GLU:O	1:B:34:LEU:HD23	2.20	0.42
3:E:281:LYS:HB2	3:E:281:LYS:HE3	1.90	0.42
2:D:86:LYS:H	2:D:86:LYS:HG2	1.70	0.42
2:D:183:THR:O	2:D:185:SER:N	2.41	0.42
2:D:721:THR:OG1	2:D:744:TYR:HB3	2.19	0.42
3:E:278:VAL:O	3:E:296:ARG:HA	2.19	0.42
2:D:447:ARG:HG3	2:D:535:LEU:HD22	2.02	0.42
2:D:507:TYR:HE2	2:D:509:TRP:CD1	2.37	0.41
2:D:83:GLU:HA	2:D:86:LYS:CE	2.47	0.41
3:E:255:ARG:HG2	3:E:614:CYS:SG	2.60	0.41
2:D:149:LEU:HD23	2:D:149:LEU:HA	1.92	0.41
2:D:176:SER:OG	2:D:177:ASN:N	2.53	0.41
3:E:193:ASN:HB3	3:E:194:PHE:H	1.52	0.41
3:E:643:GLY:O	3:E:646:THR:HG22	2.20	0.41
3:E:244:ASN:HD21	3:E:248:ASP:HB2	1.86	0.41
1:C:103:LEU:HD23	1:C:103:LEU:HA	1.87	0.41
3:E:672:ILE:HG13	3:E:673:ARG:N	2.36	0.41
1:C:93:GLY:H	1:C:94:PRO:CD	2.34	0.41
2:D:84:ASN:ND2	2:D:99:PHE:HZ	2.16	0.41
2:D:161:SER:HB3	2:D:164:LEU:HD23	2.03	0.41
3:E:386:ASP:O	3:E:393:ARG:HD2	2.21	0.41
3:E:396:LYS:HA	3:E:396:LYS:HD3	1.86	0.41
2:D:172:GLU:O	2:D:176:SER:HB3	2.21	0.41
1:A:116:PHE:HE1	1:B:51:LEU:HD22	1.86	0.40
3:E:384:ARG:NH1	3:E:386:ASP:OD1	2.54	0.40
3:E:637:ILE:HD13	3:E:637:ILE:HA	1.95	0.40
3:E:711:LEU:HD23	3:E:711:LEU:HA	1.90	0.40
3:E:53:GLU:OE2	3:E:149:ARG:NE	2.48	0.40
2:D:76:ARG:HB3	2:D:76:ARG:NH1	2.37	0.40
3:E:673:ARG:O	3:E:673:ARG:HD2	2.21	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 PDB entries followed by that with respect to all EM entries.

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	100/129 (78%)	97 (97%)	3 (3%)	0	100	100
1	B	99/129 (77%)	96 (97%)	3 (3%)	0	100	100
1	C	100/129 (78%)	96 (96%)	4 (4%)	0	100	100
2	D	668/835 (80%)	642 (96%)	23 (3%)	3 (0%)	30	58
3	E	603/721 (84%)	585 (97%)	18 (3%)	0	100	100
All	All	1570/1943 (81%)	1516 (97%)	51 (3%)	3 (0%)	45	71

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	35	HIS
2	D	84	ASN
2	D	90	LYS

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	83/106 (78%)	83 (100%)	0	100	100
1	B	82/106 (77%)	82 (100%)	0	100	100
1	C	83/106 (78%)	83 (100%)	0	100	100
2	D	634/770 (82%)	630 (99%)	4 (1%)	84	90
3	E	559/651 (86%)	559 (100%)	0	100	100
All	All	1441/1739 (83%)	1437 (100%)	4 (0%)	90	94

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	35	HIS
2	D	41	VAL

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Mol	Chain	Res	Type
2	D	85	THR
2	D	86	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	115	ASN
2	D	67	GLN
2	D	84	ASN
2	D	310	ASN
2	D	351	ASN
2	D	384	GLN
2	D	406	GLN
2	D	503	GLN
2	D	544	ASN
3	E	82	GLN
3	E	169	GLN
3	E	218	HIS
3	E	227	ASN
3	E	263	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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
5	PO4	D	901	-	4,4,4	0.95	0	6,6,6	0.43	0
4	POV	C	201	-	51,51,51	0.90	3 (5%)	57,59,59	0.75	1 (1%)
5	PO4	D	902	-	4,4,4	0.93	0	6,6,6	0.47	0
6	3PO	E	801	7	8,12,12	0.72	0	15,20,20	1.19	2 (13%)
5	PO4	E	803	-	4,4,4	0.95	0	6,6,6	0.44	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	3PO	E	801	7	-	0/12/12/12	-
4	POV	C	201	-	-	20/55/55/55	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	201	POV	P-O12	3.72	1.74	1.59
4	C	201	POV	O12-C11	-2.11	1.36	1.44
4	C	201	POV	O21-C2	-2.09	1.41	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	201	POV	O13-P-O14	3.32	128.66	112.24
6	E	801	3PO	PB-O3A-PA	-2.54	124.10	132.83
6	E	801	3PO	PB-O3B-PG	-2.32	124.86	132.83

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	201	POV	C11-O12-P-O11
4	C	201	POV	C11-O12-P-O13

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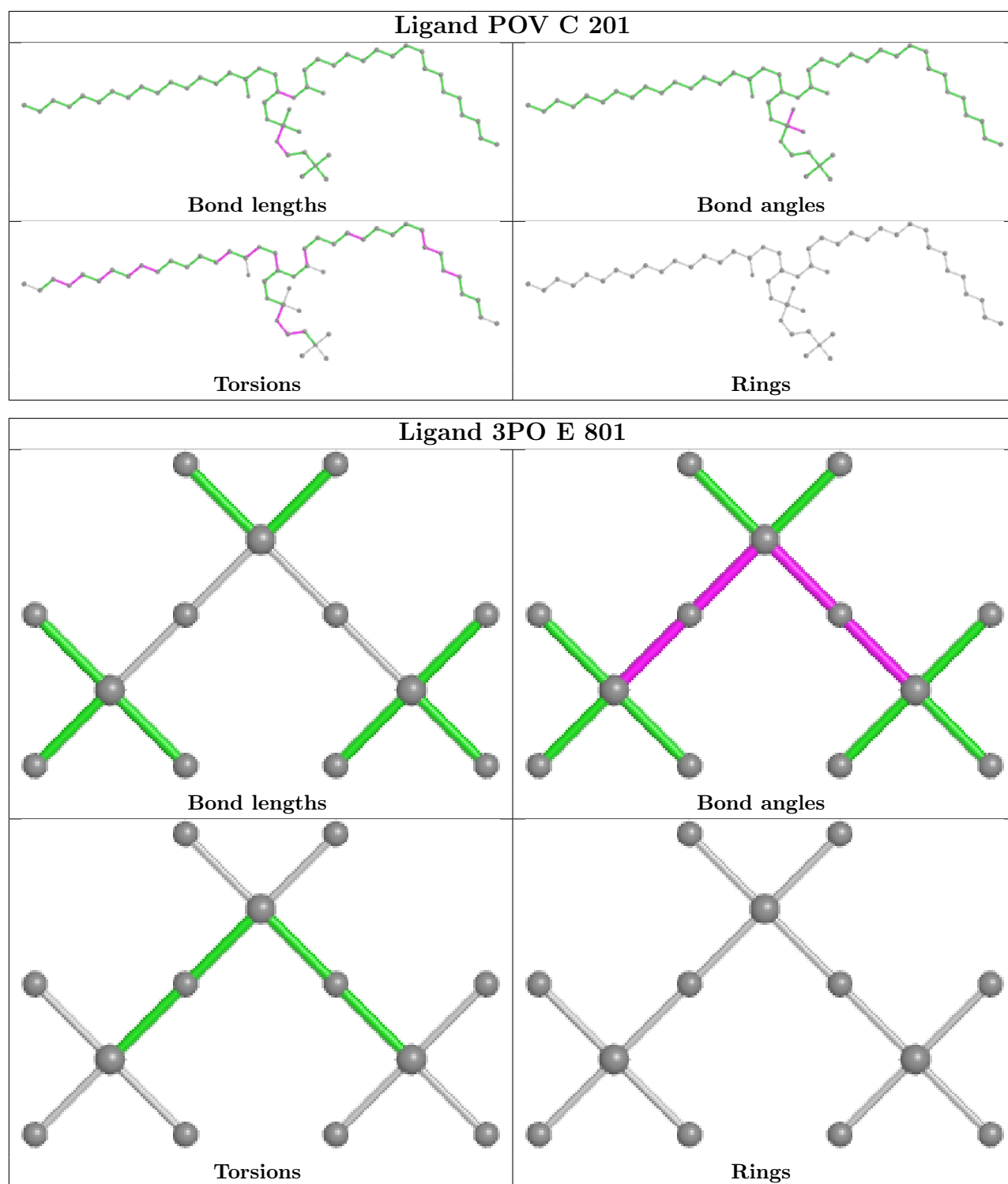
Mol	Chain	Res	Type	Atoms
4	C	201	POV	C11-O12-P-O14
4	C	201	POV	O21-C2-C3-O31
4	C	201	POV	O12-C11-C12-N
4	C	201	POV	C31-C32-C33-C34
4	C	201	POV	C36-C37-C38-C39
4	C	201	POV	C39-C310-C311-C312
4	C	201	POV	C311-C312-C313-C314
4	C	201	POV	C312-C313-C314-C315
4	C	201	POV	C37-C38-C39-C310
4	C	201	POV	C1-C2-C3-O31
4	C	201	POV	C210-C211-C212-C213
4	C	201	POV	C32-C31-O31-C3
4	C	201	POV	C212-C213-C214-C215
4	C	201	POV	O32-C31-O31-C3
4	C	201	POV	O21-C21-C22-C23
4	C	201	POV	C29-C210-C211-C212
4	C	201	POV	C24-C25-C26-C27
4	C	201	POV	C12-C11-O12-P

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	201	POV	3	0
6	E	801	3PO	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 ⓘ

There are no chain breaks in this entry.