



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:55 AM UTC

PDB ID : 8HMQ / pdb_00008hmq
Title : Crystal Structure of PKM2 mutant P403A
Authors : Upadhyay, S.; Kumar, A.; Patel, A.K.
Deposited on : 2022-12-05
Resolution : 2.50 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

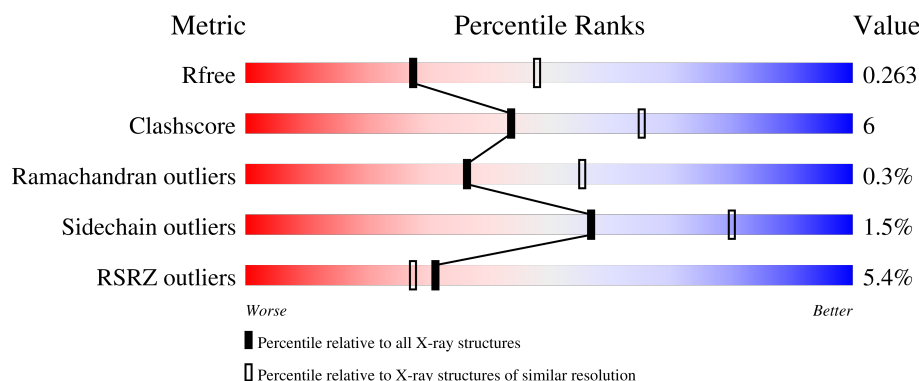
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	551	2% 76% 10% • 13%
1	B	551	4% 76% 16% 8%
1	C	551	6% 72% 15% 12%
1	D	551	7% 75% 14% 11%

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 7 unique types of molecules in this entry. The entry contains 14873 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	481	Total	C	N	O	S	0	0	0
			3593	2259	635	676	23			
1	B	509	Total	C	N	O	S	0	0	0
			3800	2387	669	719	25			
1	C	483	Total	C	N	O	S	0	0	0
			3606	2273	632	677	24			
1	D	489	Total	C	N	O	S	0	0	0
			3636	2284	639	689	24			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP P14618
A	-18	GLY	-	expression tag	UNP P14618
A	-17	SER	-	expression tag	UNP P14618
A	-16	SER	-	expression tag	UNP P14618
A	-15	HIS	-	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	SER	-	expression tag	UNP P14618
A	-8	SER	-	expression tag	UNP P14618
A	-7	GLY	-	expression tag	UNP P14618
A	-6	LEU	-	expression tag	UNP P14618
A	-5	VAL	-	expression tag	UNP P14618
A	-4	PRO	-	expression tag	UNP P14618
A	-3	ARG	-	expression tag	UNP P14618
A	-2	GLY	-	expression tag	UNP P14618
A	-1	SER	-	expression tag	UNP P14618
A	0	HIS	-	expression tag	UNP P14618
A	403	ALA	PRO	engineered mutation	UNP P14618

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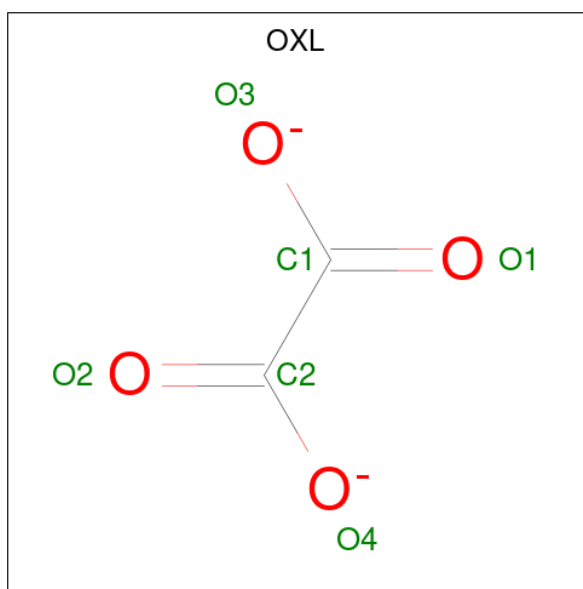
Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	initiating methionine	UNP P14618
B	-18	GLY	-	expression tag	UNP P14618
B	-17	SER	-	expression tag	UNP P14618
B	-16	SER	-	expression tag	UNP P14618
B	-15	HIS	-	expression tag	UNP P14618
B	-14	HIS	-	expression tag	UNP P14618
B	-13	HIS	-	expression 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	SER	-	expression tag	UNP P14618
B	-8	SER	-	expression tag	UNP P14618
B	-7	GLY	-	expression tag	UNP P14618
B	-6	LEU	-	expression tag	UNP P14618
B	-5	VAL	-	expression tag	UNP P14618
B	-4	PRO	-	expression tag	UNP P14618
B	-3	ARG	-	expression tag	UNP P14618
B	-2	GLY	-	expression tag	UNP P14618
B	-1	SER	-	expression tag	UNP P14618
B	0	HIS	-	expression tag	UNP P14618
B	403	ALA	PRO	engineered mutation	UNP P14618
C	-19	MET	-	initiating methionine	UNP P14618
C	-18	GLY	-	expression tag	UNP P14618
C	-17	SER	-	expression tag	UNP P14618
C	-16	SER	-	expression tag	UNP P14618
C	-15	HIS	-	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	SER	-	expression tag	UNP P14618
C	-8	SER	-	expression tag	UNP P14618
C	-7	GLY	-	expression tag	UNP P14618
C	-6	LEU	-	expression tag	UNP P14618
C	-5	VAL	-	expression tag	UNP P14618
C	-4	PRO	-	expression tag	UNP P14618
C	-3	ARG	-	expression tag	UNP P14618
C	-2	GLY	-	expression tag	UNP P14618
C	-1	SER	-	expression tag	UNP P14618
C	0	HIS	-	expression tag	UNP P14618
C	403	ALA	PRO	engineered mutation	UNP P14618

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-19	MET	-	initiating methionine	UNP P14618
D	-18	GLY	-	expression tag	UNP P14618
D	-17	SER	-	expression tag	UNP P14618
D	-16	SER	-	expression tag	UNP P14618
D	-15	HIS	-	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	SER	-	expression tag	UNP P14618
D	-8	SER	-	expression tag	UNP P14618
D	-7	GLY	-	expression tag	UNP P14618
D	-6	LEU	-	expression tag	UNP P14618
D	-5	VAL	-	expression tag	UNP P14618
D	-4	PRO	-	expression tag	UNP P14618
D	-3	ARG	-	expression tag	UNP P14618
D	-2	GLY	-	expression tag	UNP P14618
D	-1	SER	-	expression tag	UNP P14618
D	0	HIS	-	expression tag	UNP P14618
D	403	ALA	PRO	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		

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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).

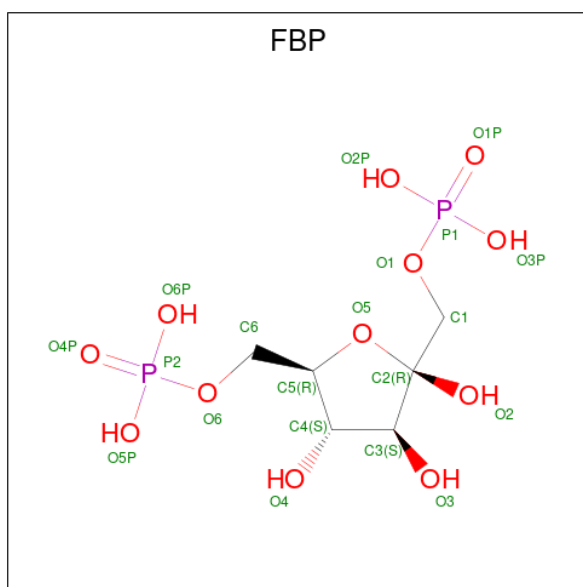


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	Mg	0	0
			3	3		
5	B	3	Total	Mg	0	0
			3	3		
5	C	1	Total	Mg	0	0
			1	1		
5	D	2	Total	Mg	0	0
			2	2		

- Molecule 6 is 1,6-di-O-phosphono-beta-D-fructofuranose (CCD ID: FBP) (formula: C₆H₁₄O₁₂P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	O	P	0	0
			20	6	12	2		
6	C	1	Total	C	O	P	0	0
			6	1	4	1		
6	D	1	Total	C	O	P	0	0
			6	1	4	1		

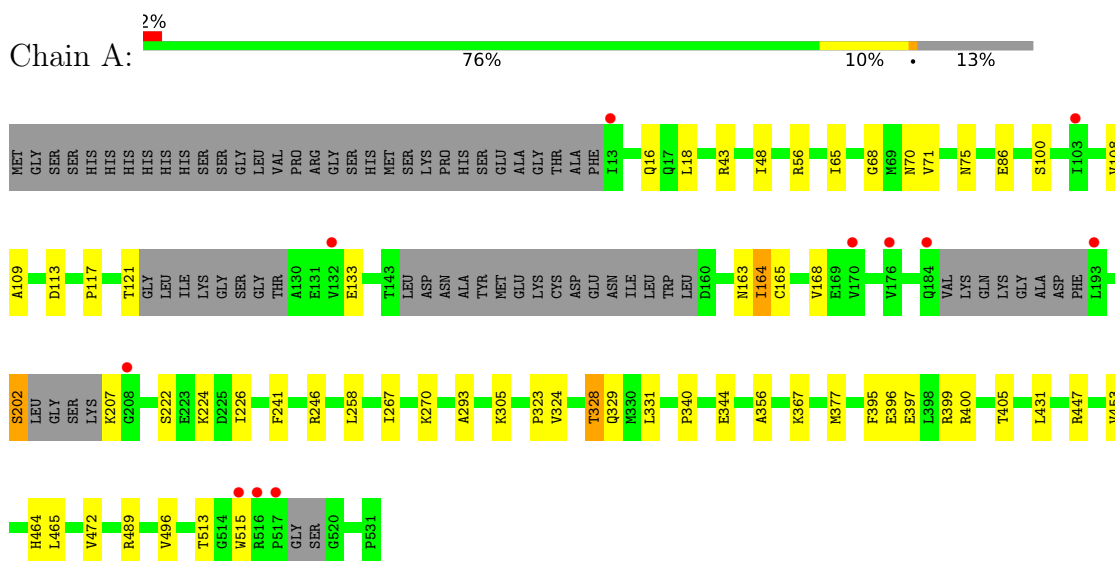
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	49	Total	O	0	0
			49	49		
7	B	32	Total	O	0	0
			32	32		
7	C	15	Total	O	0	1
			16	16		
7	D	14	Total	O	0	0
			14	14		

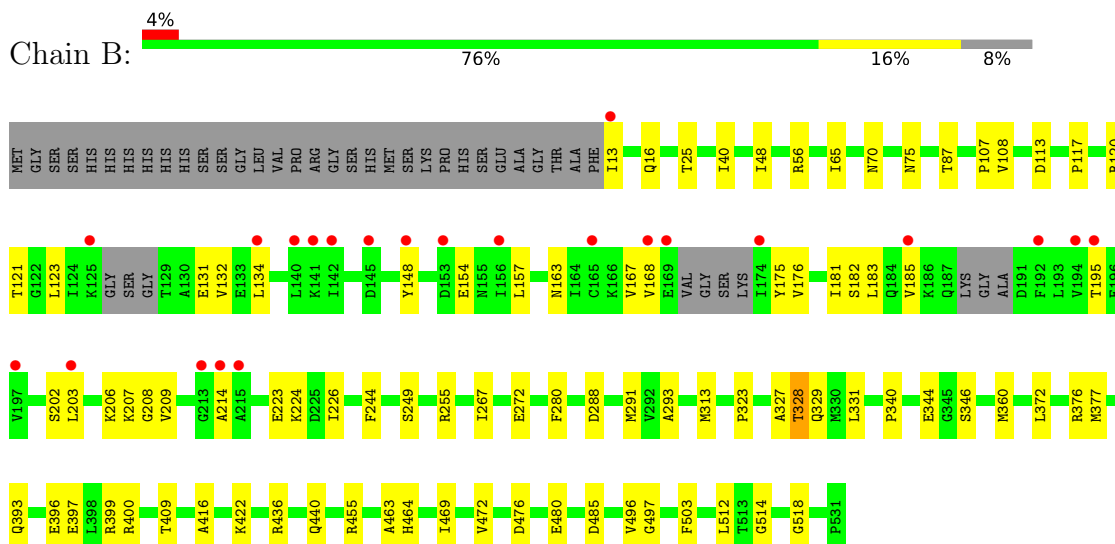
3 Residue-property plots [i](#)

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.

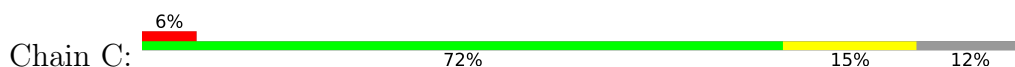
• Molecule 1: Pyruvate kinase PKM

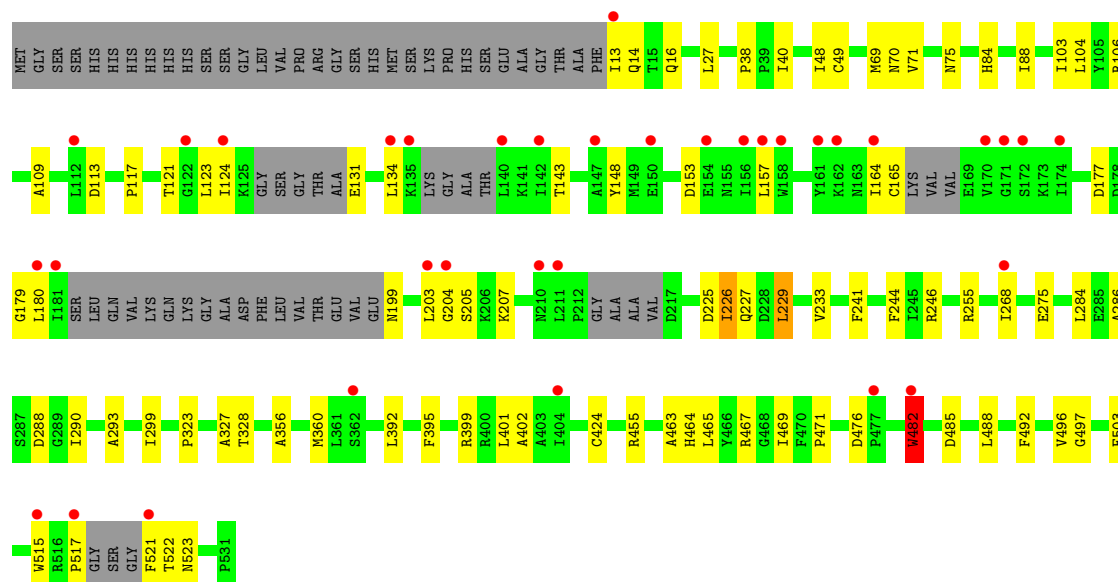


• Molecule 1: Pyruvate kinase PKM

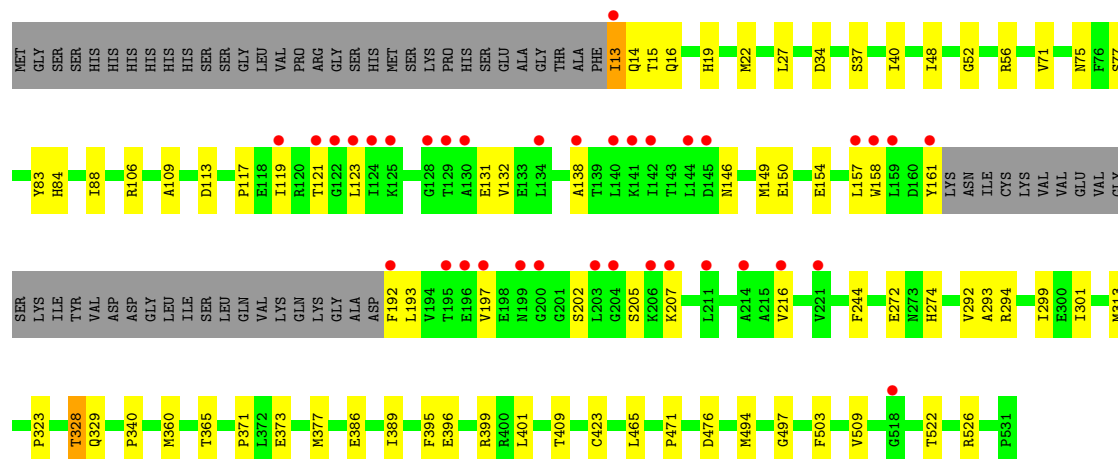
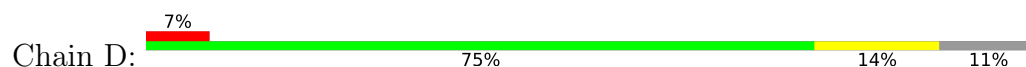


• Molecule 1: Pyruvate kinase PKM





● Molecule 1: Pyruvate kinase PKM



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.83Å 136.84Å 149.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.73 – 2.50 46.73 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.73-2.50) 99.9 (46.73-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.213 , 0.263 0.213 , 0.263	Depositor DCC
R_{free} test set	3560 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	48.3	Xtriage
Anisotropy	0.372	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14873	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% 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: OXL, FBP, GOL, EDO, MG

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	0/3647	0.36	0/4938
1	B	0.16	0/3859	0.35	0/5229
1	C	0.17	0/3662	0.43	4/4963 (0.1%)
1	D	0.18	0/3695	0.37	0/5011
All	All	0.17	0/14863	0.38	4/20141 (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	D	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	226	ILE	CA-C-N	9.23	132.44	120.44
1	C	226	ILE	C-N-CA	9.23	132.44	120.44
1	C	227	GLN	CA-CB-CG	6.30	126.70	114.10
1	C	482	TRP	CB-CG-CD2	-5.65	118.89	126.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	396	GLU	Sidechain

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	3593	0	3555	34	0
1	B	3800	0	3744	53	0
1	C	3606	0	3536	52	0
1	D	3636	0	3593	50	0
2	A	6	0	0	1	0
2	B	6	0	0	0	0
2	C	6	0	0	1	0
2	D	6	0	0	0	0
3	A	12	0	16	1	0
3	B	12	0	16	2	0
3	C	6	0	8	0	0
3	D	12	0	16	0	0
4	A	12	0	18	2	0
4	C	4	0	6	1	0
4	D	4	0	6	0	0
5	A	3	0	0	0	0
5	B	3	0	0	0	0
5	C	1	0	0	0	0
5	D	2	0	0	0	0
6	B	20	0	9	2	0
6	C	6	0	0	0	0
6	D	6	0	0	0	0
7	A	49	0	0	1	0
7	B	32	0	0	0	0
7	C	16	0	0	0	0
7	D	14	0	0	0	0
All	All	14873	0	14523	179	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 6.

All (179) 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:D:15:THR:HG22	1:D:16:GLN:HG3	1.50	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:GLU:OE1	1:B:202:SER:HB3	1.70	0.91
1:A:328:THR:HG22	1:A:329:GLN:HG3	1.65	0.77
1:B:455:ARG:NH1	1:B:476:ASP:O	2.22	0.72
1:B:185:VAL:HA	1:B:195:THR:HG22	1.74	0.70
1:B:16:GLN:HG2	1:B:40:ILE:HG23	1.72	0.70
1:B:167:VAL:HG12	1:B:214:ALA:HB1	1.74	0.69
1:C:179:GLY:HA3	1:C:299:ILE:HD11	1.75	0.68
1:B:48:ILE:HB	1:B:360:MET:HG3	1.77	0.66
1:D:409:THR:HG23	1:D:522:THR:HB	1.78	0.64
1:D:121:THR:HB	1:D:157:LEU:HD11	1.82	0.61
1:B:117:PRO:HD2	1:B:244:PHE:HB2	1.83	0.61
1:C:476:ASP:HB2	1:C:488:LEU:HD11	1.81	0.60
1:C:180:LEU:O	1:C:199:ASN:ND2	2.28	0.60
1:B:123:LEU:HD21	1:B:206:LYS:HE2	1.83	0.60
1:A:121:THR:HG1	1:A:207:LYS:N	2.00	0.60
1:B:372:LEU:O	1:B:376:ARG:HG3	2.02	0.59
1:D:395:PHE:O	1:D:399:ARG:HG3	2.03	0.59
1:C:492:PHE:O	1:C:496:VAL:HG23	2.03	0.59
1:D:132:VAL:HB	1:D:154:GLU:HG3	1.85	0.59
1:D:328:THR:HG22	1:D:329:GLN:HG3	1.83	0.59
1:C:401:LEU:HD12	1:D:27:LEU:HD23	1.84	0.58
1:B:157:LEU:HD13	1:B:203:LEU:HD21	1.84	0.58
1:D:13:ILE:O	1:D:15:THR:N	2.37	0.58
1:C:48:ILE:HB	1:C:360:MET:HG3	1.86	0.57
1:C:106:ARG:NH2	1:C:471:PRO:O	2.36	0.57
1:B:409:THR:HB	1:B:440:GLN:HE22	1.70	0.57
4:C:604:EDO:H22	1:D:329:GLN:HE22	1.69	0.56
1:B:400:ARG:HD2	1:C:392:LEU:HD21	1.86	0.56
1:C:14:GLN:O	1:C:38:PRO:HD2	2.06	0.56
1:A:515:TRP:CD2	1:D:526:ARG:HD3	2.41	0.55
1:B:399:ARG:HH22	1:C:399:ARG:HH12	1.52	0.55
1:C:103:ILE:HG22	1:C:104:LEU:HD23	1.89	0.55
1:B:436:ARG:O	1:B:440:GLN:HG3	2.07	0.55
1:C:27:LEU:HD23	1:D:401:LEU:HD22	1.87	0.55
1:B:340:PRO:HG3	1:B:377:MET:HG2	1.87	0.55
1:B:280:PHE:CE1	1:B:313:MET:HG2	2.42	0.54
1:D:292:VAL:HG12	1:D:294:ARG:HG2	1.89	0.54
1:D:48:ILE:HG12	1:D:71:VAL:HB	1.90	0.54
1:D:56:ARG:HD3	1:D:83:TYR:OH	2.07	0.54
1:A:16:GLN:HG3	1:A:18:LEU:HG	1.90	0.54
1:C:123:LEU:HD23	1:C:205:SER:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:VAL:HG22	1:A:109:ALA:HB3	1.89	0.53
1:D:149:MET:HG2	1:D:158:TRP:CE2	2.44	0.53
1:D:123:LEU:HA	1:D:205:SER:HB3	1.90	0.53
1:A:431:LEU:HD22	1:A:513:THR:HG22	1.90	0.53
1:C:121:THR:HB	1:C:157:LEU:HD11	1.91	0.52
1:B:223:GLU:HA	1:B:226:ILE:HD12	1.90	0.52
1:D:117:PRO:HD2	1:D:244:PHE:HB2	1.92	0.52
1:A:222:SER:O	1:A:226:ILE:HG13	2.10	0.52
1:D:192:PHE:O	1:D:193:LEU:HD23	2.10	0.52
1:C:49:CYS:SG	1:C:69:MET:HG3	2.50	0.52
1:B:134:LEU:HD12	1:B:181:ILE:HD13	1.91	0.51
1:B:331:LEU:HD23	1:B:344:GLU:HB3	1.91	0.51
1:D:16:GLN:HG2	1:D:40:ILE:HG22	1.92	0.51
1:B:497:GLY:HA3	1:B:503:PHE:CZ	2.45	0.51
1:C:395:PHE:CZ	1:C:399:ARG:HD2	2.46	0.51
1:D:146:ASN:HA	1:D:149:MET:HG3	1.92	0.51
1:C:84:HIS:O	1:C:88:ILE:HG13	2.11	0.50
1:A:396:GLU:O	1:A:400:ARG:HG3	2.11	0.50
1:A:56:ARG:NH2	1:A:86:GLU:HB3	2.27	0.50
1:C:482:TRP:C	1:C:482:TRP:CD1	2.88	0.49
1:D:119:ILE:HG23	1:D:161:TYR:HB2	1.93	0.49
1:C:482:TRP:CH2	1:C:517:PRO:HA	2.47	0.49
1:B:291:MET:HE2	1:B:360:MET:SD	2.52	0.49
1:D:274:HIS:CD2	1:D:301:ILE:HG22	2.47	0.49
1:B:399:ARG:HH22	1:C:399:ARG:NH1	2.10	0.49
1:C:476:ASP:CB	1:C:488:LEU:HD11	2.42	0.49
1:D:13:ILE:C	1:D:15:THR:H	2.21	0.49
1:D:494:MET:HE1	1:D:509:VAL:HG21	1.94	0.49
1:C:284:LEU:HD13	1:C:290:ILE:HG13	1.95	0.48
1:B:272:GLU:HG2	1:B:293:ALA:HB3	1.96	0.48
1:D:131:GLU:OE1	1:D:202:SER:OG	2.32	0.48
1:C:246:ARG:HB3	1:C:275:GLU:OE1	2.12	0.48
1:C:225:ASP:O	1:C:229:LEU:HD12	2.13	0.48
1:C:16:GLN:HG3	1:C:40:ILE:HG23	1.96	0.48
1:C:229:LEU:O	1:C:233:VAL:HG23	2.13	0.48
1:A:305:LYS:NZ	7:A:702:HOH:O	2.40	0.47
1:B:255:ARG:CZ	1:B:267:ILE:HD12	2.44	0.47
1:D:340:PRO:HG3	1:D:377:MET:HG2	1.96	0.47
1:C:241:PHE:HE1	1:C:268:ILE:HD13	1.80	0.47
1:A:472:VAL:HG11	1:A:496:VAL:HG11	1.97	0.47
1:B:464:HIS:CE1	3:B:604:GOL:H31	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:292:VAL:HG22	1:D:313:MET:HE2	1.97	0.47
1:C:143:THR:HG21	1:C:148:TYR:HB2	1.97	0.47
1:D:13:ILE:N	1:D:13:ILE:HD12	2.30	0.46
1:A:43:ARG:HH21	4:A:605:EDO:H21	1.80	0.46
1:A:117:PRO:HG3	1:A:246:ARG:HH21	1.79	0.46
1:C:124:ILE:HG21	1:C:131:GLU:HA	1.97	0.46
1:B:75:ASN:HA	1:B:113:ASP:HB3	1.96	0.46
1:D:106:ARG:HH22	1:D:471:PRO:HD2	1.80	0.46
1:D:497:GLY:HA3	1:D:503:PHE:CZ	2.51	0.46
1:C:482:TRP:CZ2	1:C:517:PRO:HA	2.50	0.46
1:A:48:ILE:HG12	1:A:71:VAL:HB	1.98	0.46
1:A:464:HIS:CE1	3:A:603:GOL:H31	2.51	0.46
1:C:288:ASP:O	1:C:323:PRO:HD2	2.16	0.46
1:B:327:ALA:HB1	1:B:360:MET:HE2	1.97	0.46
1:C:515:TRP:CG	1:C:523:ASN:HD21	2.34	0.45
1:A:133:GLU:OE2	1:A:202:SER:OG	2.27	0.45
1:B:518:GLY:O	6:B:602:FBP:O4	2.32	0.45
1:C:293:ALA:HB1	2:C:601:OXL:C1	2.46	0.45
1:D:71:VAL:HG22	1:D:109:ALA:HB3	1.97	0.45
1:A:395:PHE:CZ	1:A:399:ARG:HD3	2.51	0.45
1:D:476:ASP:N	1:D:476:ASP:OD1	2.50	0.45
1:D:13:ILE:HG22	1:D:14:GLN:H	1.82	0.45
1:C:356:ALA:O	1:C:467:ARG:NH2	2.38	0.45
1:C:455:ARG:NH2	1:C:485:ASP:OD1	2.47	0.45
1:B:107:PRO:O	1:B:464:HIS:NE2	2.40	0.45
1:B:464:HIS:ND1	3:B:604:GOL:H31	2.32	0.45
1:C:255:ARG:NH2	1:C:286:ALA:O	2.47	0.45
1:C:497:GLY:HA3	1:C:503:PHE:CZ	2.52	0.45
1:A:68:GLY:HA2	4:A:605:EDO:H21	1.98	0.44
1:B:132:VAL:HB	1:B:154:GLU:HG3	1.99	0.44
1:C:131:GLU:HB3	1:C:204:GLY:HA2	1.99	0.44
1:A:65:ILE:HG12	1:A:108:VAL:HG21	1.98	0.44
1:C:395:PHE:CE2	1:C:399:ARG:HD2	2.52	0.44
1:C:117:PRO:HD2	1:C:244:PHE:HB2	1.98	0.44
1:D:75:ASN:HA	1:D:113:ASP:HB3	2.00	0.44
1:B:65:ILE:HG12	1:B:108:VAL:HG21	1.99	0.44
1:D:365:THR:HA	1:D:371:PRO:HB3	1.99	0.44
1:A:75:ASN:HA	1:A:113:ASP:HB3	1.99	0.44
1:B:416:ALA:HB2	1:B:512:LEU:HD21	1.98	0.44
1:B:396:GLU:HA	1:B:399:ARG:HH21	1.83	0.44
1:D:386:GLU:HA	1:D:389:ILE:HD12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:241:PHE:HB3	1:A:270:LYS:HD2	2.01	0.43
1:C:164:ILE:HG23	1:C:165:CYS:H	1.83	0.43
1:C:323:PRO:HB3	1:C:465:LEU:O	2.18	0.43
1:C:463:ALA:HB1	1:C:469:ILE:HG21	2.00	0.43
1:C:299:ILE:HD13	1:C:299:ILE:HA	1.90	0.43
1:A:164:ILE:O	1:A:168:VAL:HG22	2.19	0.43
1:A:515:TRP:CE3	1:D:526:ARG:HD3	2.53	0.43
1:B:131:GLU:OE1	1:B:202:SER:CB	2.54	0.43
1:D:34:ASP:HB3	1:D:37:SER:HB2	1.99	0.43
1:B:163:ASN:N	1:B:163:ASN:OD1	2.51	0.43
1:A:331:LEU:HD23	1:A:344:GLU:HB3	2.00	0.42
1:B:514:GLY:HA3	6:B:602:FBP:O3	2.19	0.42
1:B:148:TYR:CD1	1:B:148:TYR:N	2.87	0.42
1:B:182:SER:C	1:B:183:LEU:HD23	2.45	0.42
1:D:52:GLY:O	1:D:56:ARG:HG3	2.20	0.42
1:A:293:ALA:HB1	2:A:601:OXL:C1	2.49	0.42
1:A:453:VAL:HG11	1:A:489:ARG:HB3	2.01	0.42
1:B:463:ALA:HB1	1:B:469:ILE:HG21	2.02	0.42
1:B:422:LYS:NZ	1:C:402:ALA:HB1	2.35	0.42
1:A:340:PRO:HG3	1:A:377:MET:HG2	2.02	0.42
1:D:84:HIS:O	1:D:88:ILE:HG13	2.19	0.42
1:D:272:GLU:HG2	1:D:293:ALA:HB3	2.02	0.42
1:A:16:GLN:NE2	1:A:447:ARG:HD3	2.35	0.42
1:A:70:ASN:HB3	1:A:464:HIS:CG	2.54	0.42
1:C:75:ASN:HA	1:C:113:ASP:HB3	2.02	0.42
1:C:521:PHE:CD1	1:C:521:PHE:N	2.88	0.42
1:D:121:THR:HG23	1:D:207:LYS:O	2.19	0.42
1:C:71:VAL:HG22	1:C:109:ALA:HB3	2.02	0.42
1:C:177:ASP:OD1	1:C:207:LYS:HD2	2.20	0.42
1:D:19:HIS:HA	1:D:22:MET:HE2	2.02	0.42
1:B:176:VAL:HA	1:B:208:GLY:O	2.20	0.41
1:A:405:THR:O	1:D:423:CYS:HA	2.21	0.41
1:B:288:ASP:O	1:B:323:PRO:HD2	2.20	0.41
1:B:472:VAL:HG11	1:B:496:VAL:HG11	2.02	0.41
1:C:70:ASN:HB3	1:C:464:HIS:CG	2.55	0.41
1:D:13:ILE:C	1:D:15:THR:N	2.79	0.41
1:B:393:GLN:O	1:B:397:GLU:HG3	2.20	0.41
1:D:323:PRO:HB3	1:D:465:LEU:O	2.21	0.41
1:B:56:ARG:NE	1:B:87:THR:OG1	2.52	0.41
1:D:48:ILE:HB	1:D:360:MET:HG3	2.02	0.41
1:D:146:ASN:CA	1:D:149:MET:HG3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:397:GLU:CD	1:B:25:THR:HB	2.45	0.41
1:B:455:ARG:NH2	1:B:485:ASP:OD1	2.53	0.41
1:C:134:LEU:HD11	1:C:203:LEU:HD13	2.03	0.41
1:A:324:VAL:HG13	1:A:356:ALA:HA	2.03	0.41
1:B:70:ASN:HB3	1:B:464:HIS:CG	2.56	0.41
1:B:121:THR:HB	1:B:157:LEU:HD11	2.02	0.41
1:C:327:ALA:HB1	1:C:360:MET:HE2	2.03	0.41
1:A:258:LEU:HD12	1:A:267:ILE:HD11	2.03	0.40
1:A:323:PRO:HB3	1:A:465:LEU:O	2.21	0.40
1:B:120:ARG:HA	1:B:207:LYS:O	2.21	0.40
1:B:328:THR:HG22	1:B:329:GLN:HG3	2.03	0.40
1:D:373:GLU:OE1	1:D:373:GLU:N	2.47	0.40
1:B:175:TYR:O	1:B:209:VAL:HA	2.22	0.40
1:D:138:ALA:O	1:D:197:VAL:HG23	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 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	469/551 (85%)	460 (98%)	7 (2%)	2 (0%)	30	49
1	B	501/551 (91%)	491 (98%)	9 (2%)	1 (0%)	43	63
1	C	469/551 (85%)	458 (98%)	9 (2%)	2 (0%)	30	49
1	D	485/551 (88%)	476 (98%)	8 (2%)	1 (0%)	43	63
All	All	1924/2204 (87%)	1885 (98%)	33 (2%)	6 (0%)	36	55

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	163	ASN

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Mol	Chain	Res	Type
1	A	328	THR
1	B	328	THR
1	C	153	ASP
1	C	328	THR
1	D	328	THR

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	368/452 (81%)	362 (98%)	6 (2%)	55	79
1	B	390/452 (86%)	384 (98%)	6 (2%)	57	80
1	C	368/452 (81%)	362 (98%)	6 (2%)	55	79
1	D	373/452 (82%)	368 (99%)	5 (1%)	61	82
All	All	1499/1808 (83%)	1476 (98%)	23 (2%)	57	80

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	100	SER
1	A	164	ILE
1	A	165	CYS
1	A	202	SER
1	A	224	LYS
1	A	367	LYS
1	B	13	ILE
1	B	168	VAL
1	B	224	LYS
1	B	249	SER
1	B	346	SER
1	B	480	GLU
1	C	13	ILE
1	C	226	ILE
1	C	229	LEU
1	C	424	CYS

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Mol	Chain	Res	Type
1	C	482	TRP
1	C	522	THR
1	D	13	ILE
1	D	77	SER
1	D	150	GLU
1	D	216	VAL
1	D	299	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	GLN
1	A	391	HIS
1	B	16	GLN
1	B	146	ASN
1	B	210	ASN
1	B	252	HIS
1	B	273	ASN
1	B	391	HIS
1	B	440	GLN
1	B	458	GLN
1	C	14	GLN
1	C	273	ASN
1	D	252	HIS
1	D	391	HIS
1	D	458	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 28 ligands modelled in this entry, 9 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
4	EDO	A	606	-	3,3,3	0.45	0	2,2,2	0.39	0
2	OXL	C	601	5	5,5,5	2.04	2 (40%)	6,6,6	2.09	2 (33%)
4	EDO	A	605	-	3,3,3	0.49	0	2,2,2	0.28	0
6	FBP	D	602	-	5,5,20	1.71	1 (20%)	7,7,32	0.62	0
3	GOL	C	603	-	5,5,5	0.83	0	5,5,5	1.17	1 (20%)
2	OXL	D	601	5	5,5,5	2.01	2 (40%)	6,6,6	2.09	2 (33%)
3	GOL	B	604	-	5,5,5	1.07	0	5,5,5	1.03	0
3	GOL	B	603	-	5,5,5	0.90	0	5,5,5	1.11	1 (20%)
3	GOL	D	605	-	5,5,5	0.94	0	5,5,5	1.00	0
3	GOL	A	603	-	5,5,5	1.04	0	5,5,5	0.97	0
4	EDO	C	604	-	3,3,3	0.45	0	2,2,2	0.37	0
3	GOL	A	602	-	5,5,5	0.90	0	5,5,5	1.10	0
2	OXL	A	601	5	5,5,5	2.04	2 (40%)	6,6,6	2.11	2 (33%)
4	EDO	D	604	-	3,3,3	0.46	0	2,2,2	0.27	0
6	FBP	C	602	-	5,5,20	1.68	1 (20%)	7,7,32	0.66	0
2	OXL	B	601	5	5,5,5	2.05	2 (40%)	6,6,6	2.06	2 (33%)
4	EDO	A	604	-	3,3,3	0.43	0	2,2,2	0.36	0
6	FBP	B	602	-	18,20,20	3.45	5 (27%)	21,32,32	0.65	0
3	GOL	D	603	-	5,5,5	0.85	0	5,5,5	1.14	1 (20%)

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	EDO	A	606	-	-	0/1/1/1	-
2	OXL	C	601	5	-	4/4/4/4	-
4	EDO	A	605	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	FBP	D	602	-	-	0/1/3/32	-
3	GOL	C	603	-	-	2/4/4/4	-
2	OXL	D	601	5	-	4/4/4/4	-
3	GOL	B	604	-	-	0/4/4/4	-
3	GOL	B	603	-	-	0/4/4/4	-
3	GOL	D	605	-	-	2/4/4/4	-
3	GOL	A	603	-	-	4/4/4/4	-
4	EDO	C	604	-	-	0/1/1/1	-
3	GOL	A	602	-	-	2/4/4/4	-
2	OXL	A	601	5	-	4/4/4/4	-
4	EDO	D	604	-	-	0/1/1/1	-
6	FBP	C	602	-	-	0/1/3/32	-
2	OXL	B	601	5	-	4/4/4/4	-
4	EDO	A	604	-	-	0/1/1/1	-
6	FBP	B	602	-	-	5/13/32/32	0/1/1/1
3	GOL	D	603	-	-	1/4/4/4	-

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	602	FBP	O5-C5	8.24	1.62	1.43
6	B	602	FBP	O5-C2	-8.22	1.30	1.43
6	B	602	FBP	C4-C5	-6.97	1.35	1.53
6	D	602	FBP	P2-O6	3.60	1.65	1.59
6	C	602	FBP	P2-O6	3.57	1.65	1.59
2	B	601	OXL	O2-C2	3.56	1.31	1.22
2	A	601	OXL	O1-C1	3.56	1.31	1.22
2	C	601	OXL	O1-C1	3.55	1.31	1.22
6	B	602	FBP	O3-C3	-3.42	1.36	1.42
2	D	601	OXL	O2-C2	3.40	1.31	1.22
2	D	601	OXL	O4-C2	-2.95	1.22	1.30
2	B	601	OXL	O4-C2	-2.87	1.22	1.30
2	C	601	OXL	O3-C1	-2.84	1.22	1.30
2	A	601	OXL	O3-C1	-2.78	1.23	1.30
6	B	602	FBP	O4-C4	2.62	1.49	1.43

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	OXL	O3-C1-C2	3.99	120.58	112.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	OXL	O3-C1-C2	3.98	120.55	112.83
2	D	601	OXL	O4-C2-C1	3.97	120.53	112.83
2	B	601	OXL	O4-C2-C1	3.91	120.42	112.83
2	A	601	OXL	O1-C1-C2	-3.09	114.20	120.63
2	D	601	OXL	O2-C2-C1	-3.05	114.28	120.63
2	B	601	OXL	O2-C2-C1	-3.02	114.34	120.63
2	C	601	OXL	O1-C1-C2	-3.02	114.34	120.63
3	B	603	GOL	C3-C2-C1	-2.03	104.34	111.80
3	D	603	GOL	C3-C2-C1	-2.02	104.39	111.80
3	C	603	GOL	C3-C2-C1	-2.01	104.44	111.80

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	603	GOL	C1-C2-C3-O3
6	B	602	FBP	O1-C1-C2-O2
6	B	602	FBP	O1-C1-C2-C3
6	B	602	FBP	O1-C1-C2-O5
6	B	602	FBP	C4-C5-C6-O6
3	A	602	GOL	C1-C2-C3-O3
3	A	603	GOL	O1-C1-C2-C3
3	A	603	GOL	C1-C2-C3-O3
3	D	603	GOL	C1-C2-C3-O3
3	D	605	GOL	O1-C1-C2-C3
3	C	603	GOL	O2-C2-C3-O3
6	B	602	FBP	O5-C5-C6-O6
3	A	602	GOL	O2-C2-C3-O3
2	A	601	OXL	O3-C1-C2-O4
2	C	601	OXL	O3-C1-C2-O4
2	B	601	OXL	O3-C1-C2-O4
2	D	601	OXL	O3-C1-C2-O4
2	A	601	OXL	O1-C1-C2-O2
2	B	601	OXL	O1-C1-C2-O2
2	C	601	OXL	O1-C1-C2-O2
2	D	601	OXL	O1-C1-C2-O2
3	D	605	GOL	O1-C1-C2-O2
3	A	603	GOL	O2-C2-C3-O3
2	A	601	OXL	O1-C1-C2-O4
2	A	601	OXL	O3-C1-C2-O2
2	B	601	OXL	O1-C1-C2-O4
2	B	601	OXL	O3-C1-C2-O2

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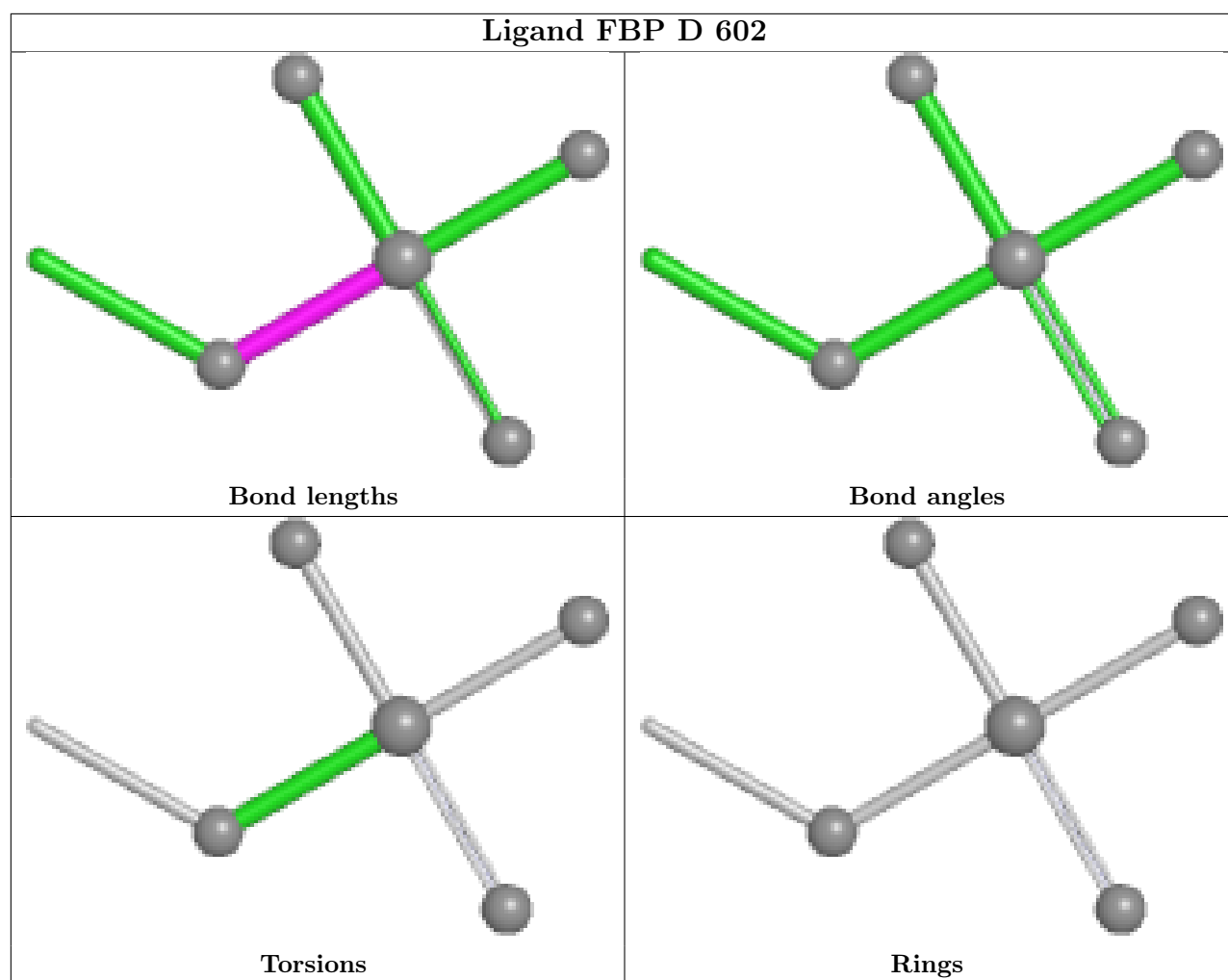
Mol	Chain	Res	Type	Atoms
2	C	601	OXL	O1-C1-C2-O4
2	C	601	OXL	O3-C1-C2-O2
2	D	601	OXL	O1-C1-C2-O4
2	D	601	OXL	O3-C1-C2-O2
3	A	603	GOL	O1-C1-C2-O2

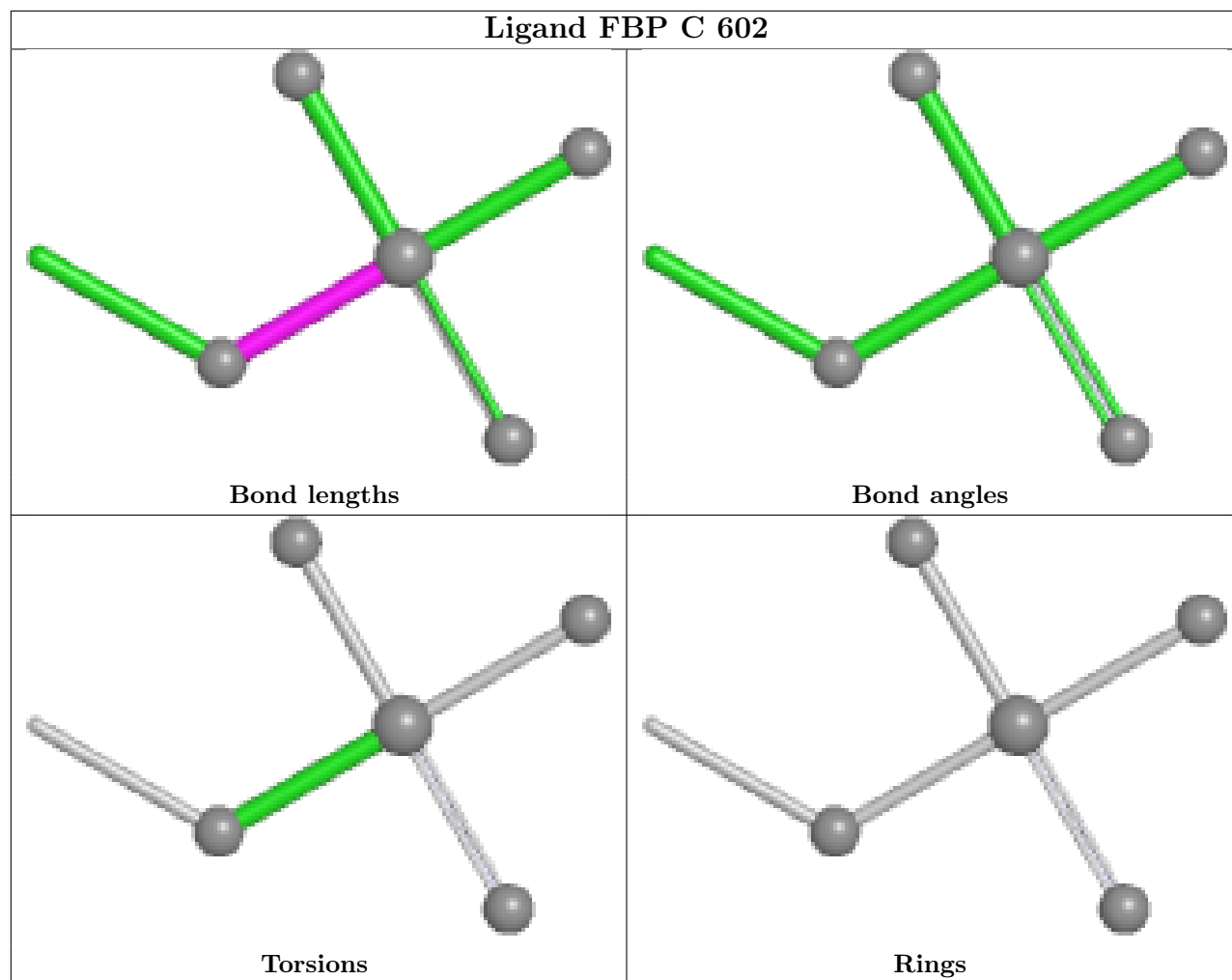
There are no ring outliers.

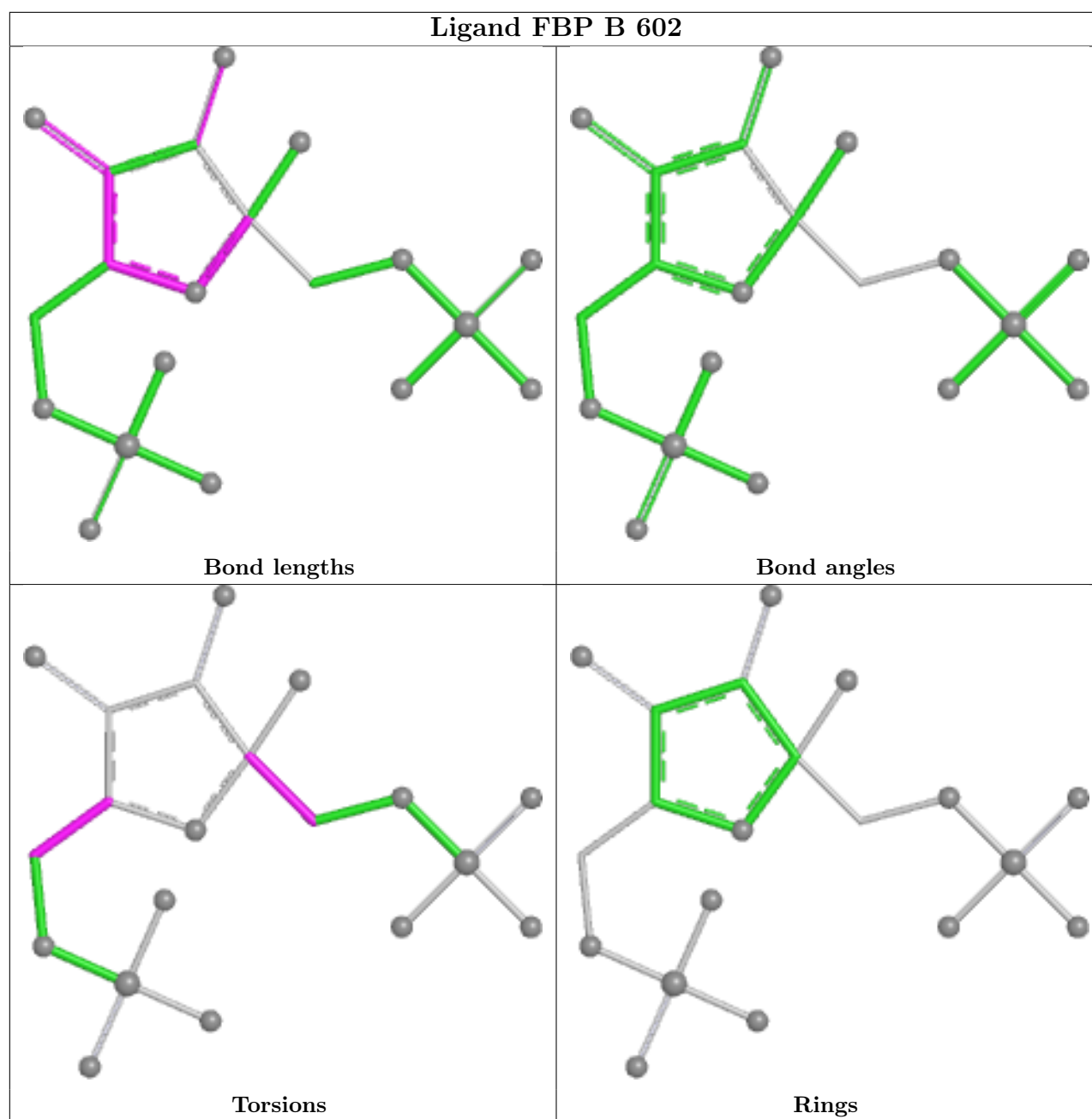
7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	601	OXL	1	0
4	A	605	EDO	2	0
3	B	604	GOL	2	0
3	A	603	GOL	1	0
4	C	604	EDO	1	0
2	A	601	OXL	1	0
6	B	602	FBP	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	481/551 (87%)	0.01	11 (2%) 61 57	32, 47, 93, 125	0
1	B	509/551 (92%)	0.17	23 (4%) 38 33	34, 53, 102, 153	0
1	C	483/551 (87%)	0.42	35 (7%) 21 19	40, 64, 105, 125	0
1	D	489/551 (88%)	0.29	36 (7%) 20 18	39, 56, 109, 153	0
All	All	1962/2204 (89%)	0.22	105 (5%) 31 27	32, 55, 103, 153	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	195	THR	4.9
1	B	169	GLU	4.8
1	C	170	VAL	4.3
1	D	121	THR	3.7
1	D	206	LYS	3.7
1	D	145	ASP	3.7
1	A	13	ILE	3.7
1	D	13	ILE	3.7
1	C	124	ILE	3.7
1	B	214	ALA	3.5
1	B	168	VAL	3.4
1	B	13	ILE	3.4
1	B	203	LEU	3.4
1	D	192	PHE	3.3
1	B	140	LEU	3.3
1	C	515	TRP	3.3
1	B	215	ALA	3.3
1	C	122	GLY	3.2
1	B	145	ASP	3.2
1	C	204	GLY	3.2
1	D	159	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	211	LEU	3.1
1	D	196	GLU	3.1
1	D	140	LEU	3.1
1	D	142	ILE	3.1
1	B	213	GLY	3.0
1	C	404	ILE	3.0
1	D	134	LEU	3.0
1	D	144	LEU	3.0
1	D	203	LEU	3.0
1	D	130	ALA	2.9
1	D	158	TRP	2.9
1	C	161	TYR	2.9
1	B	142	ILE	2.8
1	C	181	ILE	2.8
1	D	129	THR	2.8
1	C	482	TRP	2.8
1	C	156	ILE	2.8
1	C	135	LYS	2.8
1	B	174	ILE	2.7
1	C	477	PRO	2.7
1	C	268	ILE	2.6
1	C	134	LEU	2.6
1	C	517	PRO	2.6
1	C	521	PHE	2.6
1	A	515	TRP	2.5
1	D	204	GLY	2.5
1	A	176	VAL	2.5
1	D	122	GLY	2.5
1	B	156	ILE	2.5
1	C	174	ILE	2.5
1	B	194	VAL	2.5
1	D	207	LYS	2.5
1	D	197	VAL	2.5
1	C	112	LEU	2.4
1	C	171	GLY	2.4
1	D	125	LYS	2.4
1	C	13	ILE	2.4
1	C	142	ILE	2.4
1	D	123	LEU	2.4
1	B	197	VAL	2.4
1	C	147	ALA	2.4
1	C	164	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	157	LEU	2.4
1	D	214	ALA	2.4
1	C	211	LEU	2.3
1	D	221	VAL	2.3
1	B	195	THR	2.3
1	C	203	LEU	2.3
1	D	216	VAL	2.3
1	A	193	LEU	2.3
1	D	157	LEU	2.3
1	B	125	LYS	2.3
1	D	119	ILE	2.2
1	C	154	GLU	2.2
1	C	210	ASN	2.2
1	D	199	ASN	2.2
1	C	180	LEU	2.2
1	B	141	LYS	2.2
1	D	161	TYR	2.2
1	C	172	SER	2.2
1	A	517	PRO	2.2
1	C	162	LYS	2.2
1	B	165	CYS	2.2
1	D	128	GLY	2.2
1	D	124	ILE	2.2
1	B	192	PHE	2.2
1	A	132	VAL	2.1
1	D	138	ALA	2.1
1	A	208	GLY	2.1
1	A	103	ILE	2.1
1	B	148	TYR	2.1
1	B	153	ASP	2.1
1	C	362	SER	2.1
1	B	134	LEU	2.1
1	C	150	GLU	2.1
1	A	184	GLN	2.1
1	C	140	LEU	2.1
1	A	170	VAL	2.0
1	D	200	GLY	2.0
1	D	518	GLY	2.0
1	D	141	LYS	2.0
1	A	516	ARG	2.0
1	B	185	VAL	2.0
1	C	158	TRP	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
4	EDO	A	606	4/4	0.68	0.17	71,72,75,80	0
3	GOL	D	605	6/6	0.73	0.18	64,68,70,80	0
4	EDO	D	604	4/4	0.76	0.20	65,67,69,70	0
3	GOL	C	603	6/6	0.79	0.16	57,62,65,67	0
4	EDO	C	604	4/4	0.80	0.16	57,62,68,68	0
4	EDO	A	605	4/4	0.81	0.17	42,56,58,62	0
4	EDO	A	604	4/4	0.81	0.16	64,67,67,72	0
3	GOL	B	604	6/6	0.84	0.15	42,46,48,51	0
3	GOL	D	603	6/6	0.85	0.14	41,51,54,61	0
3	GOL	B	603	6/6	0.86	0.12	58,63,67,69	0
3	GOL	A	602	6/6	0.87	0.14	52,64,65,67	0
5	MG	B	607	1/1	0.87	0.27	63,63,63,63	0
5	MG	A	609	1/1	0.88	0.26	63,63,63,63	0
2	OXL	D	601	6/6	0.89	0.11	50,51,52,57	0
2	OXL	C	601	6/6	0.89	0.07	49,57,62,63	0
5	MG	B	606	1/1	0.89	0.10	54,54,54,54	0
3	GOL	A	603	6/6	0.89	0.11	32,35,40,44	0
6	FBP	B	602	20/20	0.89	0.12	44,57,67,70	20
6	FBP	C	602	6/20	0.89	0.11	56,63,70,70	6
6	FBP	D	602	6/20	0.89	0.12	51,54,64,70	6
5	MG	D	607	1/1	0.91	0.07	66,66,66,66	0
5	MG	B	605	1/1	0.91	0.14	50,50,50,50	0
2	OXL	A	601	6/6	0.92	0.08	43,45,47,49	0
2	OXL	B	601	6/6	0.92	0.07	50,53,53,55	0
5	MG	A	608	1/1	0.96	0.07	54,54,54,54	0
5	MG	C	605	1/1	0.97	0.05	62,62,62,62	0
5	MG	D	606	1/1	0.97	0.07	56,56,56,56	0

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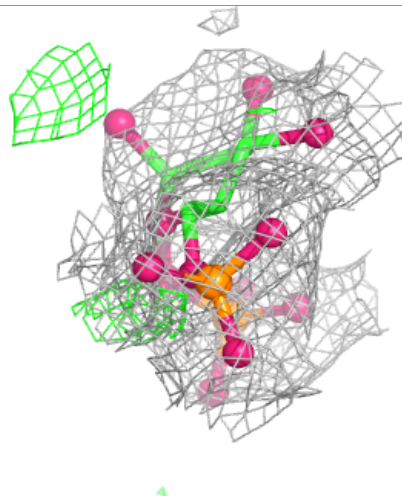
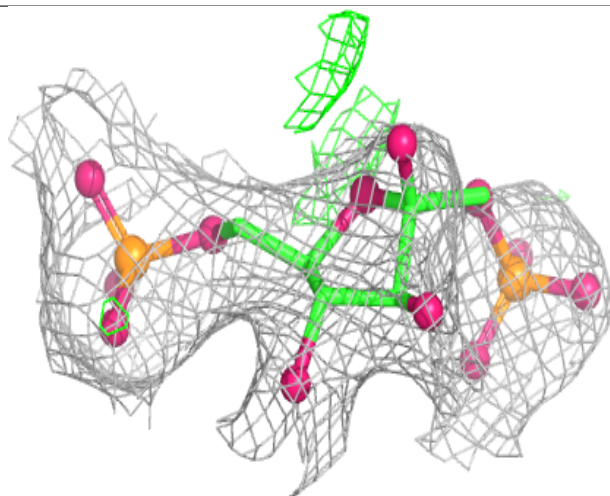
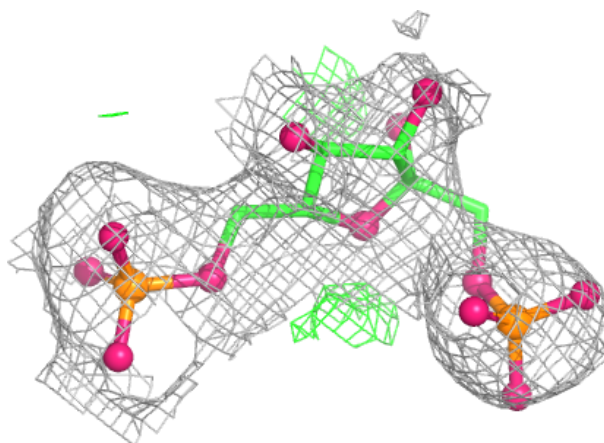
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	MG	A	607	1/1	1.00	0.06	40,40,40,40	0

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.

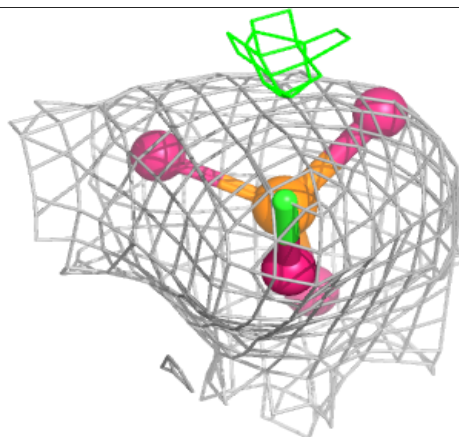
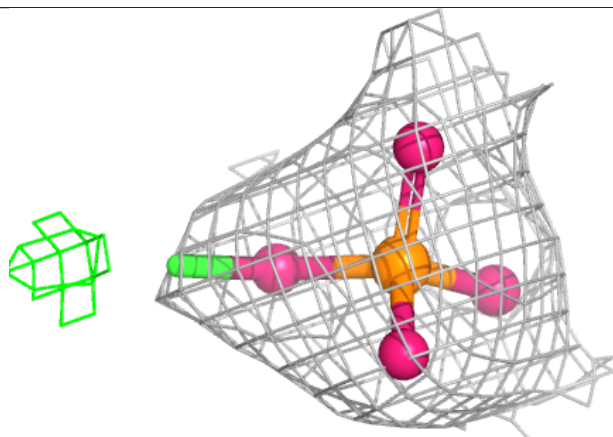
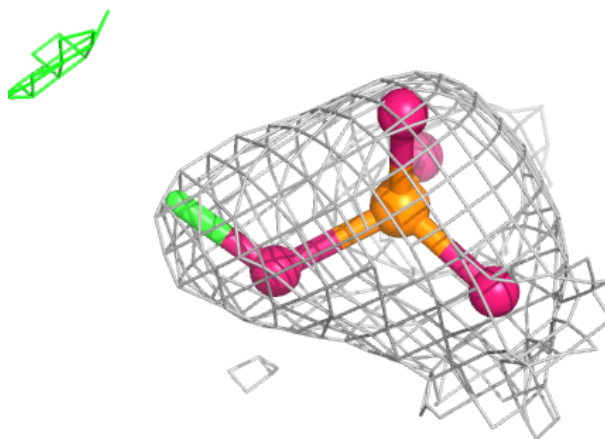
Electron density around FBP B 602:

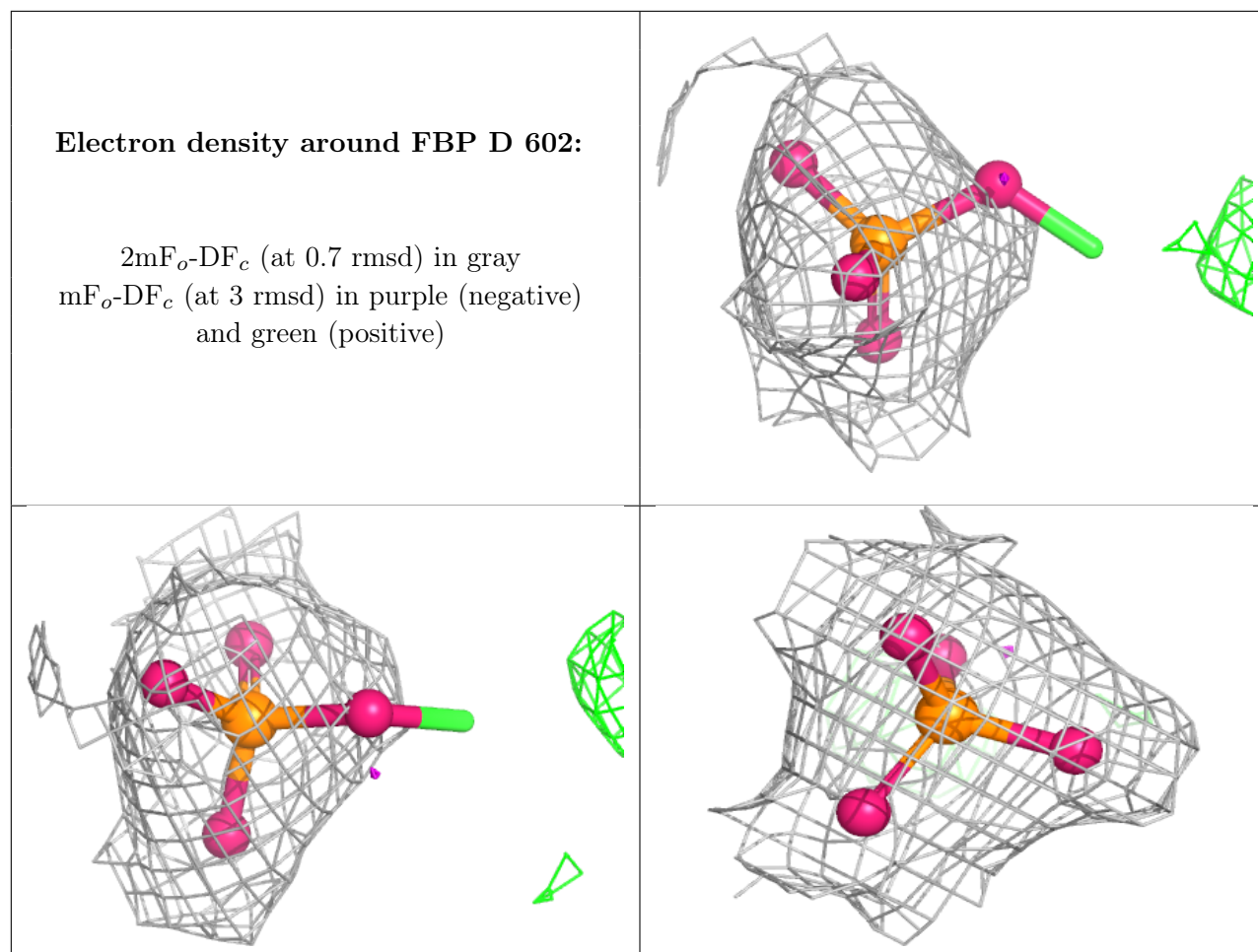
2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FBP C 602:

$2mF_o - DF_c$ (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.