



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 22, 2025 – 02:51 AM EDT

PDB ID : 7L21 / pdb_00007L21
Title : Pyruvate Kinase M2 mutant-N70D
Authors : Nandi, S.; Dey, M.
Deposited on : 2020-12-16
Resolution : 2.29 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 : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

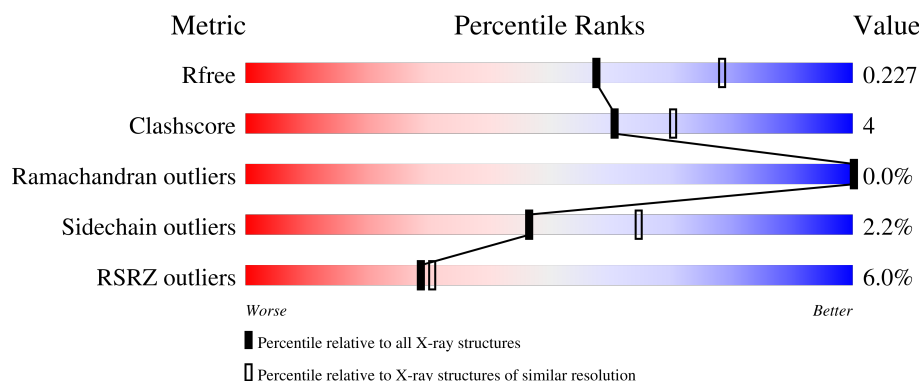
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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}	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (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	550	<div> <div>4%</div> <div>85%</div> <div>8%</div> <div>6%</div> </div>
1	B	550	<div> <div>3%</div> <div>83%</div> <div>10%</div> <div>6%</div> </div>
1	C	550	<div> <div>3%</div> <div>85%</div> <div>9%</div> <div>6%</div> </div>
1	D	550	<div> <div>12%</div> <div>79%</div> <div>12%</div> <div>8%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	OXL	A	601	-	X	-	-
2	OXL	B	601	-	X	-	-
2	OXL	C	601	-	X	-	-
2	OXL	D	601	-	X	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 16070 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 Pyruvate kinase PKM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	515	Total	C	N	O	S	0	0	0
			3878	2437	686	730	25			
1	B	515	Total	C	N	O	S	0	0	0
			3862	2430	677	730	25			
1	C	518	Total	C	N	O	S	0	0	0
			3886	2441	688	732	25			
1	D	504	Total	C	N	O	S	0	0	0
			3661	2291	659	688	23			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	initiating methionine	UNP P14618
A	-17	GLY	-	expression tag	UNP P14618
A	-16	SER	-	expression tag	UNP P14618
A	-15	SER	-	expression tag	UNP P14618
A	-14	HIS	-	expression tag	UNP P14618
A	-13	HIS	-	expression tag	UNP P14618
A	-12	HIS	-	expression tag	UNP P14618
A	-11	HIS	-	expression tag	UNP P14618
A	-10	HIS	-	expression tag	UNP P14618
A	-9	HIS	-	expression tag	UNP P14618
A	-8	SER	-	expression tag	UNP P14618
A	-7	SER	-	expression tag	UNP P14618
A	-6	GLY	-	expression tag	UNP P14618
A	-5	LEU	-	expression tag	UNP P14618
A	-4	VAL	-	expression tag	UNP P14618
A	-3	PRO	-	expression tag	UNP P14618
A	-2	ARG	-	expression tag	UNP P14618
A	-1	GLY	-	expression tag	UNP P14618
A	0	SER	-	expression tag	UNP P14618
A	70	ASP	ASN	engineered mutation	UNP P14618
B	-18	MET	-	initiating methionine	UNP P14618

Continued on next page...

Continued from previous page...

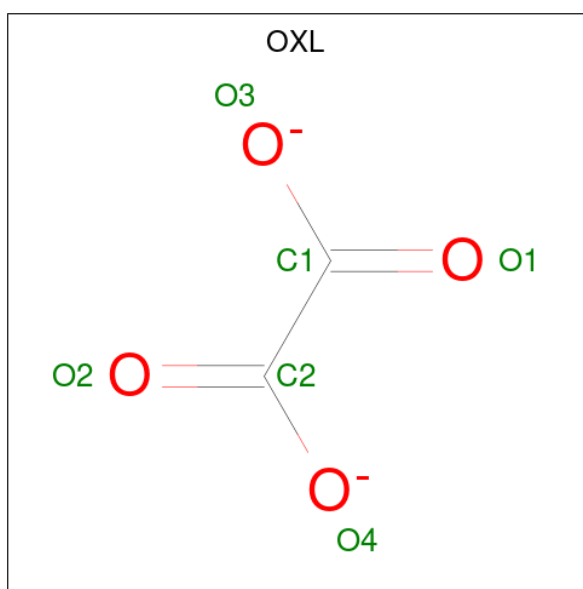
Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	GLY	-	expression tag	UNP P14618
B	-16	SER	-	expression tag	UNP P14618
B	-15	SER	-	expression tag	UNP P14618
B	-14	HIS	-	expression tag	UNP P14618
B	-13	HIS	-	expression tag	UNP P14618
B	-12	HIS	-	expression tag	UNP P14618
B	-11	HIS	-	expression tag	UNP P14618
B	-10	HIS	-	expression tag	UNP P14618
B	-9	HIS	-	expression tag	UNP P14618
B	-8	SER	-	expression tag	UNP P14618
B	-7	SER	-	expression tag	UNP P14618
B	-6	GLY	-	expression tag	UNP P14618
B	-5	LEU	-	expression tag	UNP P14618
B	-4	VAL	-	expression tag	UNP P14618
B	-3	PRO	-	expression tag	UNP P14618
B	-2	ARG	-	expression tag	UNP P14618
B	-1	GLY	-	expression tag	UNP P14618
B	0	SER	-	expression tag	UNP P14618
B	70	ASP	ASN	engineered mutation	UNP P14618
C	-18	MET	-	initiating methionine	UNP P14618
C	-17	GLY	-	expression tag	UNP P14618
C	-16	SER	-	expression tag	UNP P14618
C	-15	SER	-	expression tag	UNP P14618
C	-14	HIS	-	expression tag	UNP P14618
C	-13	HIS	-	expression tag	UNP P14618
C	-12	HIS	-	expression tag	UNP P14618
C	-11	HIS	-	expression tag	UNP P14618
C	-10	HIS	-	expression tag	UNP P14618
C	-9	HIS	-	expression tag	UNP P14618
C	-8	SER	-	expression tag	UNP P14618
C	-7	SER	-	expression tag	UNP P14618
C	-6	GLY	-	expression tag	UNP P14618
C	-5	LEU	-	expression tag	UNP P14618
C	-4	VAL	-	expression tag	UNP P14618
C	-3	PRO	-	expression tag	UNP P14618
C	-2	ARG	-	expression tag	UNP P14618
C	-1	GLY	-	expression tag	UNP P14618
C	0	SER	-	expression tag	UNP P14618
C	70	ASP	ASN	engineered mutation	UNP P14618
D	-18	MET	-	initiating methionine	UNP P14618
D	-17	GLY	-	expression tag	UNP P14618
D	-16	SER	-	expression tag	UNP P14618

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	-15	SER	-	expression tag	UNP P14618
D	-14	HIS	-	expression tag	UNP P14618
D	-13	HIS	-	expression tag	UNP P14618
D	-12	HIS	-	expression tag	UNP P14618
D	-11	HIS	-	expression tag	UNP P14618
D	-10	HIS	-	expression tag	UNP P14618
D	-9	HIS	-	expression tag	UNP P14618
D	-8	SER	-	expression tag	UNP P14618
D	-7	SER	-	expression tag	UNP P14618
D	-6	GLY	-	expression tag	UNP P14618
D	-5	LEU	-	expression tag	UNP P14618
D	-4	VAL	-	expression tag	UNP P14618
D	-3	PRO	-	expression tag	UNP P14618
D	-2	ARG	-	expression tag	UNP P14618
D	-1	GLY	-	expression tag	UNP P14618
D	0	SER	-	expression tag	UNP P14618
D	70	ASP	ASN	engineered mutation	UNP P14618

- Molecule 2 is OXALATE ION (CCD ID: OXL) (formula: C_2O_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	2	4		
2	B	1	Total	C	O	0	0
			6	2	4		
2	C	1	Total	C	O	0	0
			6	2	4		

Continued on next page...

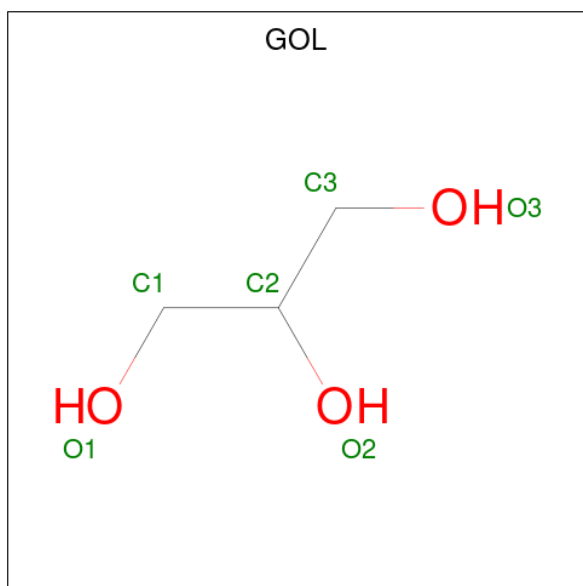
Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	C	O	0	0
			6	2	4		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



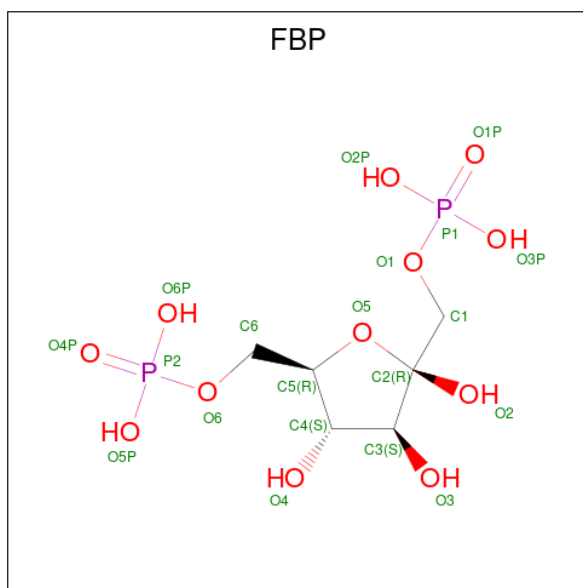
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

Continued on next page...

Continued from previous page...

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

- Molecule 5 is 1,6-di-O-phosphono-beta-D-fructofuranose (CCD ID: FBP) (formula: $C_6H_{14}O_{12}P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	O	P	0	0
			8	2	5	1		
5	B	1	Total	O	P		0	0
			5	4	1			
5	C	1	Total	O	P		0	0
			5	4	1			
5	D	1	Total	C	O	P	0	0
			7	2	4	1		

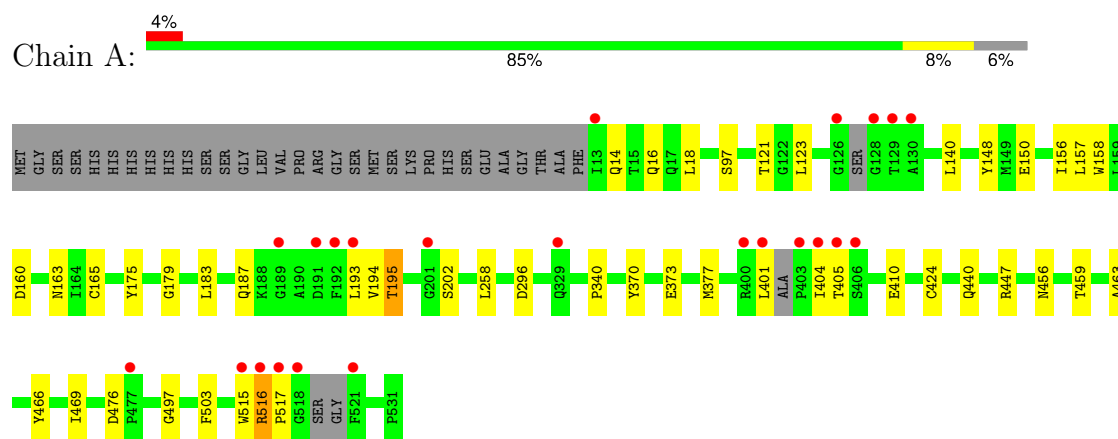
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	191	Total 191	O 191	0	0
6	B	183	Total 183	O 183	0	0
6	C	161	Total 161	O 161	0	0
6	D	129	Total 129	O 129	0	0

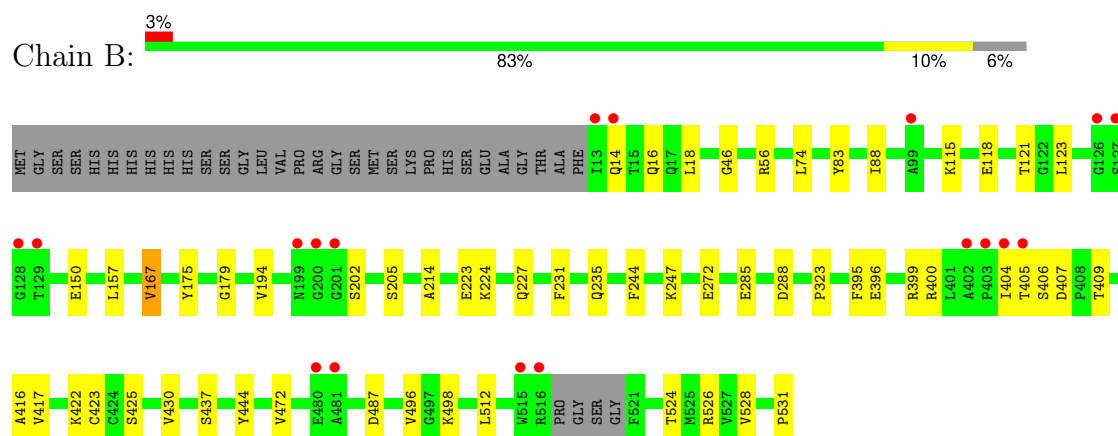
3 Residue-property plots [i](#)

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.

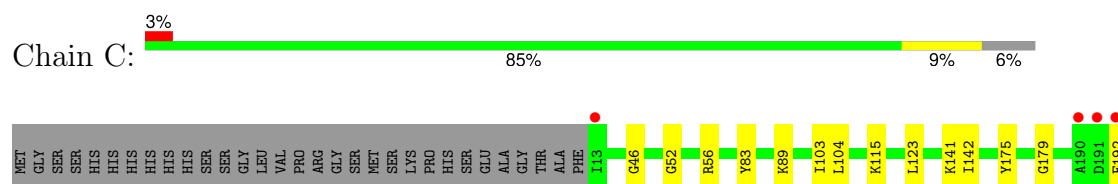
• Molecule 1: Pyruvate kinase PKM

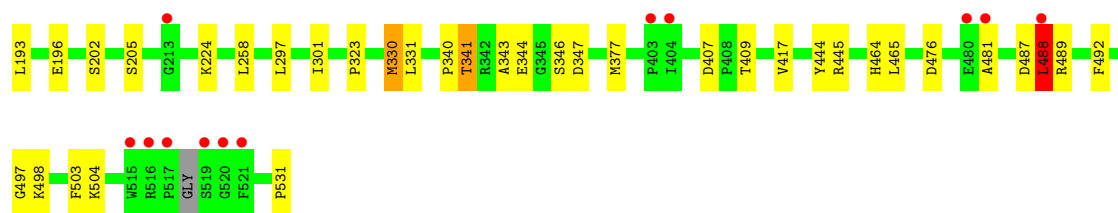


• Molecule 1: Pyruvate kinase PKM

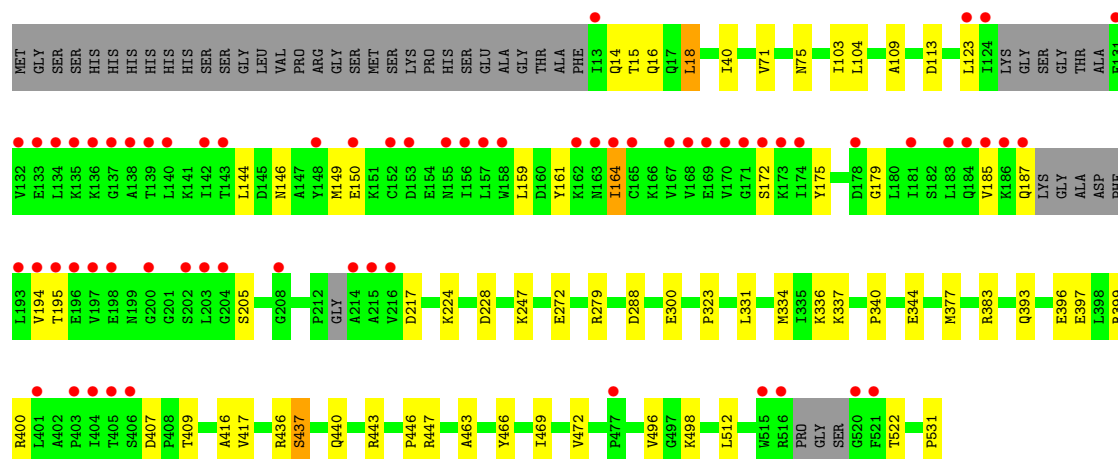
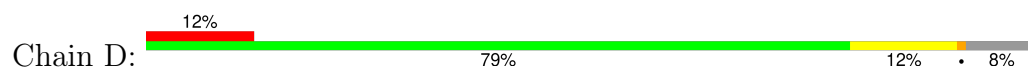


• Molecule 1: Pyruvate kinase PKM





● Molecule 1: Pyruvate kinase PKM



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	139.34Å 158.30Å 241.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	63.81 – 2.29 63.81 – 2.29	Depositor EDS
% Data completeness (in resolution range)	100.0 (63.81-2.29) 100.0 (63.81-2.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.18 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.183 , 0.229 0.184 , 0.227	Depositor DCC
R_{free} test set	5907 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	24.7	Xtriage
Anisotropy	0.674	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16070	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.75% 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: FBP, MG, OXL, GOL

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	0.41	0/3935	0.59	3/5320 (0.1%)
1	B	0.41	0/3921	0.57	0/5308
1	C	0.40	0/3944	0.58	3/5335 (0.1%)
1	D	0.37	0/3714	0.54	0/5034
All	All	0.40	0/15514	0.57	6/20997 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	488	LEU	CA-CB-CG	6.99	131.38	115.30
1	A	516	ARG	N-CA-C	-6.32	93.93	111.00
1	C	488	LEU	CB-CA-C	-6.12	98.57	110.20
1	A	515	TRP	O-C-N	-5.19	114.39	122.70
1	C	488	LEU	CB-CG-CD2	5.17	119.78	111.00
1	A	447	ARG	NE-CZ-NH2	-5.13	117.73	120.30

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	3878	0	3888	22	2

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3862	0	3867	31	2
1	C	3886	0	3898	28	0
1	D	3661	0	3503	42	0
2	A	6	0	0	0	0
2	B	6	0	0	0	0
2	C	6	0	0	0	0
2	D	6	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	12	0	16	1	0
4	B	18	0	24	6	0
4	C	18	0	24	3	0
4	D	18	0	24	0	0
5	A	8	0	2	0	0
5	B	5	0	0	1	0
5	C	5	0	0	0	0
5	D	7	0	2	1	0
6	A	191	0	0	2	0
6	B	183	0	0	2	0
6	C	161	0	0	0	0
6	D	129	0	0	2	0
All	All	16070	0	15248	124	2

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 4.

All (124) 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:488:LEU:O	1:C:488:LEU:HD22	1.53	1.06
1:C:488:LEU:O	1:C:488:LEU:CD2	2.21	0.89
1:C:341:THR:HG22	1:C:344:GLU:H	1.40	0.84
1:B:285:GLU:OE2	6:B:701:HOH:O	2.01	0.79
1:D:144:LEU:HD11	1:D:164:ILE:HD11	1.65	0.79
1:D:185:VAL:HA	1:D:195:THR:HG22	1.64	0.78
1:D:123:LEU:HB2	1:D:150:GLU:HA	1.69	0.74
1:A:183:LEU:HD13	1:A:195:THR:HG21	1.70	0.72
4:B:605:GOL:HO1	4:B:605:GOL:HO3	1.39	0.70
1:D:14:GLN:OE1	6:D:701:HOH:O	2.13	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:498:LYS:NZ	1:C:531:PRO:O	2.30	0.64
1:A:183:LEU:HB3	1:A:195:THR:HG23	1.80	0.63
1:D:123:LEU:HA	1:D:205:SER:HB2	1.79	0.63
1:D:399:ARG:NH2	6:D:704:HOH:O	2.34	0.59
1:B:167:VAL:HG13	1:B:214:ALA:HB1	1.85	0.59
1:B:123:LEU:HD23	1:B:205:SER:HB3	1.84	0.59
1:C:142:ILE:HB	1:C:193:LEU:HB3	1.86	0.58
1:D:498:LYS:NZ	1:D:531:PRO:O	2.31	0.58
1:A:516:ARG:O	1:A:517:PRO:C	2.41	0.57
1:D:103:ILE:HG22	1:D:104:LEU:HD22	1.85	0.57
1:C:487:ASP:O	1:C:488:LEU:HB3	2.05	0.56
1:D:247:LYS:HB3	1:D:279:ARG:HE	1.69	0.56
1:B:498:LYS:NZ	1:B:531:PRO:O	2.38	0.56
1:D:437:SER:OG	5:D:606:FBP:O5P	2.23	0.56
1:B:405:THR:OG1	1:B:406:SER:N	2.38	0.55
1:A:466:TYR:HB2	1:A:469:ILE:HD12	1.89	0.55
1:D:159:LEU:HD11	1:D:164:ILE:HD13	1.88	0.55
1:B:244:PHE:HZ	4:B:603:GOL:H31	1.71	0.54
1:C:497:GLY:HA3	1:C:503:PHE:CZ	2.42	0.54
1:D:161:TYR:O	1:D:164:ILE:HG12	2.06	0.54
1:C:46:GLY:HA2	4:C:603:GOL:H2	1.89	0.54
1:D:224:LYS:NZ	1:D:228:ASP:OD2	2.37	0.53
1:D:14:GLN:HG3	1:D:15:THR:H	1.72	0.53
1:A:121:THR:HB	1:A:157:LEU:HD11	1.91	0.52
1:D:417:VAL:HG13	1:D:446:PRO:HB3	1.91	0.52
1:D:14:GLN:HG2	1:D:18:LEU:HB2	1.92	0.52
1:D:175:TYR:HB3	1:D:179:GLY:HA2	1.92	0.51
1:B:472:VAL:HG11	1:B:496:VAL:HG11	1.91	0.51
1:C:341:THR:HG23	1:C:343:ALA:H	1.74	0.51
1:A:14:GLN:HB3	6:A:839:HOH:O	2.10	0.51
1:D:340:PRO:HG3	1:D:377:MET:HG2	1.92	0.51
1:C:330:MET:HB3	1:C:347:ASP:OD2	2.11	0.50
1:B:56:ARG:HD2	1:B:83:TYR:OH	2.10	0.50
1:B:396:GLU:O	1:B:400:ARG:HG3	2.11	0.50
1:D:472:VAL:HG11	1:D:496:VAL:HG11	1.93	0.50
1:B:118:GLU:HG2	4:B:603:GOL:H2	1.93	0.50
1:B:526:ARG:HB3	1:B:528:VAL:HG13	1.93	0.50
1:B:175:TYR:HB3	1:B:179:GLY:HA2	1.92	0.50
1:A:123:LEU:HD12	1:A:150:GLU:HG2	1.94	0.49
1:B:115:LYS:NZ	6:B:708:HOH:O	2.44	0.49
1:C:52:GLY:O	1:C:56:ARG:HG3	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:TYR:CE1	1:A:156:ILE:HD13	2.48	0.49
1:B:437:SER:OG	5:B:606:FBP:O4P	2.25	0.48
1:A:463:ALA:HB1	1:A:469:ILE:HG21	1.95	0.48
1:C:464:HIS:ND1	4:C:603:GOL:O2	2.37	0.48
1:C:46:GLY:CA	4:C:603:GOL:H2	2.43	0.48
1:D:407:ASP:OD2	1:D:436:ARG:NH2	2.46	0.48
1:D:40:ILE:O	1:D:383:ARG:HD2	2.13	0.48
1:A:296:ASP:OD1	4:A:603:GOL:H31	2.14	0.47
1:D:161:TYR:CD2	1:D:164:ILE:HG23	2.49	0.47
1:B:16:GLN:HG3	1:B:18:LEU:HG	1.96	0.47
1:A:183:LEU:HB3	1:A:195:THR:CG2	2.44	0.47
1:C:123:LEU:HD23	1:C:205:SER:HB3	1.96	0.47
1:A:187:GLN:HG3	1:A:194:VAL:HB	1.97	0.47
1:B:223:GLU:O	1:B:227:GLN:HG2	2.15	0.46
1:D:409:THR:HG23	1:D:522:THR:HB	1.97	0.46
1:D:16:GLN:OE1	1:D:447:ARG:HD2	2.15	0.46
1:B:231:PHE:CE2	1:B:235:GLN:HG3	2.51	0.46
1:D:334:MET:HA	1:D:337:LYS:O	2.15	0.46
1:A:16:GLN:HG3	1:A:18:LEU:HG	1.97	0.45
1:D:466:TYR:HB2	1:D:469:ILE:HD12	1.97	0.45
1:A:165:CYS:SG	6:A:867:HOH:O	2.55	0.45
1:C:56:ARG:HD2	1:C:83:TYR:OH	2.16	0.45
1:A:410:GLU:OE2	1:A:440:GLN:NE2	2.50	0.45
1:A:497:GLY:HA3	1:A:503:PHE:CZ	2.52	0.45
1:D:159:LEU:HD12	1:D:161:TYR:H	1.80	0.45
1:B:244:PHE:CZ	4:B:603:GOL:H31	2.51	0.45
1:D:463:ALA:HB1	1:D:469:ILE:HG21	1.99	0.45
1:D:161:TYR:OH	1:D:217:ASP:OD2	2.29	0.44
1:A:175:TYR:HB3	1:A:179:GLY:HA2	1.98	0.44
1:A:340:PRO:HG3	1:A:377:MET:HG2	1.98	0.44
1:B:121:THR:HB	1:B:157:LEU:HD11	1.99	0.44
1:A:140:LEU:O	1:A:195:THR:HB	2.18	0.44
1:D:336:LYS:HA	1:D:336:LYS:HD2	1.74	0.44
1:B:423:CYS:SG	1:B:425:SER:HB3	2.58	0.44
1:C:330:MET:O	1:C:331:LEU:HD23	2.17	0.44
1:B:405:THR:HB	1:B:407:ASP:H	1.83	0.43
1:C:407:ASP:OD1	1:C:409:THR:OG1	2.32	0.43
1:D:187:GLN:CB	1:D:194:VAL:H	2.31	0.43
1:B:115:LYS:HD3	1:B:224:LYS:HE3	2.00	0.43
1:C:417:VAL:HG21	1:C:444:TYR:HB2	2.01	0.43
1:D:146:ASN:O	1:D:149:MET:HG2	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:141:LYS:HE2	1:C:192:PHE:CB	2.48	0.43
1:B:288:ASP:O	1:B:323:PRO:HD2	2.19	0.43
1:A:370:TYR:HB3	1:A:373:GLU:HB2	2.01	0.43
1:B:46:GLY:HA2	4:B:604:GOL:H2	2.01	0.43
1:D:18:LEU:HD12	1:D:18:LEU:HA	1.89	0.43
1:D:272:GLU:O	1:D:300:GLU:HG3	2.19	0.43
1:A:456:ASN:HB3	1:A:459:THR:HB	2.01	0.42
1:B:46:GLY:CA	4:B:604:GOL:H2	2.48	0.42
1:B:123:LEU:HD12	1:B:150:GLU:HG2	2.00	0.42
1:B:404:ILE:HD13	1:B:404:ILE:HA	1.84	0.42
1:D:71:VAL:HG22	1:D:109:ALA:HB3	2.01	0.42
1:B:395:PHE:O	1:B:399:ARG:HG3	2.20	0.42
1:C:340:PRO:HG3	1:C:377:MET:HG2	2.01	0.42
1:C:445:ARG:HA	1:C:445:ARG:HD3	1.82	0.42
1:D:396:GLU:O	1:D:400:ARG:HG3	2.19	0.42
1:D:416:ALA:HB2	1:D:512:LEU:HD21	2.02	0.42
1:C:487:ASP:C	1:C:489:ARG:H	2.24	0.41
1:A:158:TRP:CH2	1:A:160:ASP:HB3	2.55	0.41
1:C:323:PRO:HB3	1:C:465:LEU:O	2.21	0.41
1:C:104:LEU:HD23	1:C:104:LEU:HA	1.89	0.41
1:D:331:LEU:HD23	1:D:344:GLU:HB3	2.02	0.41
1:B:416:ALA:HB2	1:B:512:LEU:HD11	2.03	0.41
1:D:75:ASN:HA	1:D:113:ASP:HB3	2.02	0.41
1:B:74:LEU:HD21	1:B:88:ILE:HG13	2.02	0.41
1:D:393:GLN:O	1:D:397:GLU:HG3	2.20	0.41
1:B:417:VAL:HG21	1:B:444:TYR:HB2	2.03	0.40
1:C:115:LYS:HD3	1:C:224:LYS:HD2	2.03	0.40
1:D:288:ASP:O	1:D:323:PRO:HD2	2.22	0.40
1:C:103:ILE:HD13	1:C:492:PHE:HE1	1.86	0.40
1:D:440:GLN:O	1:D:443:ARG:HG2	2.20	0.40
1:C:175:TYR:HB3	1:C:179:GLY:HA2	2.04	0.40
1:C:297:LEU:O	1:C:301:ILE:HG12	2.21	0.40

All (2) 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)
1:A:404:ILE:CB	1:B:422:LYS:O[3_654]	1.89	0.31
1:A:404:ILE:CA	1:B:422:LYS:O[3_654]	2.15	0.05

5.3 Torsion angles

5.3.1 Protein backbone

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	507/550 (92%)	493 (97%)	14 (3%)	0	100	100
1	B	511/550 (93%)	496 (97%)	15 (3%)	0	100	100
1	C	514/550 (94%)	501 (98%)	12 (2%)	1 (0%)	44	55
1	D	494/550 (90%)	480 (97%)	14 (3%)	0	100	100
All	All	2026/2200 (92%)	1970 (97%)	55 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	481	ALA

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	404/452 (89%)	394 (98%)	10 (2%)	42	60
1	B	402/452 (89%)	392 (98%)	10 (2%)	42	60
1	C	403/452 (89%)	393 (98%)	10 (2%)	42	60
1	D	352/452 (78%)	348 (99%)	4 (1%)	70	83
All	All	1561/1808 (86%)	1527 (98%)	34 (2%)	47	65

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	SER
1	A	163	ASN
1	A	193	LEU
1	A	195	THR
1	A	202	SER
1	A	258	LEU
1	A	401	LEU
1	A	405	THR
1	A	424	CYS
1	A	476	ASP
1	B	14	GLN
1	B	167	VAL
1	B	194	VAL
1	B	202	SER
1	B	247	LYS
1	B	272	GLU
1	B	409	THR
1	B	430	VAL
1	B	487	ASP
1	B	524	THR
1	C	89	LYS
1	C	196	GLU
1	C	202	SER
1	C	258	LEU
1	C	330	MET
1	C	341	THR
1	C	346	SER
1	C	476	ASP
1	C	488	LEU
1	C	504	LYS
1	D	18	LEU
1	D	164	ILE
1	D	172	SER
1	D	437	SER

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

Mol	Chain	Res	Type
1	B	199	ASN
1	D	14	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 23 ligands modelled in this entry, 4 are monoatomic - leaving 19 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	FBP	A	605	-	7,7,20	1.72	2 (28%)	9,9,32	0.89	1 (11%)
2	OXL	C	601	3	5,5,5	1.43	0	6,6,6	3.07	4 (66%)
4	GOL	B	604	-	5,5,5	0.39	0	5,5,5	1.28	0
4	GOL	D	605	-	5,5,5	0.96	0	5,5,5	1.04	0
5	FBP	B	606	-	4,4,20	2.07	1 (25%)	6,6,32	0.44	0
5	FBP	D	606	-	6,6,20	1.03	0	7,8,32	0.89	0
4	GOL	D	604	-	5,5,5	0.81	0	5,5,5	1.17	0
4	GOL	B	603	-	5,5,5	0.53	0	5,5,5	1.53	1 (20%)
4	GOL	A	604	-	5,5,5	1.21	1 (20%)	5,5,5	1.08	0
4	GOL	B	605	-	5,5,5	0.81	0	5,5,5	1.37	1 (20%)
4	GOL	D	603	-	5,5,5	1.00	0	5,5,5	1.11	0
4	GOL	C	604	-	5,5,5	1.30	0	5,5,5	0.80	0
2	OXL	A	601	3	5,5,5	1.36	0	6,6,6	2.69	4 (66%)
4	GOL	A	603	-	5,5,5	0.67	0	5,5,5	1.16	0
4	GOL	C	605	-	5,5,5	0.90	0	5,5,5	1.21	1 (20%)
2	OXL	D	601	3	5,5,5	1.30	0	6,6,6	2.64	4 (66%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	FBP	C	606	-	4,4,20	3.33	1 (25%)	6,6,32	0.63	0
2	OXL	B	601	3	5,5,5	1.44	0	6,6,6	2.68	4 (66%)
4	GOL	C	603	-	5,5,5	1.17	0	5,5,5	1.02	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
4	GOL	A	604	-	-	4/4/4/4	-
4	GOL	C	605	-	-	2/4/4/4	-
4	GOL	B	605	-	-	0/4/4/4	-
5	FBP	A	605	-	-	1/5/5/32	-
2	OXL	C	601	3	-	4/4/4/4	-
2	OXL	D	601	3	-	4/4/4/4	-
4	GOL	B	604	-	-	3/4/4/4	-
2	OXL	A	601	3	-	4/4/4/4	-
4	GOL	D	603	-	-	0/4/4/4	-
4	GOL	D	605	-	-	2/4/4/4	-
2	OXL	B	601	3	-	4/4/4/4	-
4	GOL	C	603	-	-	4/4/4/4	-
4	GOL	C	604	-	-	4/4/4/4	-
5	FBP	D	606	-	-	2/4/4/32	-
4	GOL	D	604	-	-	4/4/4/4	-
4	GOL	A	603	-	-	3/4/4/4	-
4	GOL	B	603	-	-	1/4/4/4	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	606	FBP	P2-O4P	6.47	1.65	1.50
5	B	606	FBP	P2-O6	3.91	1.66	1.54
5	A	605	FBP	O5-C5	3.89	1.61	1.42
4	A	604	GOL	C3-C2	2.39	1.60	1.51
5	A	605	FBP	P2-O6	2.14	1.67	1.60

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	OXL	O4-C2-C1	5.13	122.78	112.83
2	A	601	OXL	O4-C2-C1	4.38	121.32	112.83
2	D	601	OXL	O3-C1-C2	4.31	121.19	112.83
2	B	601	OXL	O4-C2-C1	4.25	121.08	112.83
2	C	601	OXL	O3-C1-C2	4.14	120.86	112.83
2	D	601	OXL	O4-C2-C1	3.81	120.22	112.83
2	B	601	OXL	O3-C1-C2	3.80	120.20	112.83
2	A	601	OXL	O3-C1-C2	3.23	119.10	112.83
4	B	603	GOL	C3-C2-C1	-2.81	101.50	111.80
2	C	601	OXL	O3-C1-O1	-2.64	117.61	123.90
2	A	601	OXL	O4-C2-O2	-2.59	117.73	123.90
2	A	601	OXL	O3-C1-O1	-2.43	118.10	123.90
4	B	605	GOL	C3-C2-C1	-2.39	103.04	111.80
2	B	601	OXL	O3-C1-O1	-2.37	118.25	123.90
5	A	605	FBP	O6P-P2-O6	2.35	112.80	106.67
2	C	601	OXL	O4-C2-O2	-2.22	118.60	123.90
2	B	601	OXL	O4-C2-O2	-2.19	118.68	123.90
2	D	601	OXL	O3-C1-O1	-2.15	118.79	123.90
4	C	605	GOL	C3-C2-C1	-2.09	104.15	111.80
2	D	601	OXL	O4-C2-O2	-2.01	119.12	123.90

There are no chirality outliers.

All (46) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	601	OXL	O1-C1-C2-O2
2	D	601	OXL	O1-C1-C2-O4
2	D	601	OXL	O3-C1-C2-O4
4	A	603	GOL	C1-C2-C3-O3
4	B	604	GOL	O1-C1-C2-C3
4	C	603	GOL	O1-C1-C2-O2
4	C	603	GOL	O1-C1-C2-C3
4	C	604	GOL	O1-C1-C2-C3
4	C	604	GOL	C1-C2-C3-O3
4	C	605	GOL	C1-C2-C3-O3
4	C	605	GOL	O2-C2-C3-O3
4	D	604	GOL	O1-C1-C2-C3
4	D	605	GOL	C1-C2-C3-O3
5	D	606	FBP	C6-O6-P2-O5P
5	D	606	FBP	C6-O6-P2-O6P
2	D	601	OXL	O3-C1-C2-O2
2	A	601	OXL	O1-C1-C2-O2
4	C	604	GOL	O2-C2-C3-O3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
4	D	605	GOL	O2-C2-C3-O3
4	A	604	GOL	O1-C1-C2-C3
4	A	604	GOL	C1-C2-C3-O3
4	B	603	GOL	C1-C2-C3-O3
4	C	603	GOL	C1-C2-C3-O3
4	D	604	GOL	C1-C2-C3-O3
4	A	604	GOL	O1-C1-C2-O2
4	B	604	GOL	O1-C1-C2-O2
4	D	604	GOL	O1-C1-C2-O2
4	D	604	GOL	O2-C2-C3-O3
2	A	601	OXL	O3-C1-C2-O4
2	A	601	OXL	O1-C1-C2-O4
2	A	601	OXL	O3-C1-C2-O2
4	A	604	GOL	O2-C2-C3-O3
4	C	604	GOL	O1-C1-C2-O2
2	B	601	OXL	O1-C1-C2-O2
2	B	601	OXL	O3-C1-C2-O4
4	A	603	GOL	O2-C2-C3-O3
4	C	603	GOL	O2-C2-C3-O3
5	A	605	FBP	O5-C5-C6-O6
2	C	601	OXL	O3-C1-C2-O4
2	B	601	OXL	O1-C1-C2-O4
2	C	601	OXL	O1-C1-C2-O2
2	B	601	OXL	O3-C1-C2-O2
4	A	603	GOL	O1-C1-C2-O2
4	B	604	GOL	C1-C2-C3-O3
2	C	601	OXL	O1-C1-C2-O4
2	C	601	OXL	O3-C1-C2-O2

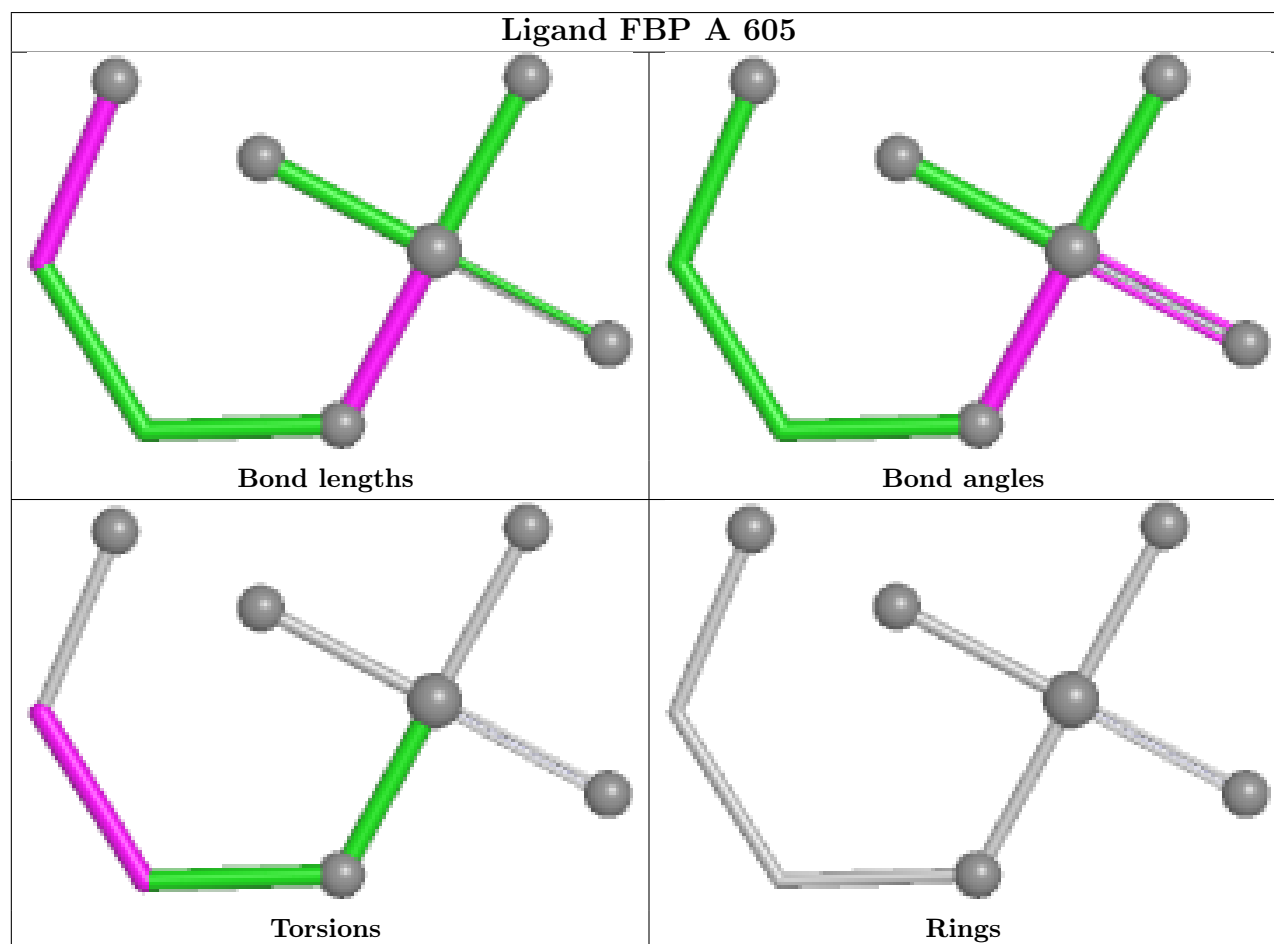
There are no ring outliers.

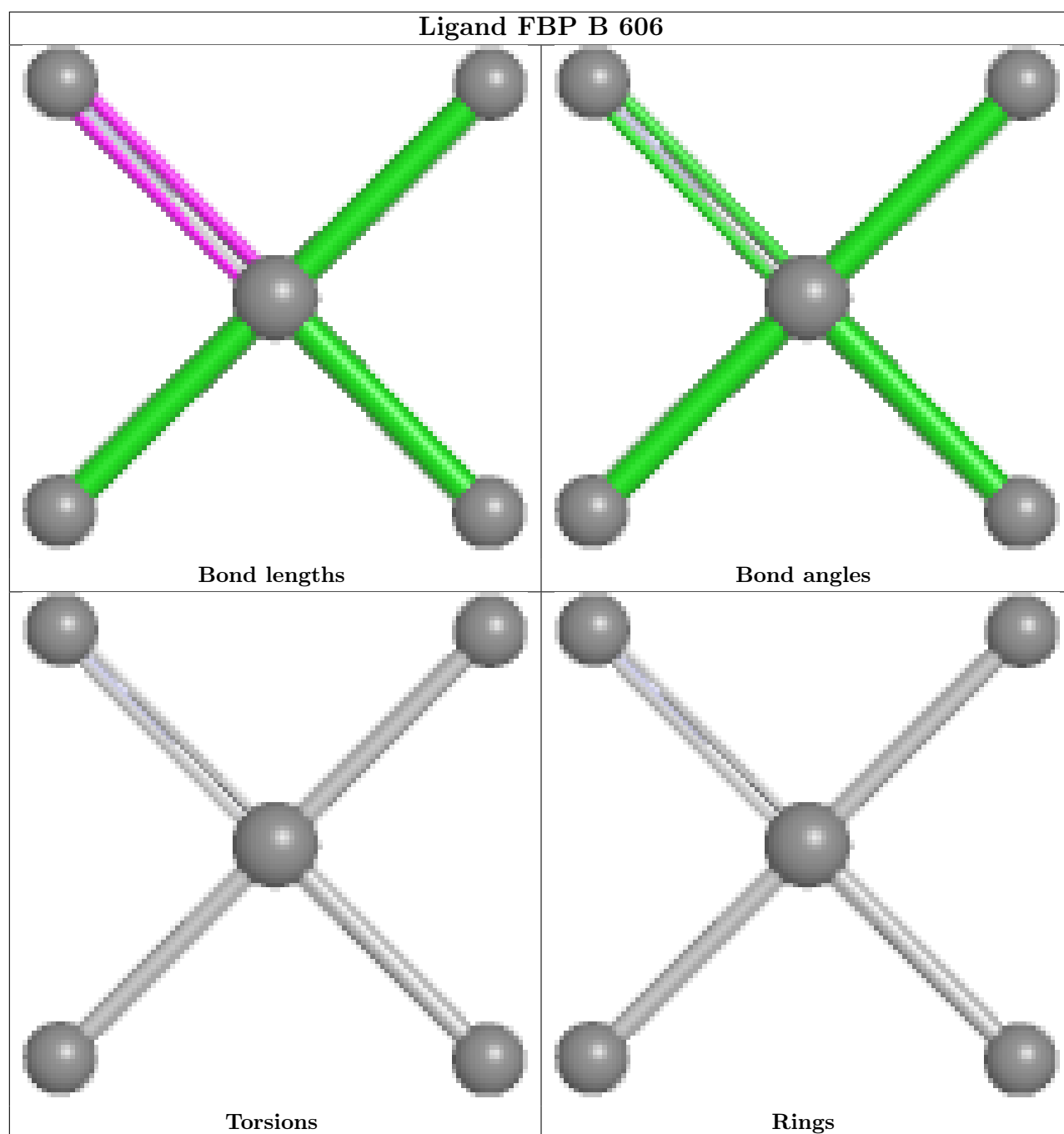
7 monomers are involved in 12 short contacts:

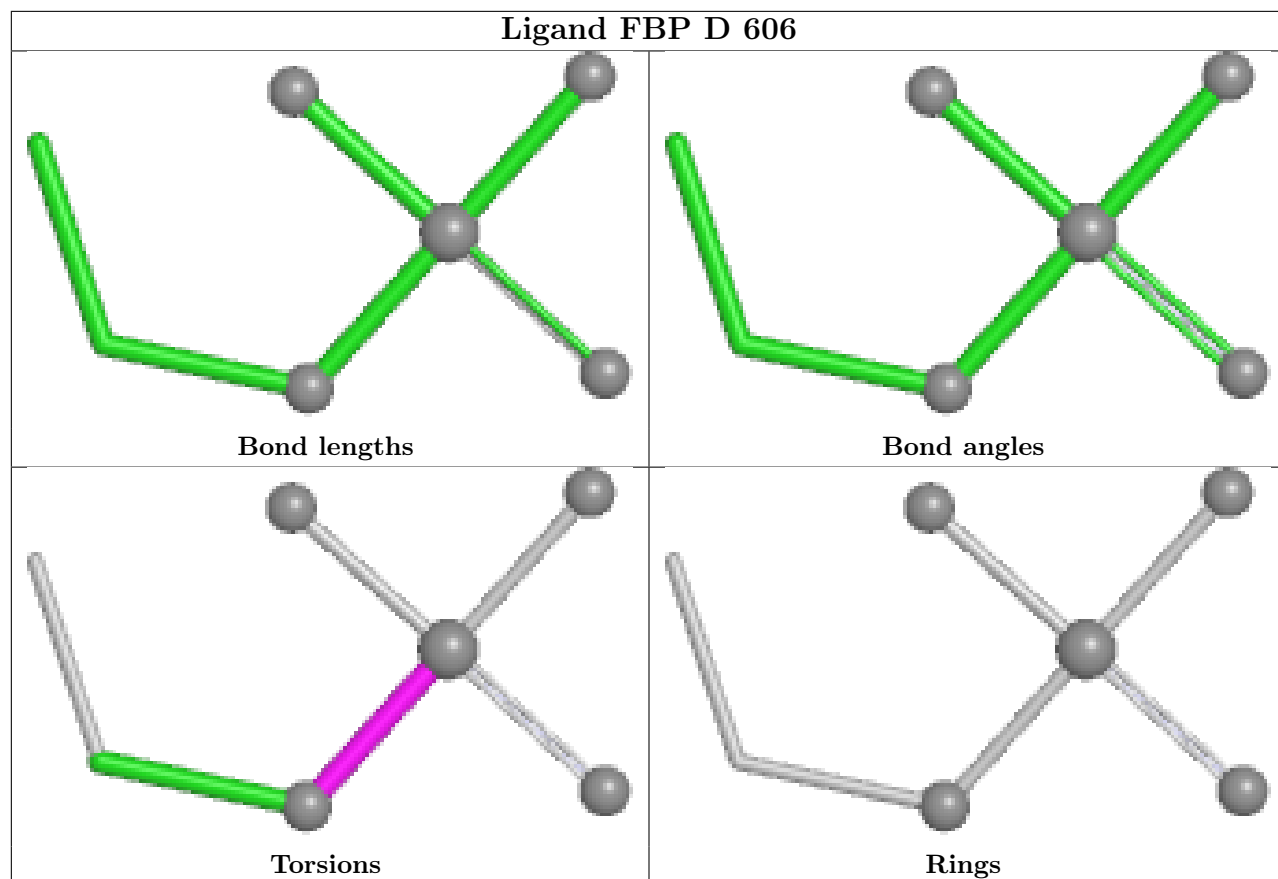
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	604	GOL	2	0
5	B	606	FBP	1	0
5	D	606	FBP	1	0
4	B	603	GOL	3	0
4	B	605	GOL	1	0
4	A	603	GOL	1	0
4	C	603	GOL	3	0

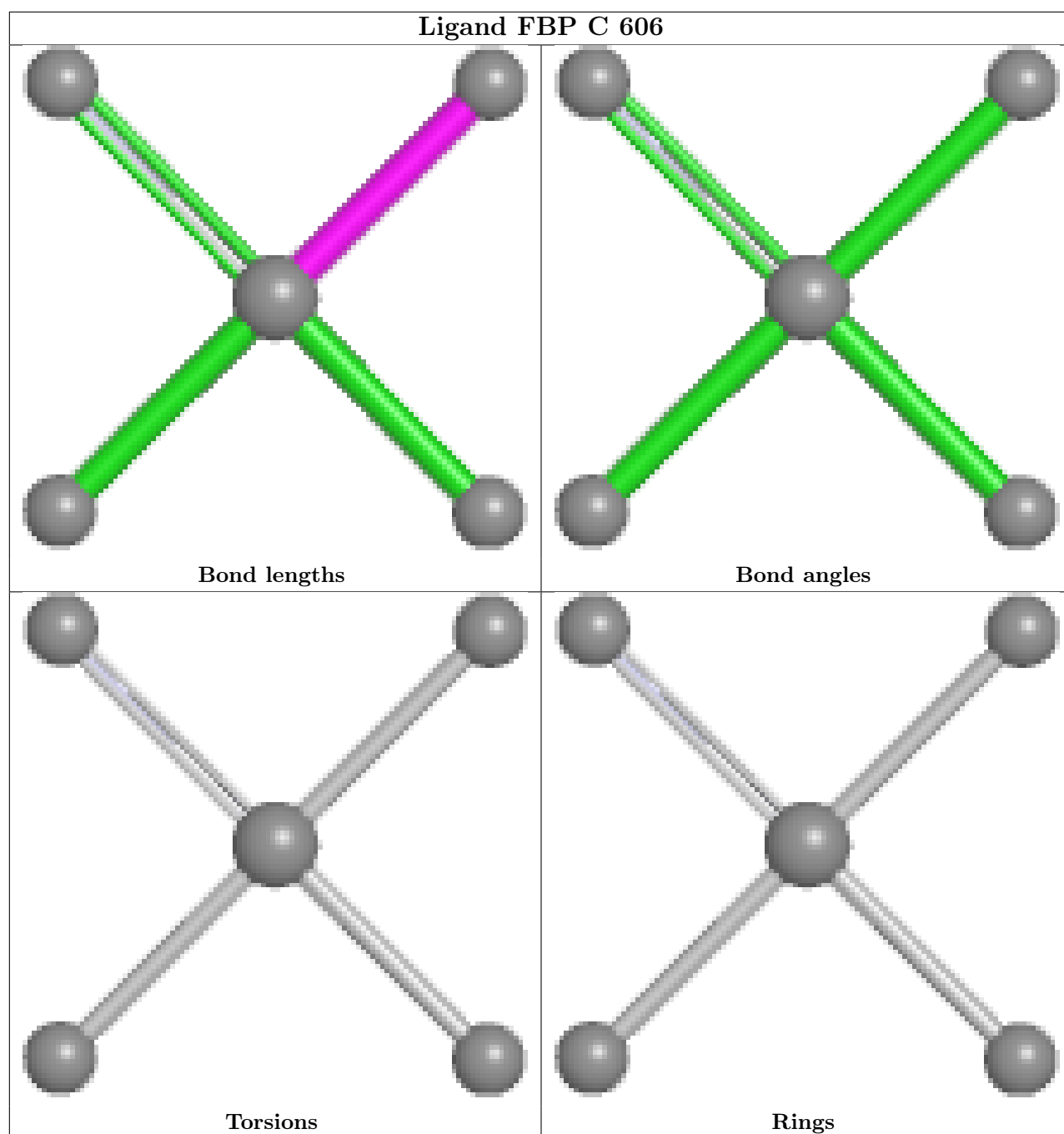
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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	515/550 (93%)	-0.25	23 (4%) 39 40	13, 25, 45, 76	0
1	B	515/550 (93%)	-0.21	18 (3%) 47 49	12, 27, 48, 67	0
1	C	518/550 (94%)	-0.22	16 (3%) 51 53	14, 27, 50, 66	0
1	D	504/550 (91%)	0.29	66 (13%) 8 9	14, 32, 70, 89	0
All	All	2052/2200 (93%)	-0.10	123 (5%) 29 31	12, 27, 58, 89	0

All (123) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	403	PRO	8.6
1	A	404	ILE	6.9
1	A	518	GLY	6.8
1	A	192	PHE	6.0
1	D	170	VAL	5.8
1	D	515	TRP	5.8
1	B	13	ILE	5.8
1	C	404	ILE	5.8
1	A	517	PRO	5.7
1	A	405	THR	5.6
1	C	519	SER	5.6
1	D	137	GLY	5.4
1	D	165	CYS	5.4
1	D	124	ILE	5.0
1	A	516	ARG	4.9
1	D	153	ASP	4.9
1	C	403	PRO	4.8
1	D	13	ILE	4.8
1	D	138	ALA	4.7
1	A	13	ILE	4.6
1	D	171	GLY	4.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	404	ILE	4.3
1	A	129	THR	4.3
1	D	520	GLY	4.2
1	D	157	LEU	4.2
1	D	194	VAL	4.1
1	D	403	PRO	4.1
1	A	193	LEU	4.1
1	A	329	GLN	4.1
1	D	123	LEU	4.1
1	D	193	LEU	4.1
1	D	152	CYS	4.0
1	D	156	ILE	4.0
1	B	14	GLN	3.9
1	C	520	GLY	3.9
1	D	215	ALA	3.9
1	D	195	THR	3.8
1	D	169	GLU	3.8
1	A	401	LEU	3.8
1	B	403	PRO	3.8
1	D	183	LEU	3.7
1	A	191	ASP	3.7
1	B	201	GLY	3.6
1	D	162	LYS	3.6
1	C	517	PRO	3.6
1	A	521	PHE	3.6
1	D	134	LEU	3.6
1	D	143	THR	3.5
1	D	516	ARG	3.5
1	B	200	GLY	3.5
1	C	191	ASP	3.5
1	D	148	TYR	3.5
1	C	13	ILE	3.4
1	D	406	SER	3.4
1	D	139	THR	3.4
1	D	136	LYS	3.3
1	D	187	GLN	3.3
1	D	132	VAL	3.3
1	D	186	LYS	3.2
1	D	405	THR	3.2
1	C	515	TRP	3.2
1	B	126	GLY	3.2
1	D	184	GLN	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	128	GLY	3.0
1	D	155	ASN	3.0
1	D	174	ILE	3.0
1	B	127	SER	3.0
1	D	150	GLU	2.9
1	D	163	ASN	2.9
1	B	516	ARG	2.9
1	D	198	GLU	2.9
1	D	202	SER	2.8
1	C	516	ARG	2.8
1	C	488	LEU	2.8
1	D	477	PRO	2.7
1	D	168	VAL	2.7
1	B	515	TRP	2.7
1	A	406	SER	2.7
1	B	404	ILE	2.7
1	B	99	ALA	2.7
1	D	173	LYS	2.6
1	C	521	PHE	2.6
1	A	515	TRP	2.6
1	C	481	ALA	2.6
1	B	129	THR	2.6
1	D	140	LEU	2.6
1	A	130	ALA	2.5
1	D	200	GLY	2.5
1	D	181	ILE	2.5
1	D	197	VAL	2.5
1	D	164	ILE	2.4
1	B	481	ALA	2.4
1	C	480	GLU	2.4
1	D	196	GLU	2.4
1	D	178	ASP	2.4
1	B	402	ALA	2.4
1	C	192	PHE	2.4
1	D	167	VAL	2.4
1	A	126	GLY	2.4
1	D	521	PHE	2.4
1	D	172	SER	2.4
1	A	201	GLY	2.4
1	D	158	TRP	2.3
1	A	400	ARG	2.3
1	D	142	ILE	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	190	ALA	2.3
1	D	131	GLU	2.2
1	D	203	LEU	2.2
1	B	128	GLY	2.2
1	D	214	ALA	2.2
1	B	405	THR	2.2
1	D	216	VAL	2.2
1	D	204	GLY	2.1
1	D	133	GLU	2.1
1	D	135	LYS	2.1
1	C	213	GLY	2.1
1	D	185	VAL	2.0
1	A	189	GLY	2.0
1	D	208	GLY	2.0
1	D	401	LEU	2.0
1	B	480	GLU	2.0
1	A	477	PRO	2.0
1	B	199	ASN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	D	603	6/6	0.76	0.18	27,31,35,36	0
4	GOL	C	604	6/6	0.84	0.14	38,39,43,44	0
5	FBP	A	605	8/20	0.84	0.16	27,33,39,43	8
5	FBP	D	606	7/20	0.85	0.17	33,44,48,51	7
4	GOL	B	604	6/6	0.86	0.18	26,27,30,30	0

Continued on next page...

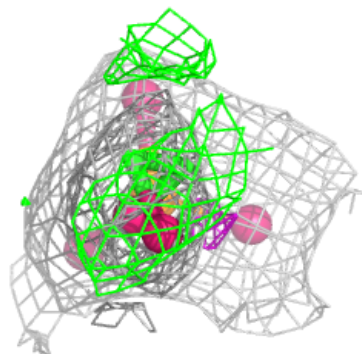
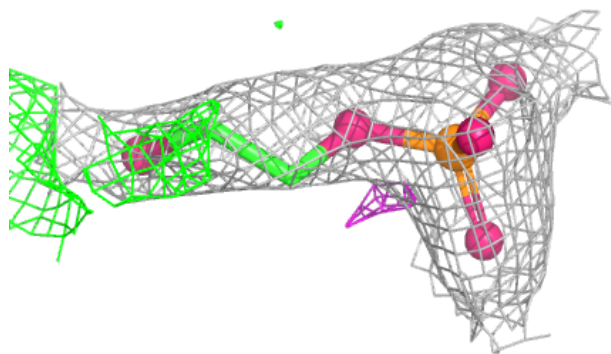
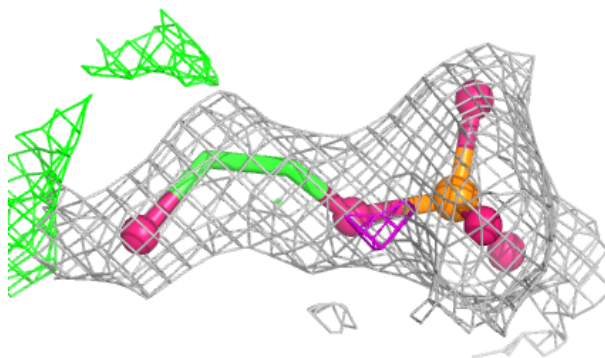
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	GOL	C	603	6/6	0.87	0.18	27,31,34,34	0
4	GOL	A	603	6/6	0.88	0.14	24,28,34,41	0
4	GOL	B	603	6/6	0.88	0.14	24,29,31,38	0
4	GOL	D	604	6/6	0.89	0.12	33,38,40,50	0
4	GOL	B	605	6/6	0.90	0.18	35,39,42,42	0
4	GOL	D	605	6/6	0.91	0.15	40,40,44,46	0
5	FBP	C	606	5/20	0.92	0.09	32,32,43,44	5
4	GOL	A	604	6/6	0.92	0.15	29,31,34,35	0
3	MG	D	602	1/1	0.93	0.08	35,35,35,35	0
2	OXL	B	601	6/6	0.94	0.08	21,22,30,31	0
2	OXL	D	601	6/6	0.94	0.08	25,31,35,42	0
4	GOL	C	605	6/6	0.94	0.08	23,34,36,40	0
5	FBP	B	606	5/20	0.95	0.07	24,29,37,41	5
2	OXL	C	601	6/6	0.96	0.09	21,23,29,36	0
2	OXL	A	601	6/6	0.96	0.07	22,24,32,33	0
3	MG	C	602	1/1	0.98	0.03	19,19,19,19	0
3	MG	B	602	1/1	0.99	0.02	24,24,24,24	0
3	MG	A	602	1/1	0.99	0.03	23,23,23,23	0

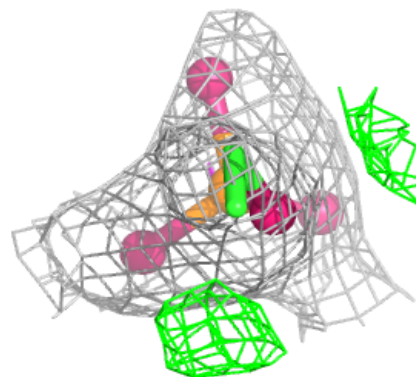
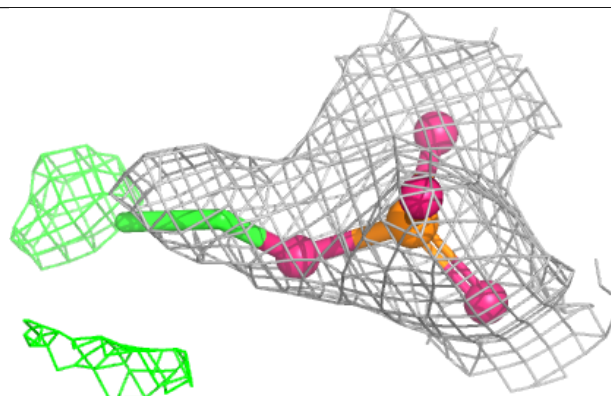
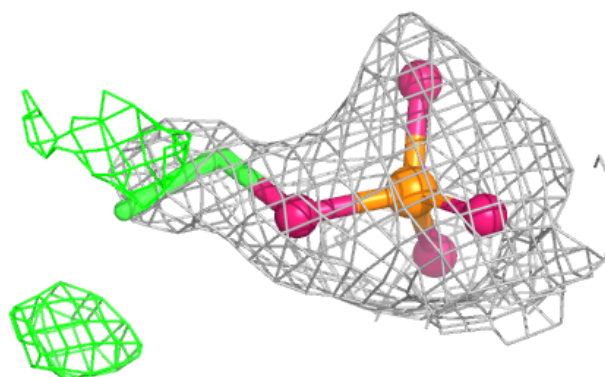
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FBP A 605:

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

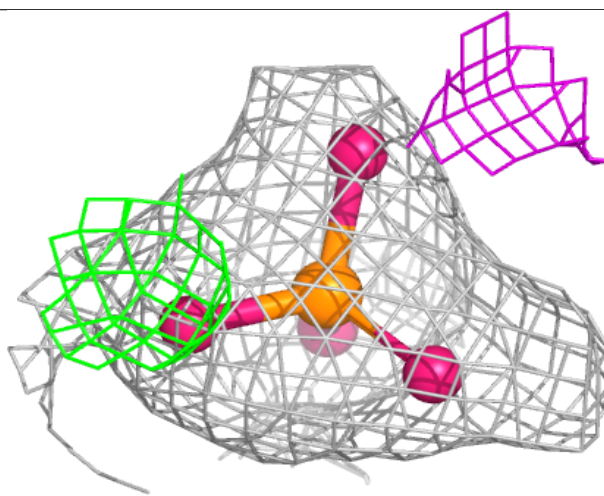
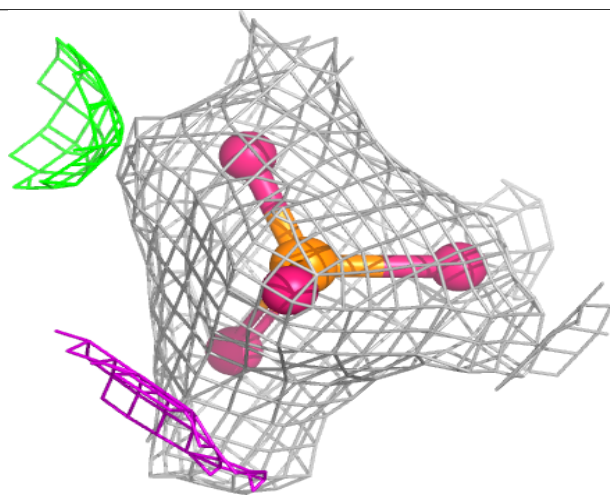
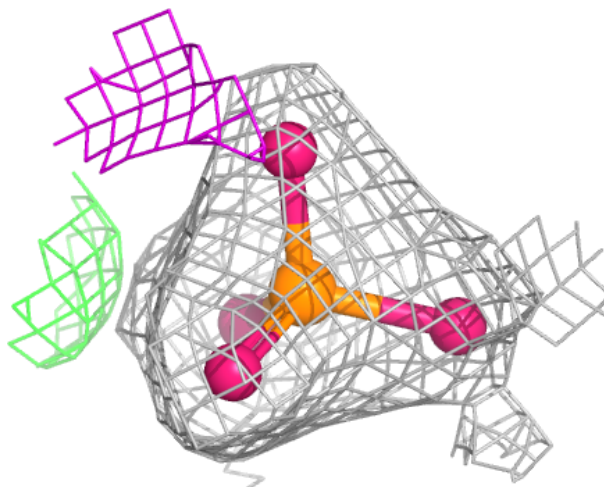
**Electron density around FBP D 606:**

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



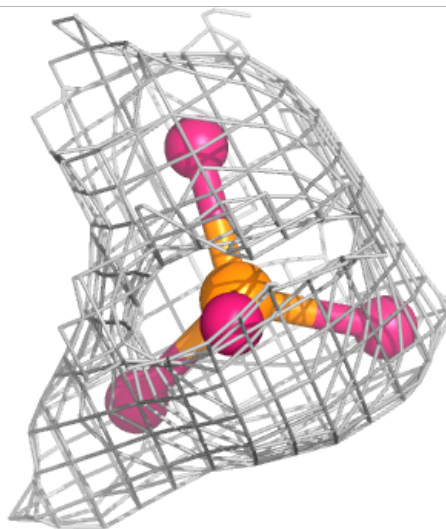
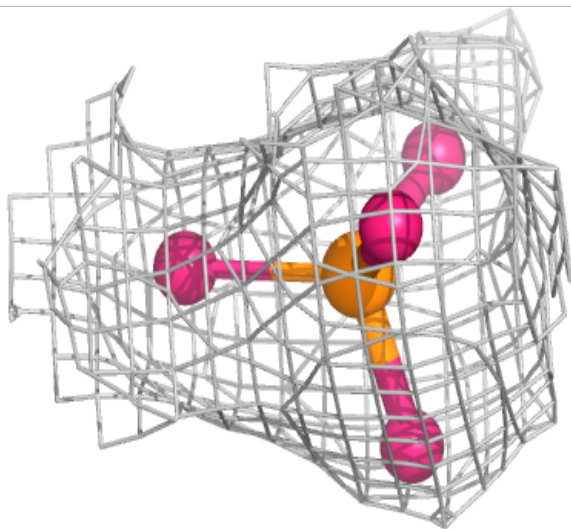
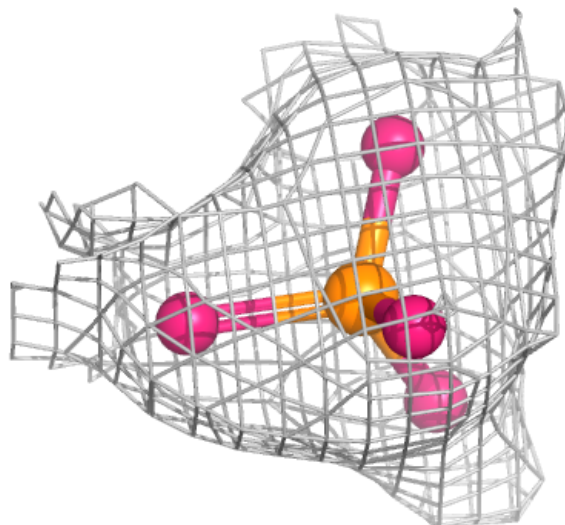
Electron density around FBP C 606:

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



Electron density around FBP B 606:

$2mF_o-DF_c$ (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.