



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:27 AM UTC

PDB ID : 8XFX / pdb_00008xfx
Title : Archaeal exosome subcomplex (Rrp41-Rrp42)
Authors : Kim, H.S.; Park, S.H.; Kim, S.H.; Hwang, K.Y.
Deposited on : 2023-12-14
Resolution : 2.30 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

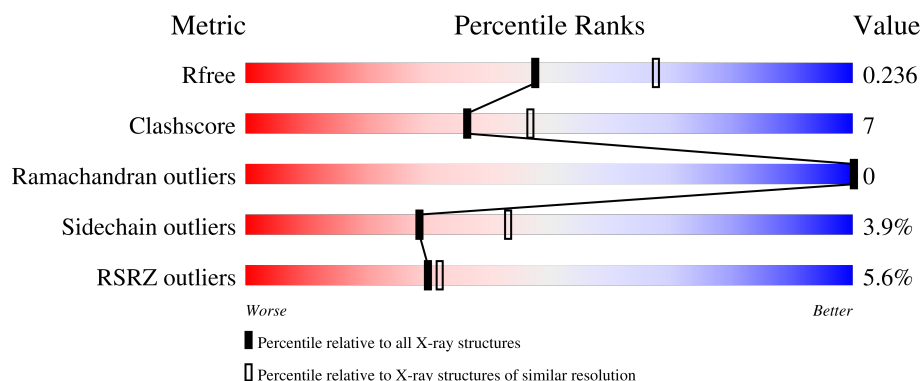
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

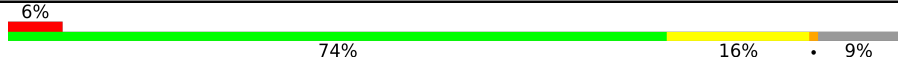
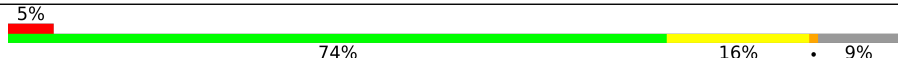
The reported resolution of this entry is 2.30 Å.

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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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 $\leq 5\%$. 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	508	
1	B	508	

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
2	PO4	A	602	-	-	X	-

2 Entry composition [i](#)

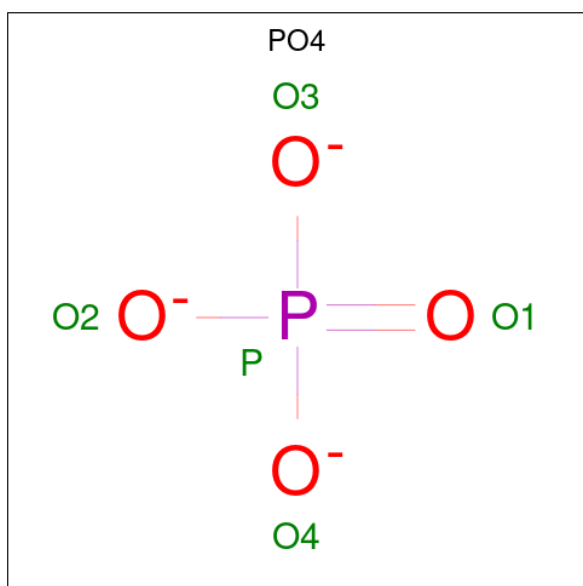
There are 3 unique types of molecules in this entry. The entry contains 7408 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Exosome complex component Rrp41,Exosome complex component Rrp42.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	463	Total	C	N	O	S	0	0	0
			3544	2225	607	693	19			
1	B	463	Total	C	N	O	S	0	0	0
			3559	2239	608	693	19			

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P) (labeled as "Ligand of Interest" by depositor).



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

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	129	Total	O	0	0
			129	129		
3	B	156	Total	O	0	0
			156	156		

- Molecule 1: Exosome complex component Rrp41,Exosome complex component Rrp42



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	164.59Å 164.59Å 164.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.10 – 2.30 29.10 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.3 (29.10-2.30) 99.2 (29.10-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.19.1_4122: ???)	Depositor
R, R_{free}	0.204 , 0.236 0.204 , 0.236	Depositor DCC
R_{free} test set	2027 reflections (3.06%)	wwPDB-VP
Wilson B-factor (Å ²)	41.6	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 35.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.033 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7408	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.17% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.16	0/3595	0.53	3/4862 (0.1%)
1	B	0.16	0/3609	0.45	0/4875
All	All	0.16	0/7204	0.49	3/9737 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	1
All	All	0	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	379	GLY	CA-C-N	9.31	149.34	127.00
1	A	379	GLY	C-N-CA	9.31	149.34	127.00
1	A	379	GLY	C-N-CD	-8.14	102.68	120.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	380	PRO	Peptide
1	A	454	GLY	Peptide
1	B	132	ALA	Peptide

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	3544	0	3586	57	0
1	B	3559	0	3598	53	0
2	A	15	0	0	3	0
2	B	5	0	0	0	0
3	A	129	0	0	2	0
3	B	156	0	0	6	0
All	All	7408	0	7184	103	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 7.

All (103) 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:177:LYS:NZ	3:A:701:HOH:O	2.09	0.84
1:A:446:ALA:HB1	1:A:460:LEU:HB3	1.64	0.79
1:A:377:GLU:H	1:A:380:PRO:HB3	1.48	0.76
1:A:446:ALA:HB1	1:A:460:LEU:H	1.55	0.70
1:B:11:ILE:HG21	1:B:167:VAL:HG11	1.72	0.69
1:B:408:VAL:HA	1:B:415:VAL:HG12	1.75	0.69
1:A:120:ARG:NH2	1:B:66:HIS:O	2.26	0.69
1:B:96:ARG:NH2	3:B:704:HOH:O	2.27	0.68
1:B:72:HIS:HB2	1:B:115:ILE:HG23	1.76	0.68
1:A:319:THR:HG23	1:A:335:ALA:HB3	1.77	0.66
1:B:70:ILE:HG23	1:B:120:ARG:NH1	2.10	0.66
1:A:62:ALA:HB3	1:A:68:GLN:HG2	1.76	0.66
1:A:228:GLN:O	1:A:232:GLU:HG3	1.96	0.66
1:B:242:ASP:O	3:B:701:HOH:O	2.14	0.65
1:A:446:ALA:HB1	1:A:460:LEU:N	2.11	0.64
1:B:355:ASP:OD1	1:B:355:ASP:N	2.23	0.62
1:A:74:ILE:HD11	1:B:70:ILE:HD11	1.83	0.61
1:A:311:LEU:HB2	1:A:314:GLU:HG3	1.82	0.60
1:B:62:ALA:HB3	1:B:68:GLN:HG2	1.82	0.60
1:B:484:LEU:O	1:B:488:GLN:HG3	2.04	0.58
1:A:114:MET:HE3	1:A:154:PRO:HB2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:197:ASP:HB3	1:B:514:ALA:HB1	1.87	0.57
1:B:410:GLU:HG2	1:B:413:LYS:HB2	1.86	0.56
1:B:65:LYS:HA	1:B:68:GLN:HG3	1.87	0.56
1:A:207:VAL:HG22	1:A:211:GLU:HB2	1.87	0.56
1:B:306:ARG:HD2	1:B:486:GLU:OE2	2.07	0.55
1:A:485:GLU:OE2	1:B:114:MET:HE1	2.07	0.54
1:B:319:THR:HG23	1:B:335:ALA:HB3	1.89	0.54
1:A:373:PHE:CD2	1:A:374:PRO:HD2	2.42	0.54
1:B:156:ARG:HA	1:B:241:GLN:O	2.07	0.53
1:B:41:GLY:HA3	1:B:151:ALA:HB2	1.90	0.53
1:B:407:LEU:HB3	1:B:416:TRP:HB2	1.90	0.53
1:B:91:ARG:NE	1:B:91:ARG:H	2.08	0.52
1:A:409:ILE:HD11	1:A:416:TRP:CZ2	2.45	0.52
1:A:189:ILE:HD11	1:A:201:MET:HE3	1.92	0.52
1:A:69:ASP:HB2	1:B:70:ILE:HD11	1.93	0.50
1:B:19:ASP:OD1	1:B:19:ASP:N	2.41	0.50
1:A:306:ARG:HD2	1:A:486:GLU:OE2	2.11	0.50
1:A:13:GLU:OE1	1:A:14:ASP:HB2	2.11	0.50
1:B:75:VAL:CG2	1:B:115:ILE:HD11	2.42	0.50
1:B:460:LEU:HD12	1:B:461:PRO:HD2	1.94	0.50
1:A:407:LEU:HB3	1:A:416:TRP:HB2	1.93	0.50
1:B:216:MET:O	1:B:220:PHE:HD2	1.95	0.50
1:B:430:ASN:ND2	1:B:481:ASP:HA	2.27	0.49
1:A:204:ASP:CG	1:A:394:ARG:HD3	2.37	0.49
1:B:204:ASP:HB2	1:B:398:GLU:HG3	1.93	0.49
1:B:79:TYR:HE1	1:B:81:MET:HE2	1.77	0.49
1:B:75:VAL:HG23	1:B:115:ILE:HD11	1.93	0.49
1:A:410:GLU:HG2	1:A:413:LYS:HB2	1.95	0.48
1:B:220:PHE:O	1:B:223:THR:OG1	2.29	0.48
1:A:73:ALA:HB2	1:A:118:PHE:HB2	1.96	0.48
1:B:17:ARG:HD2	1:B:179:GLU:OE2	2.14	0.48
1:A:197:ASP:HB3	1:A:514:ALA:HB1	1.96	0.48
1:B:81:MET:HE1	1:B:97:ARG:HH21	1.78	0.48
1:A:446:ALA:HB1	1:A:460:LEU:CB	2.40	0.48
1:A:306:ARG:NH2	1:A:480:CYS:O	2.45	0.48
1:A:370:PRO:HA	1:A:376:PHE:HB3	1.95	0.48
1:B:535:ARG:NH2	3:B:714:HOH:O	2.46	0.48
1:A:209:GLU:HG2	1:A:213:TYR:CE2	2.49	0.47
1:A:232:GLU:O	1:A:236:ASN:ND2	2.35	0.47
1:A:307:ILE:HD11	1:B:242:ASP:HB2	1.96	0.47
1:A:532:LYS:NZ	1:A:536:GLU:HG3	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:81:MET:HE1	1:B:97:ARG:HE	1.79	0.47
1:B:52:ILE:HD11	1:B:136:THR:HG23	1.97	0.46
1:A:446:ALA:HB3	1:A:459:LYS:HG3	1.98	0.46
1:A:364:THR:HB	1:A:393:ASP:HB2	1.97	0.45
1:A:413:LYS:O	1:A:414:LYS:HD3	2.16	0.45
1:A:41:GLY:HA3	1:A:151:ALA:HB2	1.99	0.45
1:A:390:ARG:NH2	2:A:602:PO4:O1	2.46	0.45
1:A:485:GLU:HA	1:B:117:GLN:HE22	1.82	0.45
1:B:385:ALA:O	1:B:389:SER:OG	2.31	0.44
1:A:446:ALA:CB	1:A:460:LEU:H	2.28	0.44
1:A:338:ASN:HB2	1:A:428:ASP:OD2	2.17	0.44
1:B:14:ASP:O	1:B:15:ASN:HB2	2.18	0.44
1:A:95:ASP:OD1	1:A:98:THR:HG23	2.18	0.44
1:B:137:ARG:HG2	3:B:751:HOH:O	2.17	0.43
1:A:407:LEU:HD21	1:A:460:LEU:HD12	1.99	0.43
1:A:521:LYS:NZ	3:A:706:HOH:O	2.33	0.43
1:A:355:ASP:OD1	1:A:355:ASP:N	2.51	0.43
1:A:373:PHE:HB3	1:A:376:PHE:CG	2.53	0.43
1:B:365:ASN:HB2	3:B:840:HOH:O	2.19	0.43
1:B:364:THR:HB	1:B:393:ASP:HB2	2.01	0.42
1:A:340:ARG:NH1	2:A:603:PO4:O1	2.51	0.42
1:B:401:MET:HE1	1:B:440:VAL:HA	2.01	0.42
1:A:117:GLN:OE1	1:B:485:GLU:HA	2.19	0.42
1:A:202:GLN:NE2	2:A:602:PO4:O2	2.53	0.42
1:A:14:ASP:O	1:A:15:ASN:HB2	2.20	0.41
1:B:19:ASP:OD2	1:B:21:ARG:HD3	2.20	0.41
1:A:21:ARG:HB3	1:A:25:GLU:HB3	2.03	0.41
1:B:203:MET:O	1:B:506:ALA:HA	2.20	0.41
1:B:404:PRO:HA	1:B:407:LEU:HG	2.03	0.41
1:A:70:ILE:O	1:A:119:PRO:HB3	2.21	0.41
1:B:219:ILE:O	1:B:223:THR:HG23	2.21	0.41
1:A:19:ASP:OD2	1:A:21:ARG:HG3	2.21	0.41
1:B:11:ILE:HG21	1:B:167:VAL:CG1	2.45	0.41
1:A:446:ALA:CB	1:A:459:LYS:HG3	2.52	0.40
1:B:427:TYR:CE2	1:B:431:LEU:HG	2.55	0.40
1:A:377:GLU:N	1:A:380:PRO:HB3	2.24	0.40
1:B:128:GLU:HB3	3:B:716:HOH:O	2.21	0.40
1:A:203:MET:HE2	1:A:204:ASP:C	2.46	0.40
1:A:427:TYR:CE2	1:A:484:LEU:HD13	2.56	0.40
1:B:189:ILE:HD11	1:B:201:MET:HE3	2.03	0.40
1:A:166:LYS:HD2	1:A:211:GLU:OE2	2.22	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	459/508 (90%)	457 (100%)	2 (0%)	0	100	100
1	B	455/508 (90%)	454 (100%)	1 (0%)	0	100	100
All	All	914/1016 (90%)	911 (100%)	3 (0%)	0	100	100

There are no Ramachandran outliers to report.

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	384/424 (91%)	371 (97%)	13 (3%)	32	49
1	B	385/424 (91%)	368 (96%)	17 (4%)	25	38
All	All	769/848 (91%)	739 (96%)	30 (4%)	28	43

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	ILE
1	A	104	VAL
1	A	129	VAL
1	A	319	THR
1	A	342	VAL

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Mol	Chain	Res	Type
1	A	355	ASP
1	A	363	THR
1	A	375	SER
1	A	402	ILE
1	A	448	VAL
1	A	452	LYS
1	A	489	ILE
1	A	529	GLU
1	B	70	ILE
1	B	104	VAL
1	B	115	ILE
1	B	129	VAL
1	B	207	VAL
1	B	319	THR
1	B	342	VAL
1	B	355	ASP
1	B	356	THR
1	B	389	SER
1	B	448	VAL
1	B	463	SER
1	B	465	THR
1	B	479	VAL
1	B	499	THR
1	B	529	GLU
1	B	532	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	ASN
1	A	423	ASN
1	B	12	ASN
1	B	32	GLN
1	B	117	GLN
1	B	170	HIS
1	B	323	ASN
1	B	423	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	PO4	A	603	-	4,4,4	0.97	0	6,6,6	0.46	0
2	PO4	A	602	-	4,4,4	0.97	0	6,6,6	0.54	0
2	PO4	B	601	-	4,4,4	0.96	0	6,6,6	0.48	0
2	PO4	A	601	-	4,4,4	0.96	0	6,6,6	0.47	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

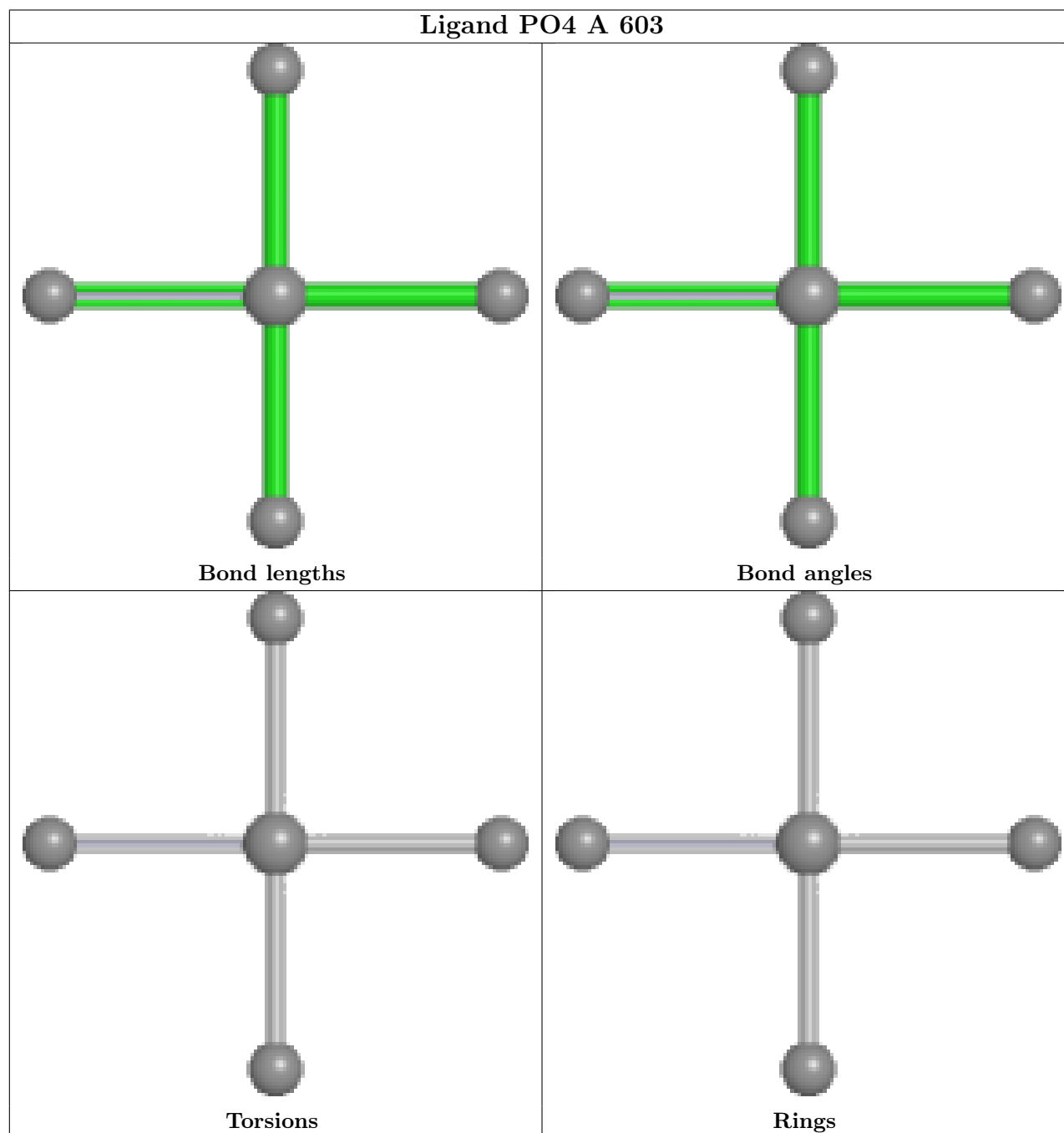
There are no ring outliers.

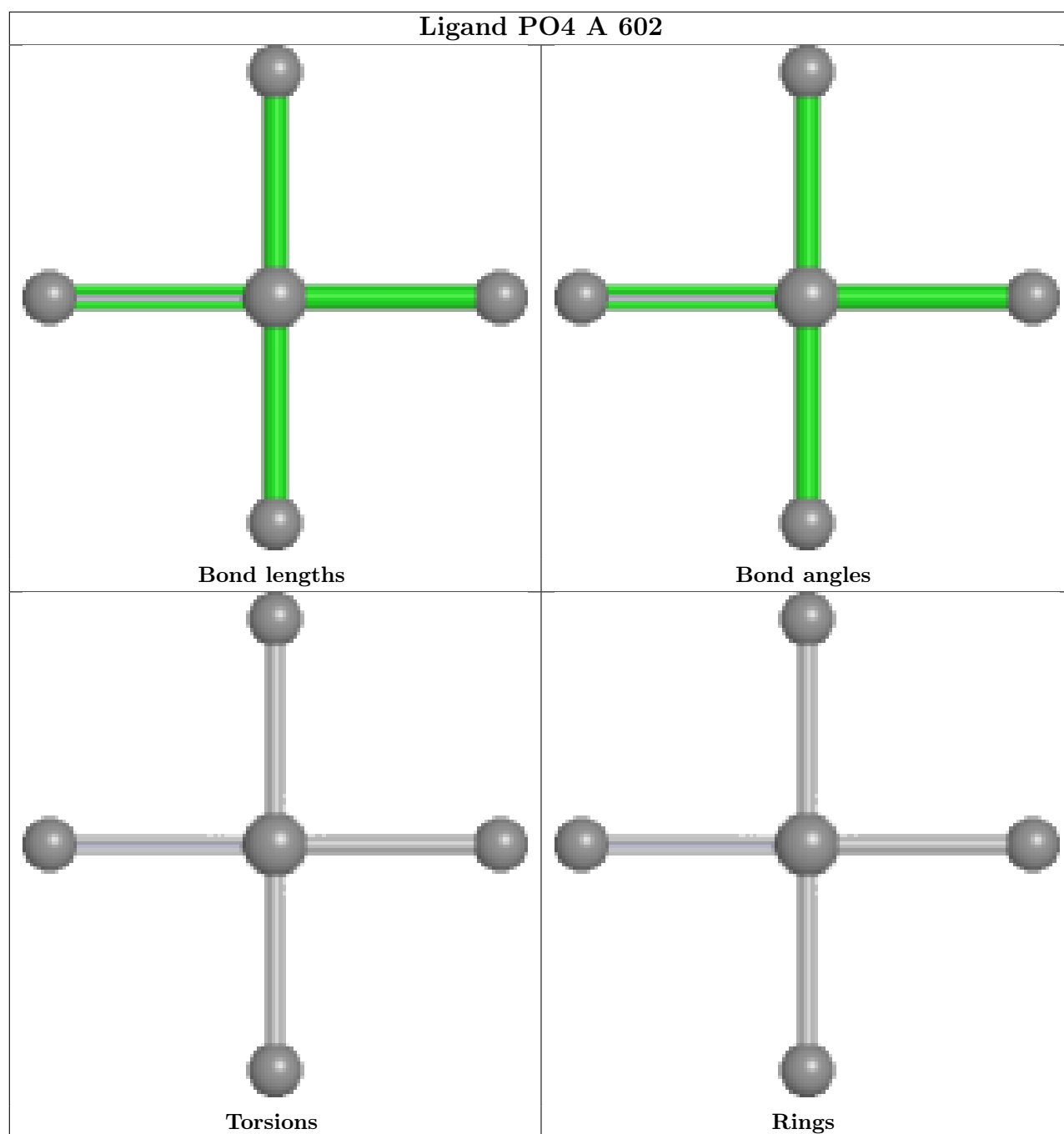
2 monomers are involved in 3 short contacts:

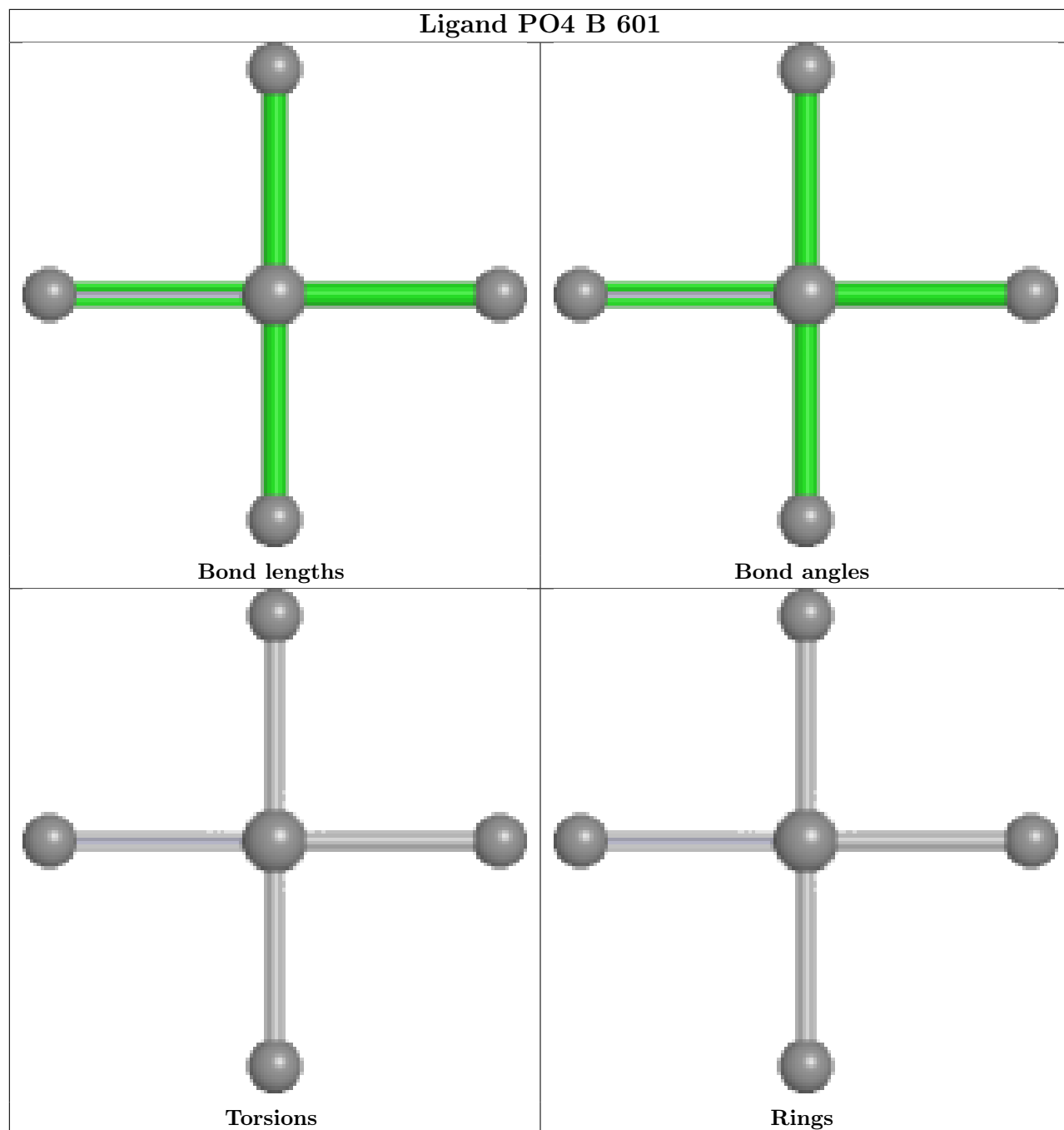
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	603	PO4	1	0
2	A	602	PO4	2	0

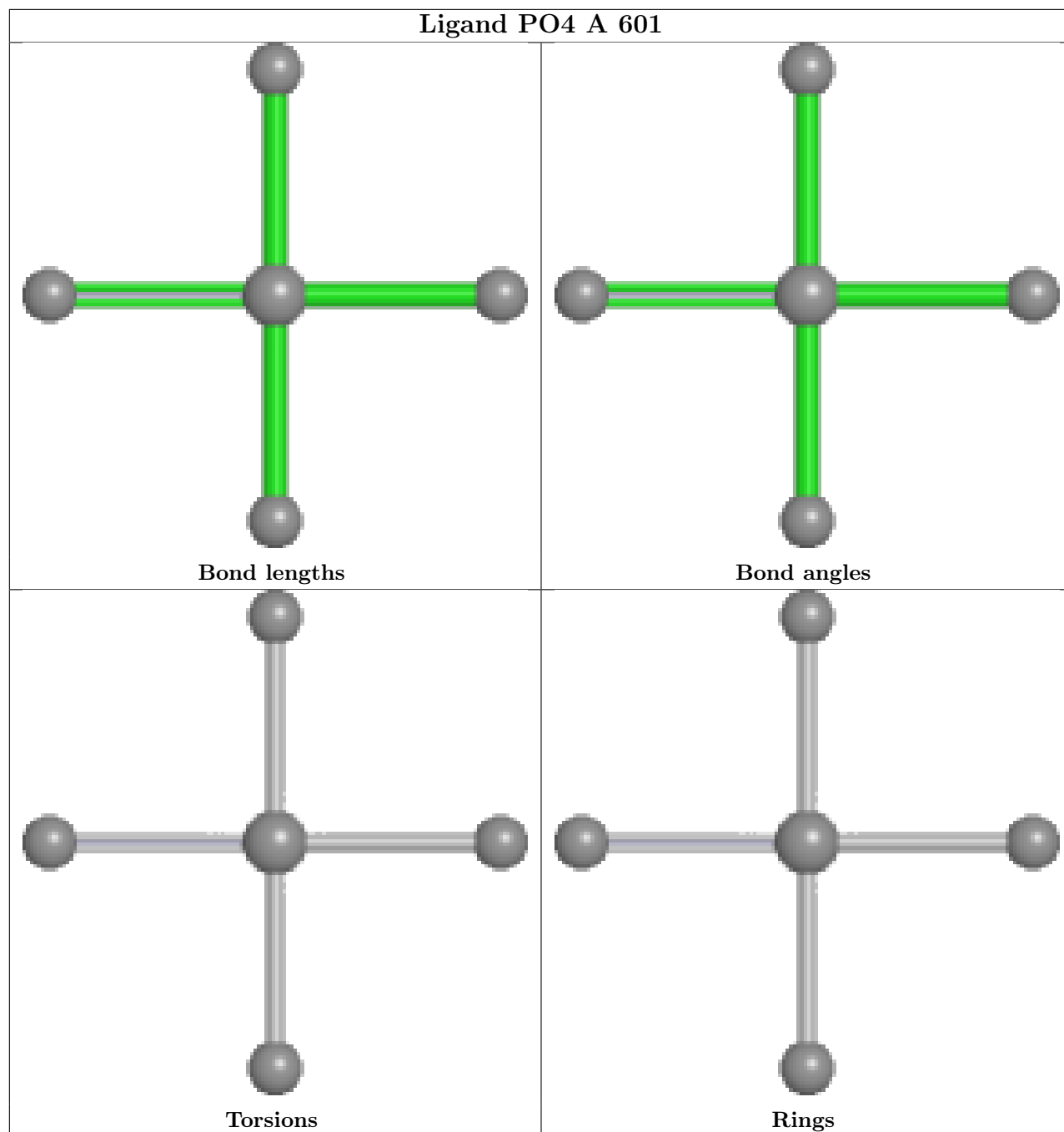
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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	463/508 (91%)	0.20	28 (6%)	27 29	33, 48, 90, 124	0
1	B	463/508 (91%)	0.06	24 (5%)	33 34	28, 44, 91, 117	0
All	All	926/1016 (91%)	0.13	52 (5%)	30 32	28, 47, 90, 124	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	490	CYS	6.8
1	B	376	PHE	6.6
1	A	378	ALA	6.3
1	B	10	LEU	5.3
1	A	381	PRO	4.9
1	A	380	PRO	4.5
1	B	381	PRO	4.3
1	A	379	GLY	4.2
1	A	66	HIS	4.2
1	A	446	ALA	4.0
1	B	9	LYS	3.9
1	A	376	PHE	3.7
1	B	210	ASP	3.3
1	B	66	HIS	3.3
1	B	375	SER	3.1
1	B	238	TYR	3.1
1	A	10	LEU	3.1
1	A	375	SER	3.0
1	A	447	VAL	3.0
1	A	63	TYR	3.0
1	B	358	ASP	2.9
1	B	354	PRO	2.9
1	A	9	LYS	2.9
1	B	489	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	304	GLY	2.8
1	A	373	PHE	2.8
1	B	304	GLY	2.7
1	B	11	ILE	2.7
1	B	454	GLY	2.7
1	A	454	GLY	2.6
1	B	242	ASP	2.6
1	A	11	ILE	2.6
1	A	445	ASN	2.5
1	A	64	PRO	2.5
1	B	373	PHE	2.5
1	A	489	ILE	2.4
1	B	63	TYR	2.4
1	B	357	PRO	2.4
1	A	235	LEU	2.3
1	A	14	ASP	2.3
1	A	133	ASP	2.3
1	B	12	ASN	2.3
1	A	403	SER	2.3
1	A	455	GLY	2.2
1	B	133	ASP	2.2
1	B	65	LYS	2.2
1	B	359	GLN	2.2
1	A	353	PHE	2.1
1	A	88	GLU	2.1
1	B	14	ASP	2.1
1	B	241	GLN	2.0
1	A	65	LYS	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 oligosaccharides in this entry.

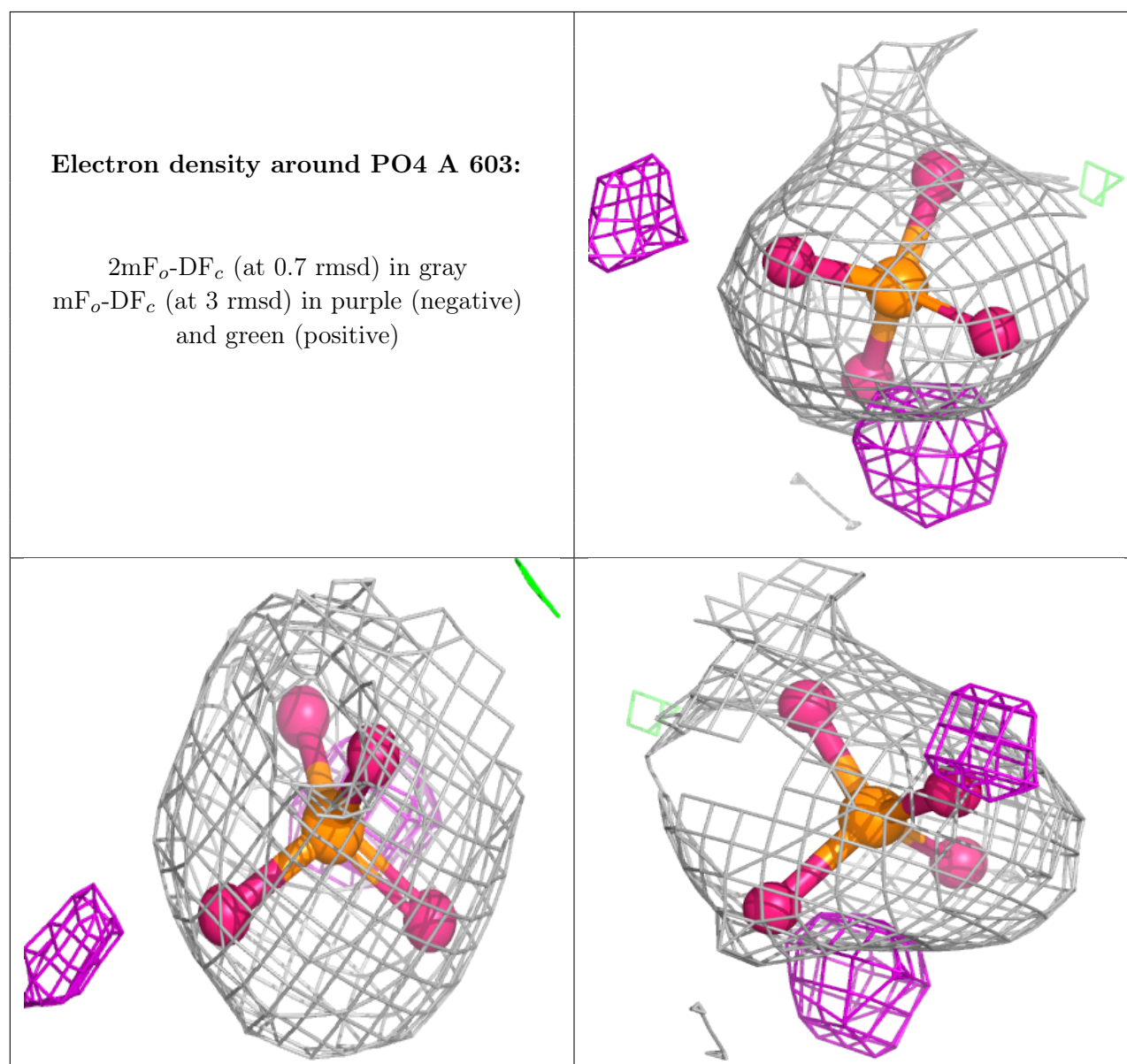
6.4 Ligands [i](#)

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.

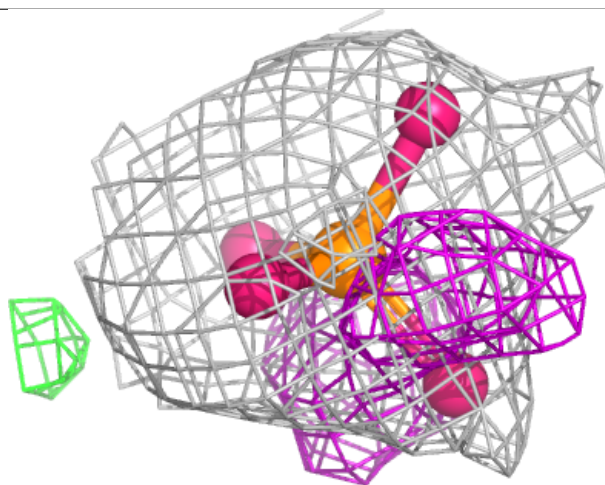
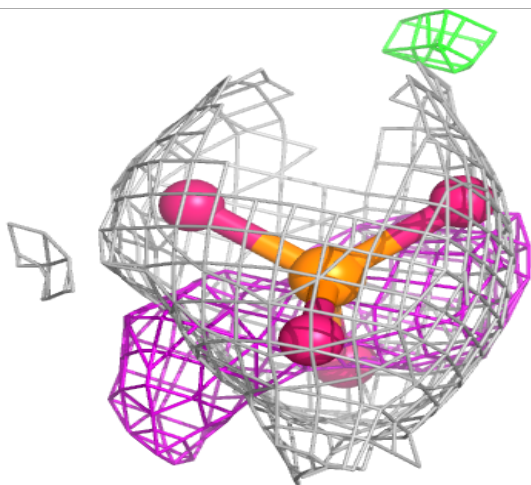
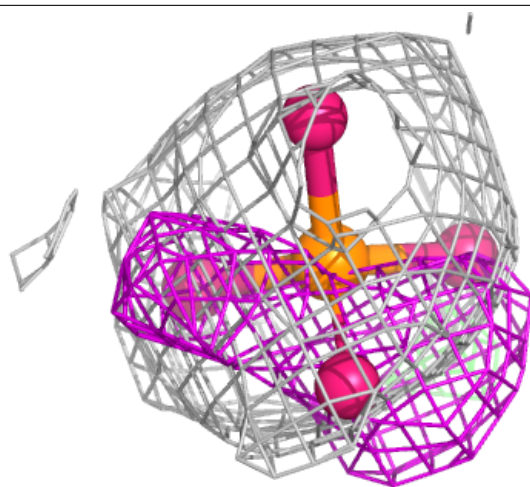
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PO4	A	603	5/5	0.85	0.08	79,84,91,100	0
2	PO4	A	602	5/5	0.88	0.17	60,66,77,82	0
2	PO4	A	601	5/5	0.98	0.05	43,43,46,61	0
2	PO4	B	601	5/5	0.98	0.05	37,42,48,57	0

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.



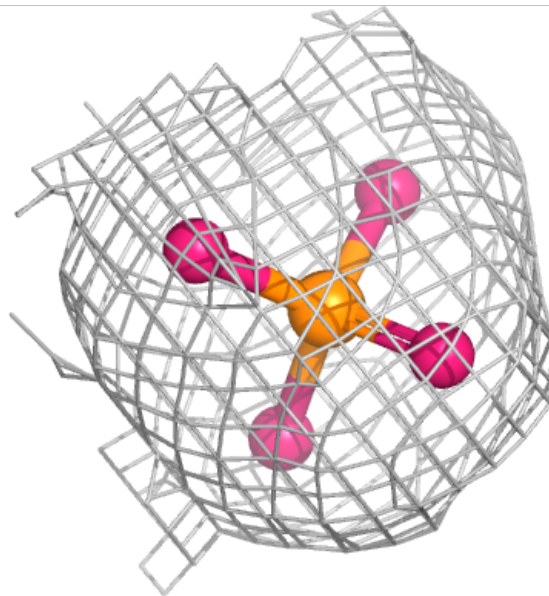
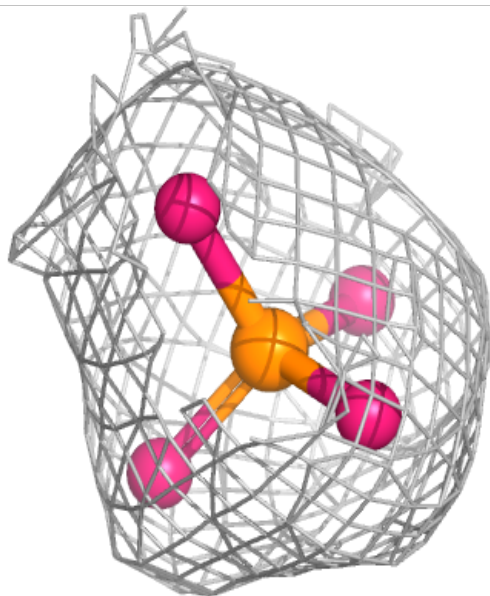
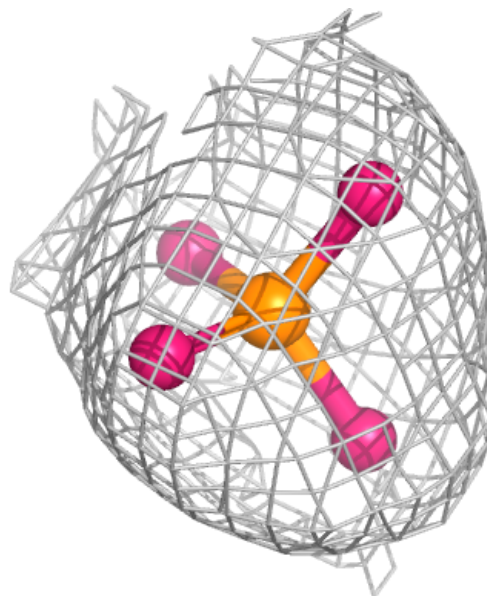
Electron density around PO4 A 602:

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



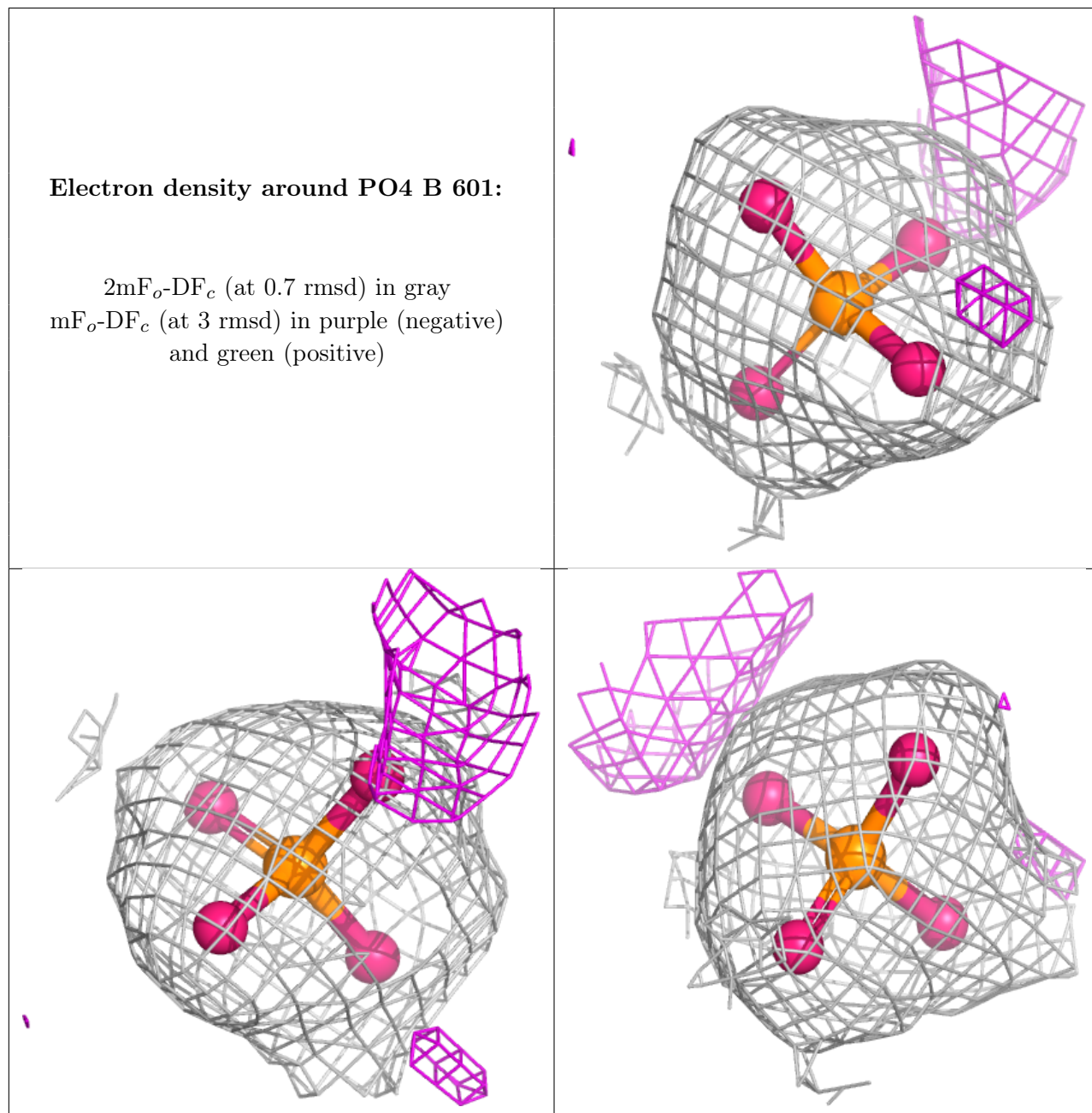
Electron density around PO4 A 601:

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



Electron density around PO4 B 601:

$2mF_o-DF_c$ (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.