



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:17 AM UTC

PDB ID : 3SRD / pdb_00003srd
Title : Human M2 pyruvate kinase in complex with fructose 1-6 biphosphate and Oxalate.
Authors : Morgan, H.P.; O'Reilly, F.; Palmer, R.; McNae, I.W.; Nowicki, M.W.; Wear, M.A.; Fothergill-Gilmore, L.A.; Walkinshaw, M.D.
Deposited on : 2011-07-07
Resolution : 2.90 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

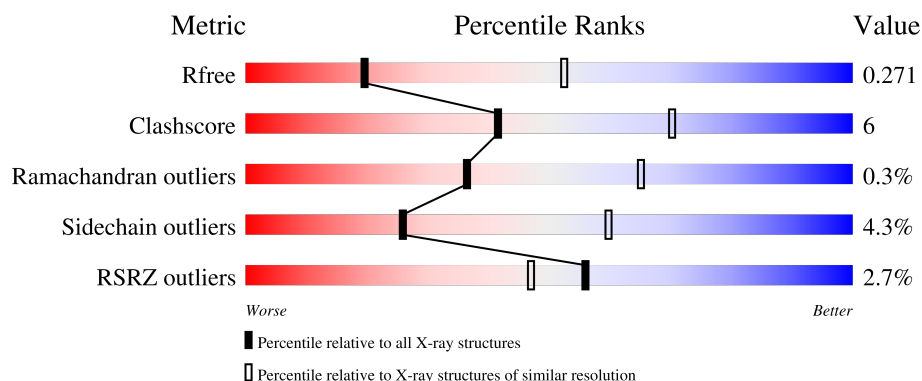
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	
1	B	551	
1	C	551	
1	D	551	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 16047 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 isozymes M1/M2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	515	Total	C	N	O	S	0	0	0
			3951	2486	701	739	25			
1	B	512	Total	C	N	O	S	0	0	0
			3930	2473	698	734	25			
1	C	514	Total	C	N	O	S	0	0	0
			3947	2484	700	738	25			
1	D	515	Total	C	N	O	S	0	1	0
			3952	2484	702	741	25			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	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
B	-19	MET	-	expression tag	UNP P14618

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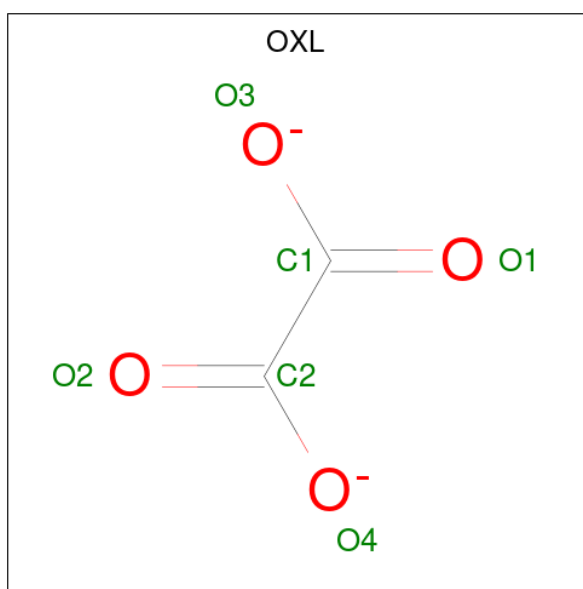
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP P14618
B	-17	SER	-	expression tag	UNP P14618
B	-16	SER	-	expression tag	UNP P14618
B	-15	HIS	-	expression tag	UNP P14618
B	-14	HIS	-	expression tag	UNP P14618
B	-13	HIS	-	expression tag	UNP P14618
B	-12	HIS	-	expression tag	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
C	-19	MET	-	expression tag	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
D	-19	MET	-	expression tag	UNP P14618
D	-18	GLY	-	expression tag	UNP P14618
D	-17	SER	-	expression tag	UNP P14618

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Chain	Residue	Modelled	Actual	Comment	Reference
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

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



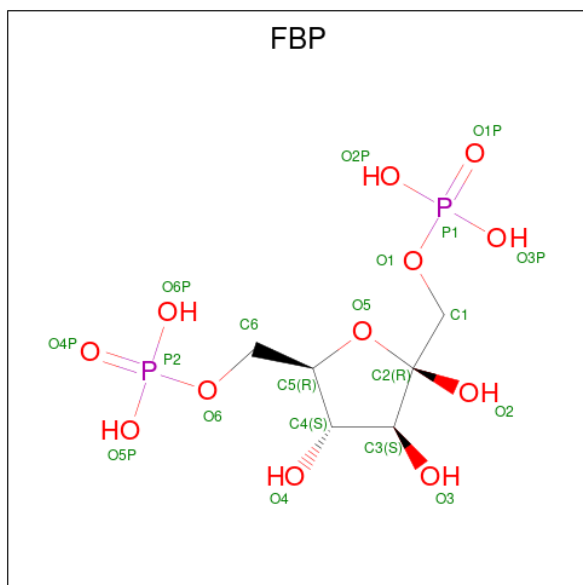
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	2	4		
2	B	1	Total	C	O	0	0
			6	2	4		
2	C	1	Total	C	O	0	0
			6	2	4		

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

- Molecule 3 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
3	A	1	Total	C	O	P	0	0
			20	6	12	2		
3	B	1	Total	C	O	P	0	0
			20	6	12	2		
3	C	1	Total	C	O	P	0	0
			20	6	12	2		
3	D	1	Total	C	O	P	0	0
			20	6	12	2		

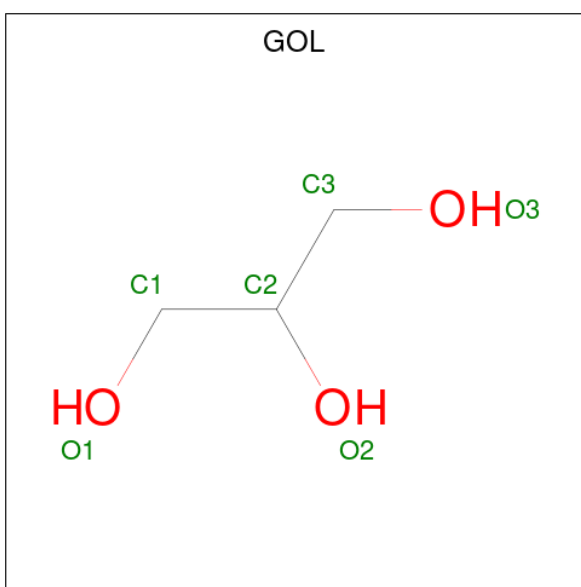
- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K).

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

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

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

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

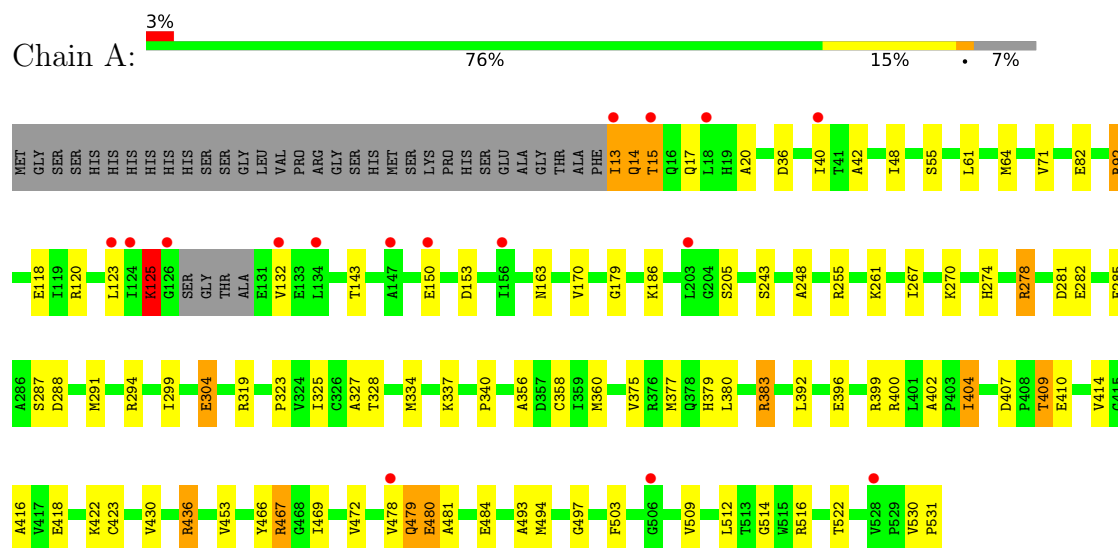
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	34	Total 34	O 34	0	0
7	B	34	Total 34	O 34	0	0
7	C	31	Total 31	O 31	0	0
7	D	27	Total 27	O 27	0	0

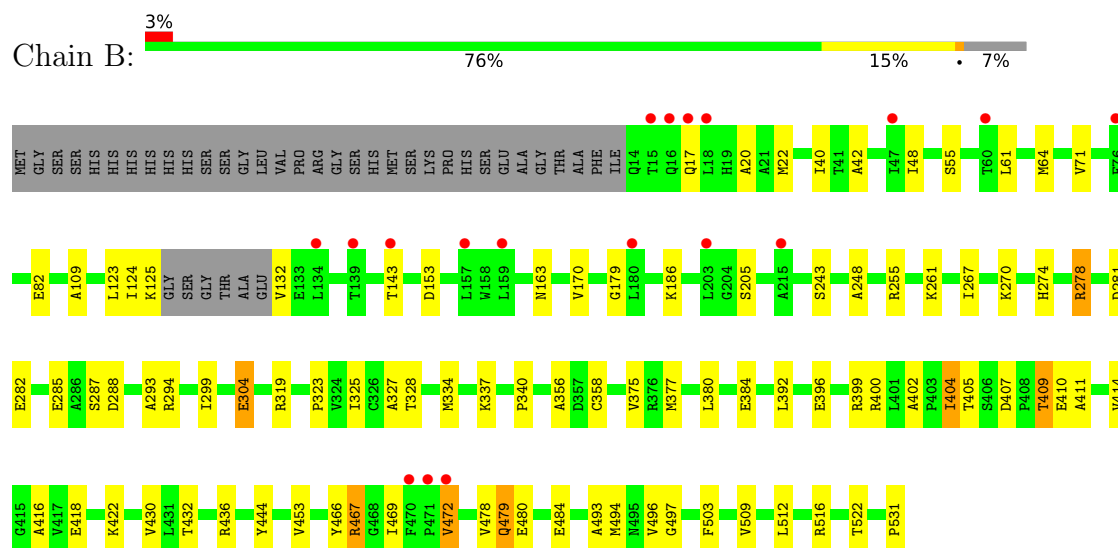
3 Residue-property plots [i](#)

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.

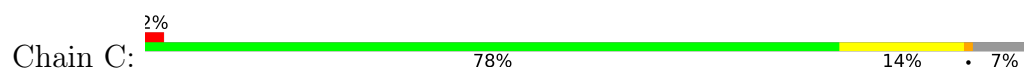
• Molecule 1: Pyruvate kinase isozymes M1/M2

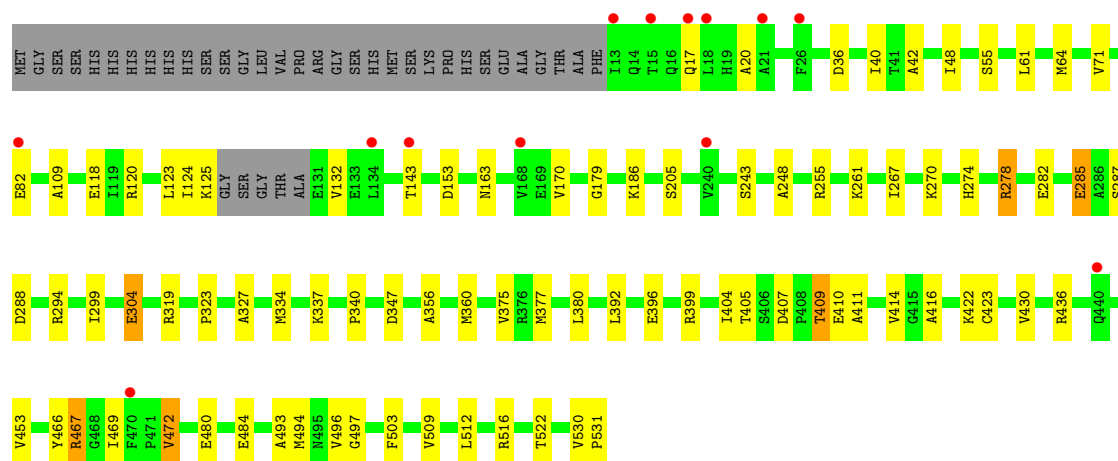


• Molecule 1: Pyruvate kinase isozymes M1/M2

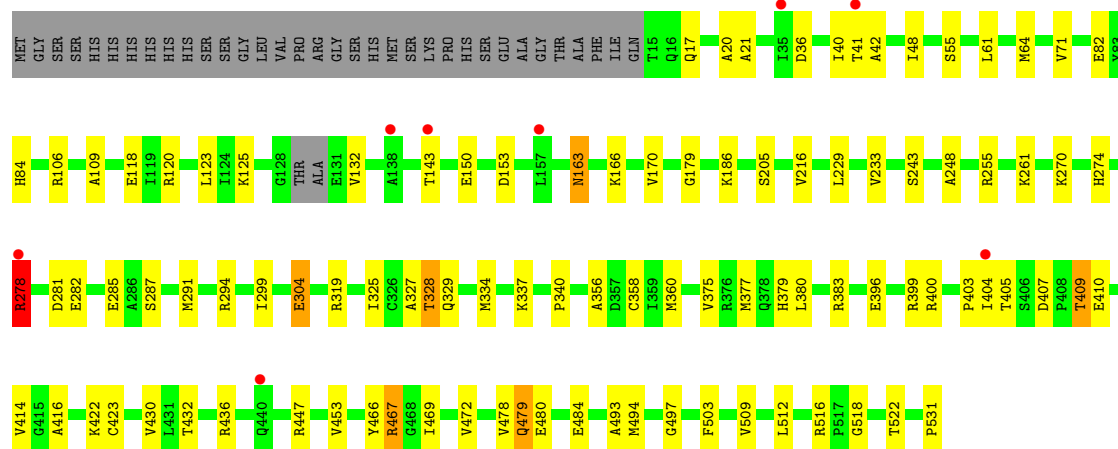
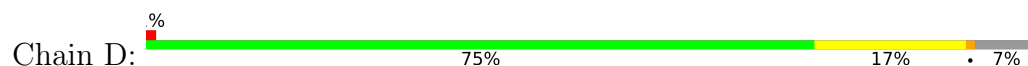


• Molecule 1: Pyruvate kinase isozymes M1/M2





• Molecule 1: Pyruvate kinase isozymes M1/M2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	95.05Å 117.37Å 110.46Å 90.00° 113.56° 90.00°	Depositor
Resolution (Å)	54.18 – 2.90 54.18 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (54.18-2.90) 91.9 (54.18-2.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.253 , 0.279 0.249 , 0.271	Depositor DCC
R_{free} test set	2283 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	71.0	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 69.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	16047	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.96% 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: MG, FBP, GOL, OXL, K

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	0.49	0/4014	0.96	15/5419 (0.3%)
1	B	0.49	0/3993	0.84	3/5391 (0.1%)
1	C	0.49	0/4010	0.85	4/5414 (0.1%)
1	D	0.51	1/4015 (0.0%)	0.86	7/5420 (0.1%)
All	All	0.50	1/16032 (0.0%)	0.88	29/21644 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	436	ARG	CG-CD	-5.67	1.35	1.52

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	14	GLN	N-CA-C	17.12	135.02	111.39
1	A	14	GLN	CB-CA-C	-13.52	92.69	111.89
1	A	15	THR	N-CA-C	12.78	128.25	110.35
1	A	92	ARG	NE-CZ-NH2	9.63	127.87	119.20
1	A	383	ARG	NE-CZ-NH2	8.71	127.04	119.20
1	A	92	ARG	NE-CZ-NH1	-8.46	113.04	121.50
1	C	285	GLU	CA-CB-CG	8.08	130.26	114.10
1	A	436	ARG	NE-CZ-NH2	7.98	126.38	119.20
1	A	125	LYS	CB-CA-C	-7.97	97.02	109.61
1	A	383	ARG	NE-CZ-NH1	-7.92	113.58	121.50
1	D	436	ARG	CB-CG-CD	-7.06	95.06	111.30
1	D	278	ARG	NE-CZ-NH2	7.05	125.55	119.20
1	A	436	ARG	NE-CZ-NH1	-6.70	114.80	121.50
1	A	278	ARG	CG-CD-NE	-6.69	97.28	112.00
1	D	436	ARG	CG-CD-NE	6.46	126.22	112.00
1	C	278	ARG	CG-CD-NE	-6.40	97.92	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	92	ARG	CD-NE-CZ	6.39	133.35	124.40
1	B	278	ARG	CG-CD-NE	-6.25	98.25	112.00
1	D	436	ARG	NE-CZ-NH2	5.50	124.15	119.20
1	D	407	ASP	CA-C-N	5.42	124.88	119.24
1	D	407	ASP	C-N-CA	5.42	124.88	119.24
1	B	407	ASP	CA-C-N	5.34	124.80	119.24
1	B	407	ASP	C-N-CA	5.34	124.80	119.24
1	A	383	ARG	CD-NE-CZ	5.22	131.70	124.40
1	D	436	ARG	N-CA-C	5.20	116.95	111.28
1	A	407	ASP	CA-C-N	5.16	124.60	119.24
1	A	407	ASP	C-N-CA	5.16	124.60	119.24
1	C	407	ASP	CA-C-N	5.12	124.57	119.24
1	C	407	ASP	C-N-CA	5.12	124.57	119.24

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	3951	0	4039	64	0
1	B	3930	0	4019	53	0
1	C	3947	0	4036	50	0
1	D	3952	0	4033	64	0
2	A	6	0	0	1	0
2	B	6	0	0	1	0
2	C	6	0	0	0	0
2	D	6	0	0	0	0
3	A	20	0	10	1	0
3	B	20	0	10	1	0
3	C	20	0	10	0	0
3	D	20	0	10	2	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	6	0	8	0	0
6	B	6	0	8	0	0
6	C	6	0	8	0	0
6	D	12	0	16	1	0
7	A	34	0	0	0	0
7	B	34	0	0	2	0
7	C	31	0	0	0	0
7	D	27	0	0	4	0
All	All	16047	0	16207	204	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 (204) 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:14:GLN:O	1:A:14:GLN:CG	1.70	1.32
1:D:274:HIS:CD2	1:D:278:ARG:HH22	1.52	1.27
1:A:480:GLU:H	1:A:480:GLU:CD	1.54	1.12
1:D:278:ARG:NH2	1:D:278:ARG:HG3	1.56	1.06
1:D:278:ARG:HH21	1:D:278:ARG:CG	1.72	1.03
1:A:380:LEU:HB3	1:C:304:GLU:HG2	1.37	1.03
1:D:278:ARG:HG3	1:D:278:ARG:HH21	0.91	1.02
1:D:274:HIS:CD2	1:D:278:ARG:NH2	2.29	0.99
1:C:405:THR:O	1:D:423:CYS:HA	1.63	0.98
1:B:380:LEU:HB3	1:D:304:GLU:HG2	1.44	0.97
1:D:274:HIS:HD2	1:D:278:ARG:HH22	1.11	0.97
1:D:274:HIS:HD2	1:D:278:ARG:NH2	1.64	0.93
1:B:304:GLU:HG2	1:D:380:LEU:HB3	1.51	0.92
1:C:274:HIS:CD2	1:C:278:ARG:NH2	2.39	0.91
1:D:216:VAL:HG21	6:D:535:GOL:H32	1.54	0.89
1:A:274:HIS:CD2	1:A:278:ARG:NH2	2.42	0.88
1:B:274:HIS:CD2	1:B:278:ARG:NH2	2.42	0.87
1:D:278:ARG:NH2	1:D:278:ARG:CG	2.30	0.87
1:A:304:GLU:HG2	1:C:380:LEU:HB3	1.57	0.86
1:A:14:GLN:O	1:A:14:GLN:HG2	0.99	0.81
1:C:274:HIS:CD2	1:C:278:ARG:HH22	1.99	0.80
1:B:274:HIS:CD2	1:B:278:ARG:HH22	2.00	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:480:GLU:CD	1:A:480:GLU:N	2.31	0.78
1:A:423:CYS:HA	1:B:405:THR:O	1.85	0.77
1:A:409:THR:HG22	1:A:522:THR:HB	1.68	0.76
1:B:494:MET:HG2	1:B:531:PRO:HD2	1.69	0.75
1:A:274:HIS:CD2	1:A:278:ARG:HH22	2.02	0.75
1:C:494:MET:HG2	1:C:531:PRO:HD2	1.68	0.75
1:D:409:THR:HG22	1:D:522:THR:HB	1.69	0.74
1:A:494:MET:HG2	1:A:531:PRO:HD2	1.69	0.74
1:C:409:THR:HG22	1:C:522:THR:HB	1.70	0.74
1:D:494:MET:HG2	1:D:531:PRO:HD2	1.69	0.73
1:C:399:ARG:HH21	1:D:399:ARG:HH21	1.34	0.73
1:D:518:GLY:O	3:D:532:FBP:O4	2.07	0.73
1:C:422:LYS:NZ	1:D:403:PRO:O	2.22	0.71
1:B:409:THR:HG22	1:B:522:THR:HB	1.71	0.70
1:B:278:ARG:NH1	1:D:36:ASP:OD1	2.25	0.69
1:A:36:ASP:OD1	1:C:278:ARG:NH1	2.25	0.69
1:D:123:LEU:HD23	1:D:205:SER:HB3	1.80	0.62
1:B:123:LEU:HD23	1:B:205:SER:HB3	1.81	0.62
1:A:123:LEU:HD23	1:A:205:SER:HB3	1.81	0.61
1:C:123:LEU:HD23	1:C:205:SER:HB3	1.80	0.61
1:D:179:GLY:HA3	1:D:299:ILE:HD12	1.81	0.61
1:C:274:HIS:HD2	1:C:278:ARG:NH2	1.98	0.60
1:D:432:THR:HA	3:D:532:FBP:H61	1.83	0.60
1:A:294:ARG:HD3	1:A:327:ALA:O	2.01	0.60
1:A:179:GLY:HA3	1:A:299:ILE:HD12	1.82	0.60
1:B:179:GLY:HA3	1:B:299:ILE:HD12	1.84	0.59
1:C:399:ARG:NH2	1:D:399:ARG:HH21	2.00	0.59
1:C:179:GLY:HA3	1:C:299:ILE:HD12	1.82	0.59
1:A:400:ARG:HE	1:B:392:LEU:HD11	1.67	0.59
1:A:13:ILE:CG2	1:A:13:ILE:O	2.50	0.58
1:D:356:ALA:O	1:D:467:ARG:NH1	2.37	0.57
1:C:294:ARG:HD3	1:C:327:ALA:O	2.05	0.57
1:D:84:HIS:HD2	7:D:555:HOH:O	1.88	0.57
1:B:274:HIS:HD2	1:B:278:ARG:NH2	2.01	0.57
1:C:356:ALA:O	1:C:467:ARG:NH1	2.37	0.57
1:D:497:GLY:HA3	1:D:503:PHE:CZ	2.41	0.56
1:B:356:ALA:O	1:B:467:ARG:NH1	2.38	0.55
1:C:497:GLY:HA3	1:C:503:PHE:CZ	2.42	0.55
1:D:294:ARG:HD3	1:D:327:ALA:O	2.07	0.55
1:C:392:LEU:HD11	1:D:400:ARG:HE	1.72	0.55
1:A:497:GLY:HA3	1:A:503:PHE:CZ	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:ARG:HD3	1:B:327:ALA:O	2.07	0.54
1:B:432:THR:HA	3:B:532:FBP:H61	1.89	0.54
1:A:356:ALA:O	1:A:467:ARG:NH1	2.41	0.53
1:A:423:CYS:HB3	1:B:411:ALA:HB2	1.89	0.53
1:D:453:VAL:HG21	1:D:493:ALA:HB2	1.91	0.53
1:B:17:GLN:HB3	1:B:20:ALA:HB3	1.91	0.53
1:A:453:VAL:HG21	1:A:493:ALA:HB2	1.91	0.52
1:B:453:VAL:HG21	1:B:493:ALA:HB2	1.91	0.52
1:B:466:TYR:HB2	1:B:469:ILE:HD12	1.92	0.52
1:C:17:GLN:HB3	1:C:20:ALA:HB3	1.91	0.52
1:C:422:LYS:HE3	1:D:405:THR:HG22	1.91	0.52
1:B:497:GLY:HA3	1:B:503:PHE:CZ	2.45	0.52
1:A:380:LEU:CB	1:C:304:GLU:HG2	2.26	0.51
1:A:17:GLN:HB3	1:A:20:ALA:HB3	1.92	0.51
1:D:17:GLN:HB3	1:D:20:ALA:HB3	1.91	0.51
1:D:243:SER:HA	1:D:270:LYS:HE2	1.93	0.51
1:C:40:ILE:HD12	1:C:42:ALA:HB3	1.92	0.50
1:C:453:VAL:HG21	1:C:493:ALA:HB2	1.94	0.50
1:A:278:ARG:NH1	1:C:36:ASP:OD1	2.45	0.50
1:B:430:VAL:HG22	1:B:512:LEU:HD12	1.94	0.50
1:C:248:ALA:HB2	1:C:282:GLU:HG2	1.94	0.50
1:D:40:ILE:HD12	1:D:42:ALA:HB3	1.93	0.50
1:A:430:VAL:HG22	1:A:512:LEU:HD12	1.94	0.49
1:D:340:PRO:HG3	1:D:377:MET:HG2	1.94	0.49
1:C:423:CYS:HA	1:D:405:THR:O	2.11	0.49
1:A:40:ILE:HD12	1:A:42:ALA:HB3	1.93	0.49
1:A:392:LEU:HD11	1:B:400:ARG:HE	1.77	0.49
1:A:410:GLU:O	1:A:414:VAL:HG23	2.13	0.49
1:B:340:PRO:HG3	1:B:377:MET:HG2	1.94	0.49
1:B:410:GLU:O	1:B:414:VAL:HG23	2.13	0.49
1:D:410:GLU:O	1:D:414:VAL:HG23	2.13	0.49
1:A:118:GLU:OE2	1:A:120:ARG:NH1	2.46	0.48
1:C:410:GLU:O	1:C:414:VAL:HG23	2.13	0.48
1:A:243:SER:HA	1:A:270:LYS:HE2	1.95	0.48
1:A:466:TYR:HB2	1:A:469:ILE:HD12	1.95	0.48
1:A:248:ALA:HB2	1:A:282:GLU:HG2	1.95	0.48
1:D:430:VAL:HG22	1:D:512:LEU:HD12	1.94	0.48
1:B:40:ILE:HD12	1:B:42:ALA:HB3	1.95	0.48
1:C:170:VAL:HG13	1:C:186:LYS:O	2.13	0.48
1:D:64:MET:HE2	1:D:375:VAL:HG21	1.95	0.48
1:D:466:TYR:HB2	1:D:469:ILE:HD12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:48:ILE:HG12	1:D:71:VAL:HB	1.94	0.48
1:B:248:ALA:HB2	1:B:282:GLU:HG2	1.96	0.48
1:B:170:VAL:HG13	1:B:186:LYS:O	2.13	0.48
1:C:411:ALA:HB2	1:D:423:CYS:HB3	1.96	0.48
1:C:430:VAL:HG22	1:C:512:LEU:HD12	1.96	0.48
1:C:410:GLU:HG3	1:D:422:LYS:HE2	1.96	0.48
1:A:340:PRO:HG3	1:A:377:MET:HG2	1.96	0.47
1:A:480:GLU:OE1	1:A:481:ALA:N	2.47	0.47
1:B:293:ALA:HB1	2:B:533:OXL:C2	2.43	0.47
1:A:170:VAL:HG13	1:A:186:LYS:O	2.14	0.47
1:C:340:PRO:HG3	1:C:377:MET:HG2	1.95	0.47
1:A:327:ALA:HB1	1:A:360:MET:HE2	1.96	0.47
1:B:404:ILE:H	1:B:404:ILE:HG13	1.44	0.47
1:A:13:ILE:O	1:A:13:ILE:HG22	2.13	0.47
1:C:124:ILE:O	1:C:125:LYS:C	2.56	0.47
1:C:466:TYR:HB2	1:C:469:ILE:HD12	1.97	0.47
1:B:124:ILE:O	1:B:125:LYS:C	2.58	0.47
1:D:118:GLU:OE2	1:D:120:ARG:NH1	2.47	0.47
1:D:270:LYS:HD2	1:D:291:MET:SD	2.54	0.47
1:B:243:SER:HA	1:B:270:LYS:HE2	1.97	0.47
1:D:41:THR:HG21	7:D:553:HOH:O	2.14	0.47
1:D:106:ARG:HG2	7:D:562:HOH:O	2.14	0.47
1:D:327:ALA:HB1	1:D:360:MET:HE2	1.97	0.47
1:A:40:ILE:O	1:A:383:ARG:HD3	2.15	0.46
1:B:64:MET:HE2	1:B:375:VAL:HG21	1.96	0.46
1:B:384:GLU:HG2	7:B:561:HOH:O	2.15	0.46
1:D:170:VAL:HG13	1:D:186:LYS:O	2.16	0.46
1:D:248:ALA:HB2	1:D:282:GLU:HG2	1.97	0.46
1:A:274:HIS:HD2	1:A:278:ARG:NH2	2.03	0.46
1:D:255:ARG:NH1	7:D:559:HOH:O	2.45	0.46
1:A:132:VAL:HG21	1:A:153:ASP:HA	1.97	0.46
1:C:243:SER:HA	1:C:270:LYS:HE2	1.98	0.46
1:A:64:MET:HE2	1:A:375:VAL:HG21	1.97	0.46
1:A:379:HIS:HE2	1:A:383:ARG:HH11	1.62	0.46
1:D:379:HIS:HE2	1:D:383:ARG:NH1	2.13	0.45
1:D:132:VAL:HG21	1:D:153:ASP:HA	1.99	0.45
1:C:71:VAL:HG22	1:C:109:ALA:HB3	1.98	0.45
1:C:64:MET:HE2	1:C:375:VAL:HG21	1.98	0.45
1:D:325:ILE:HG12	1:D:358:CYS:HB2	1.98	0.44
1:A:48:ILE:HG12	1:A:71:VAL:HB	1.98	0.44
1:A:270:LYS:HD2	1:A:291:MET:SD	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:327:ALA:HB1	1:C:360:MET:HE2	1.98	0.44
1:A:55:SER:O	1:A:61:LEU:HD13	2.17	0.44
1:A:255:ARG:HG2	1:A:267:ILE:HD12	2.00	0.44
1:A:288:ASP:O	1:A:323:PRO:HD2	2.18	0.44
1:C:334:MET:HA	1:C:337:LYS:O	2.17	0.44
1:D:55:SER:O	1:D:61:LEU:HD13	2.17	0.44
1:A:270:LYS:NZ	2:A:533:OXL:O1	2.48	0.44
1:D:281:ASP:O	1:D:285:GLU:HB2	2.17	0.44
1:B:132:VAL:HG21	1:B:153:ASP:HA	1.99	0.44
1:B:281:ASP:O	1:B:285:GLU:HB2	2.18	0.44
1:A:416:ALA:HB2	1:A:512:LEU:HD21	2.00	0.43
1:B:48:ILE:HG12	1:B:71:VAL:HB	2.00	0.43
1:B:416:ALA:HB2	1:B:512:LEU:HD21	2.00	0.43
1:D:334:MET:HA	1:D:337:LYS:O	2.19	0.43
1:D:478:VAL:HG12	1:D:479:GLN:O	2.19	0.43
1:B:55:SER:O	1:B:61:LEU:HD13	2.18	0.43
1:C:132:VAL:HG21	1:C:153:ASP:HA	2.00	0.43
1:C:416:ALA:HB2	1:C:512:LEU:HD21	2.00	0.43
1:D:416:ALA:HB2	1:D:512:LEU:HD21	2.01	0.43
1:B:255:ARG:HG2	1:B:267:ILE:HD12	2.01	0.43
1:B:288:ASP:O	1:B:323:PRO:HD2	2.19	0.43
1:D:123:LEU:HD12	1:D:150:GLU:HG2	2.02	0.42
1:B:478:VAL:HG12	1:B:479:GLN:O	2.19	0.42
1:C:255:ARG:HG2	1:C:267:ILE:HD12	2.01	0.42
1:A:281:ASP:O	1:A:285:GLU:HB2	2.19	0.42
1:A:404:ILE:H	1:A:404:ILE:HG13	1.43	0.42
1:B:325:ILE:HG12	1:B:358:CYS:HB2	2.02	0.42
1:C:118:GLU:OE2	1:C:120:ARG:NH1	2.52	0.42
1:A:325:ILE:HG12	1:A:358:CYS:HB2	2.01	0.42
1:A:402:ALA:HB1	1:B:422:LYS:NZ	2.34	0.42
1:C:405:THR:HG22	1:D:422:LYS:HE3	2.00	0.42
1:A:125:LYS:HE2	1:A:125:LYS:HB3	1.16	0.41
1:C:48:ILE:HG12	1:C:71:VAL:HB	2.02	0.41
1:A:514:GLY:HA3	3:A:532:FBP:O3	2.20	0.41
1:A:399:ARG:HH21	1:B:399:ARG:HH21	1.67	0.41
1:B:334:MET:HA	1:B:337:LYS:O	2.20	0.41
1:A:418:GLU:HB2	1:B:418:GLU:HG2	2.03	0.41
1:B:472:VAL:HG21	1:B:496:VAL:HG11	2.02	0.41
1:B:478:VAL:C	1:B:479:GLN:O	2.64	0.41
1:A:418:GLU:HG2	1:B:418:GLU:HB2	2.02	0.41
1:B:22:MET:HE2	7:B:551:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:288:ASP:O	1:C:323:PRO:HD2	2.21	0.41
1:B:414:VAL:HG22	1:B:444:TYR:CZ	2.56	0.41
1:D:71:VAL:HG22	1:D:109:ALA:HB3	2.03	0.41
1:A:123:LEU:HD12	1:A:150:GLU:HG2	2.02	0.41
1:A:334:MET:HA	1:A:337:LYS:O	2.20	0.41
1:A:494:MET:HG3	1:A:530:VAL:HG13	2.02	0.41
1:A:480:GLU:N	1:A:480:GLU:OE1	2.46	0.40
1:D:163:ASN:OD1	1:D:166:LYS:HD2	2.20	0.40
1:B:71:VAL:HG22	1:B:109:ALA:HB3	2.02	0.40
1:D:21:ALA:CB	1:D:447:ARG:HH22	2.34	0.40
1:C:494:MET:HG3	1:C:530:VAL:HG13	2.02	0.40
1:C:55:SER:O	1:C:61:LEU:HD13	2.21	0.40
1:C:294:ARG:NH2	1:C:347:ASP:OD1	2.54	0.40
1:A:422:LYS:NZ	1:B:402:ALA:HB1	2.36	0.40
1:A:478:VAL:HG12	1:A:479:GLN:O	2.21	0.40
1:C:472:VAL:HG21	1:C:496:VAL:HG11	2.02	0.40
1:D:229:LEU:O	1:D:233:VAL:HG23	2.21	0.40
1:D:328:THR:HG22	1:D:329:GLN:HG3	2.03	0.40

There are no symmetry-related clashes.

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	511/551 (93%)	485 (95%)	24 (5%)	2 (0%)	30	59
1	B	508/551 (92%)	480 (94%)	26 (5%)	2 (0%)	30	59
1	C	510/551 (93%)	480 (94%)	30 (6%)	0	100	100
1	D	512/551 (93%)	483 (94%)	26 (5%)	3 (1%)	21	51
All	All	2041/2204 (93%)	1928 (94%)	106 (5%)	7 (0%)	36	65

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	125	LYS
1	B	479	GLN
1	D	479	GLN
1	A	479	GLN
1	A	328	THR
1	B	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	425/453 (94%)	404 (95%)	21 (5%)	22	54
1	B	423/453 (93%)	406 (96%)	17 (4%)	28	62
1	C	425/453 (94%)	407 (96%)	18 (4%)	26	60
1	D	425/453 (94%)	408 (96%)	17 (4%)	28	62
All	All	1698/1812 (94%)	1625 (96%)	73 (4%)	26	60

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ILE
1	A	15	THR
1	A	82	GLU
1	A	92	ARG
1	A	125	LYS
1	A	143	THR
1	A	163	ASN
1	A	261	LYS
1	A	287	SER
1	A	304	GLU
1	A	319	ARG
1	A	396	GLU
1	A	404	ILE
1	A	409	THR
1	A	436	ARG

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Mol	Chain	Res	Type
1	A	467	ARG
1	A	472	VAL
1	A	480	GLU
1	A	484	GLU
1	A	509	VAL
1	A	516	ARG
1	B	82	GLU
1	B	143	THR
1	B	163	ASN
1	B	261	LYS
1	B	287	SER
1	B	304	GLU
1	B	319	ARG
1	B	396	GLU
1	B	404	ILE
1	B	409	THR
1	B	436	ARG
1	B	467	ARG
1	B	472	VAL
1	B	480	GLU
1	B	484	GLU
1	B	509	VAL
1	B	516	ARG
1	C	82	GLU
1	C	143	THR
1	C	163	ASN
1	C	261	LYS
1	C	285	GLU
1	C	287	SER
1	C	304	GLU
1	C	319	ARG
1	C	396	GLU
1	C	404	ILE
1	C	409	THR
1	C	436	ARG
1	C	467	ARG
1	C	472	VAL
1	C	480	GLU
1	C	484	GLU
1	C	509	VAL
1	C	516	ARG
1	D	82	GLU

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Mol	Chain	Res	Type
1	D	143	THR
1	D	163	ASN
1	D	261	LYS
1	D	278	ARG
1	D	287	SER
1	D	304	GLU
1	D	319	ARG
1	D	396	GLU
1	D	404	ILE
1	D	409	THR
1	D	467	ARG
1	D	472	VAL
1	D	480	GLU
1	D	484	GLU
1	D	509	VAL
1	D	516	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	ASN
1	A	274	HIS
1	A	318	ASN
1	A	378	GLN
1	A	439	HIS
1	A	479	GLN
1	B	78	HIS
1	B	146	ASN
1	B	274	HIS
1	B	318	ASN
1	B	378	GLN
1	B	479	GLN
1	C	78	HIS
1	C	146	ASN
1	C	318	ASN
1	C	378	GLN
1	C	439	HIS
1	C	479	GLN
1	D	78	HIS
1	D	84	HIS
1	D	146	ASN
1	D	274	HIS

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Mol	Chain	Res	Type
1	D	318	ASN
1	D	479	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 20 ligands modelled in this entry, 7 are monoatomic - leaving 13 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	$\# Z > 2$
3	FBP	B	532	-	18,20,20	0.93	1 (5%)	21,32,32	0.63	0
6	GOL	D	534	-	5,5,5	0.36	0	5,5,5	0.22	0
3	FBP	D	532	-	18,20,20	0.95	1 (5%)	21,32,32	0.90	1 (4%)
6	GOL	D	535	-	5,5,5	0.36	0	5,5,5	0.44	0
2	OXL	D	533	5	5,5,5	1.53	1 (20%)	6,6,6	2.03	2 (33%)
6	GOL	B	534	-	5,5,5	0.37	0	5,5,5	0.28	0
6	GOL	C	534	-	5,5,5	0.41	0	5,5,5	0.20	0
3	FBP	C	532	-	18,20,20	0.90	1 (5%)	21,32,32	0.78	1 (4%)
3	FBP	A	532	-	18,20,20	0.94	1 (5%)	21,32,32	0.69	0
2	OXL	C	533	5	5,5,5	1.41	0	6,6,6	1.64	2 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	GOL	A	536	-	5,5,5	0.38	0	5,5,5	0.27	0
2	OXL	A	533	5	5,5,5	1.32	0	6,6,6	1.88	2 (33%)
2	OXL	B	533	5	5,5,5	1.40	0	6,6,6	1.79	2 (33%)

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
3	FBP	B	532	-	-	8/13/32/32	0/1/1/1
6	GOL	D	534	-	-	0/4/4/4	-
3	FBP	D	532	-	-	6/13/32/32	0/1/1/1
6	GOL	D	535	-	-	4/4/4/4	-
2	OXL	D	533	5	-	0/4/4/4	-
6	GOL	B	534	-	-	2/4/4/4	-
6	GOL	C	534	-	-	2/4/4/4	-
3	FBP	C	532	-	-	4/13/32/32	0/1/1/1
3	FBP	A	532	-	-	4/13/32/32	0/1/1/1
2	OXL	C	533	5	-	0/4/4/4	-
6	GOL	A	536	-	-	1/4/4/4	-
2	OXL	A	533	5	-	0/4/4/4	-
2	OXL	B	533	5	-	0/4/4/4	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	532	FBP	O2-C2	2.90	1.45	1.40
3	D	532	FBP	O2-C2	2.76	1.45	1.40
3	A	532	FBP	O2-C2	2.75	1.45	1.40
3	C	532	FBP	O2-C2	2.71	1.45	1.40
2	D	533	OXL	O4-C2	-2.31	1.24	1.30

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	533	OXL	O3-C1-C2	4.11	120.80	112.83
2	A	533	OXL	O3-C1-C2	3.25	119.13	112.83
2	B	533	OXL	O3-C1-C2	2.92	118.49	112.83
2	C	533	OXL	O3-C1-C2	2.61	117.90	112.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	533	OXL	O1-C1-C2	-2.61	115.19	120.63
2	A	533	OXL	O4-C2-C1	2.55	117.78	112.83
3	D	532	FBP	O5-C5-C6	2.45	115.26	109.50
2	C	533	OXL	O4-C2-C1	2.35	117.39	112.83
2	B	533	OXL	O4-C2-C1	2.27	117.22	112.83
3	C	532	FBP	O6P-P2-O6	2.25	112.53	106.67

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	532	FBP	C6-O6-P2-O5P
3	A	532	FBP	C6-O6-P2-O6P
3	B	532	FBP	O1-C1-C2-O2
3	B	532	FBP	O1-C1-C2-C3
3	B	532	FBP	O1-C1-C2-O5
3	B	532	FBP	C6-O6-P2-O5P
3	B	532	FBP	C6-O6-P2-O6P
3	C	532	FBP	C6-O6-P2-O4P
3	D	532	FBP	O1-C1-C2-O2
3	D	532	FBP	O1-C1-C2-C3
3	D	532	FBP	O1-C1-C2-O5
3	D	532	FBP	C6-O6-P2-O5P
6	C	534	GOL	O1-C1-C2-O2
6	C	534	GOL	O1-C1-C2-C3
6	D	535	GOL	C1-C2-C3-O3
3	A	532	FBP	C4-C5-C6-O6
3	D	532	FBP	C4-C5-C6-O6
6	B	534	GOL	O1-C1-C2-C3
6	D	535	GOL	O2-C2-C3-O3
3	B	532	FBP	C4-C5-C6-O6
3	B	532	FBP	O5-C5-C6-O6
3	D	532	FBP	O5-C5-C6-O6
3	A	532	FBP	O5-C5-C6-O6
6	B	534	GOL	O1-C1-C2-O2
3	C	532	FBP	C4-C5-C6-O6
6	A	536	GOL	O2-C2-C3-O3
6	D	535	GOL	O1-C1-C2-O2
3	C	532	FBP	C6-O6-P2-O5P
6	D	535	GOL	O1-C1-C2-C3
3	B	532	FBP	C6-O6-P2-O4P
3	C	532	FBP	C6-O6-P2-O6P

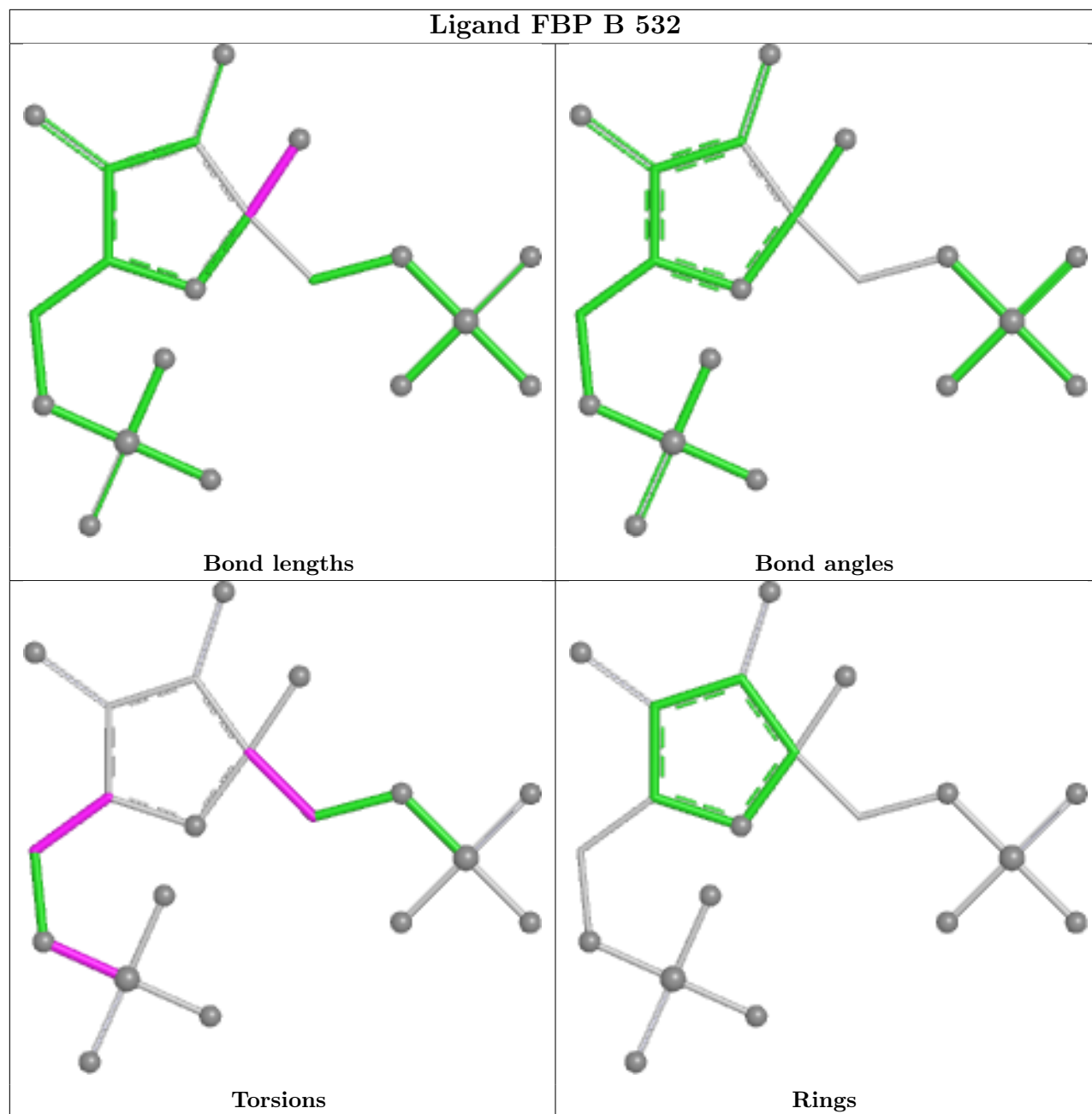
There are no ring outliers.

6 monomers are involved in 7 short contacts:

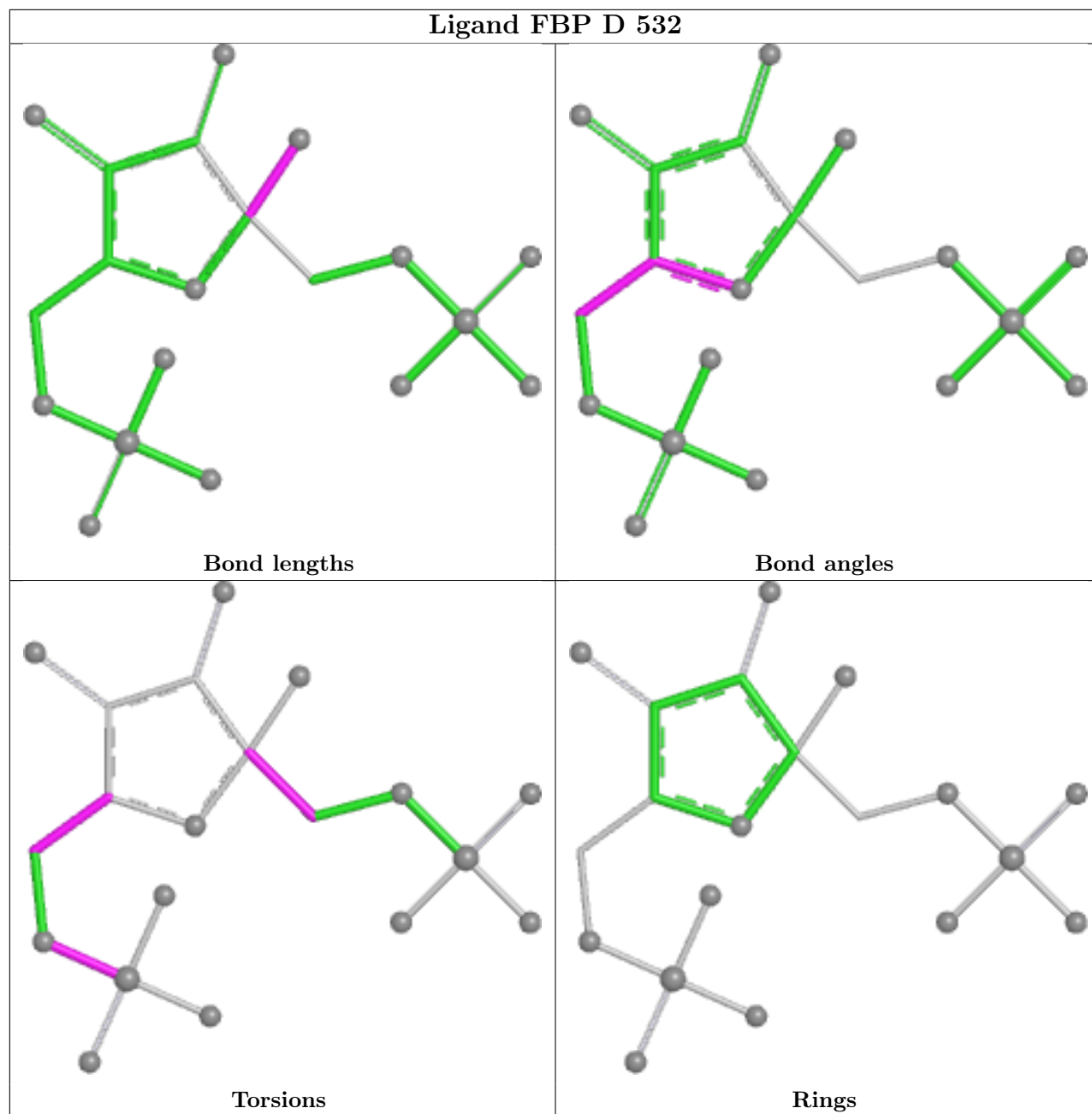
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	532	FBP	1	0
3	D	532	FBP	2	0
6	D	535	GOL	1	0
3	A	532	FBP	1	0
2	A	533	OXL	1	0
2	B	533	OXL	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

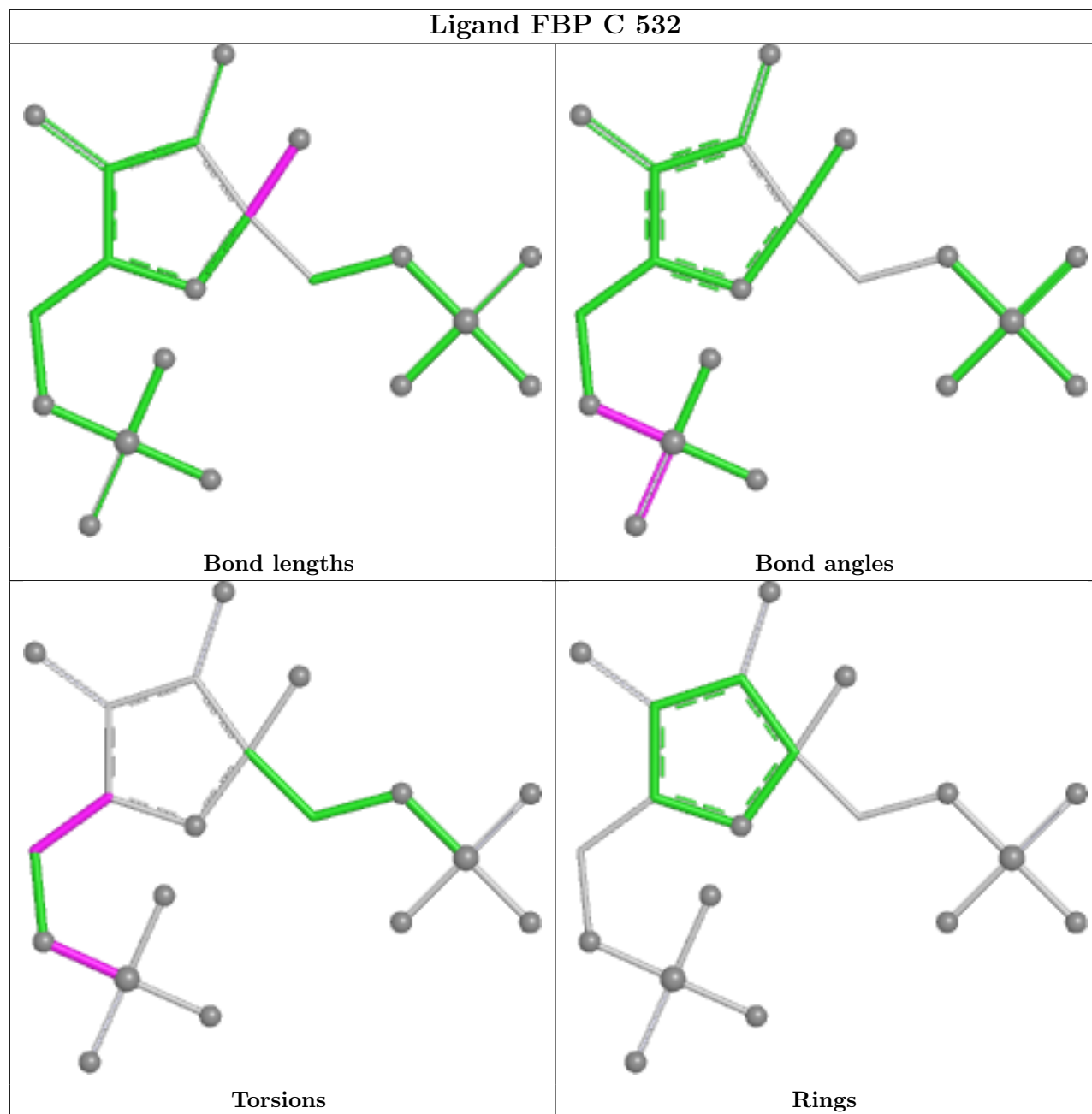
Ligand FBP B 532

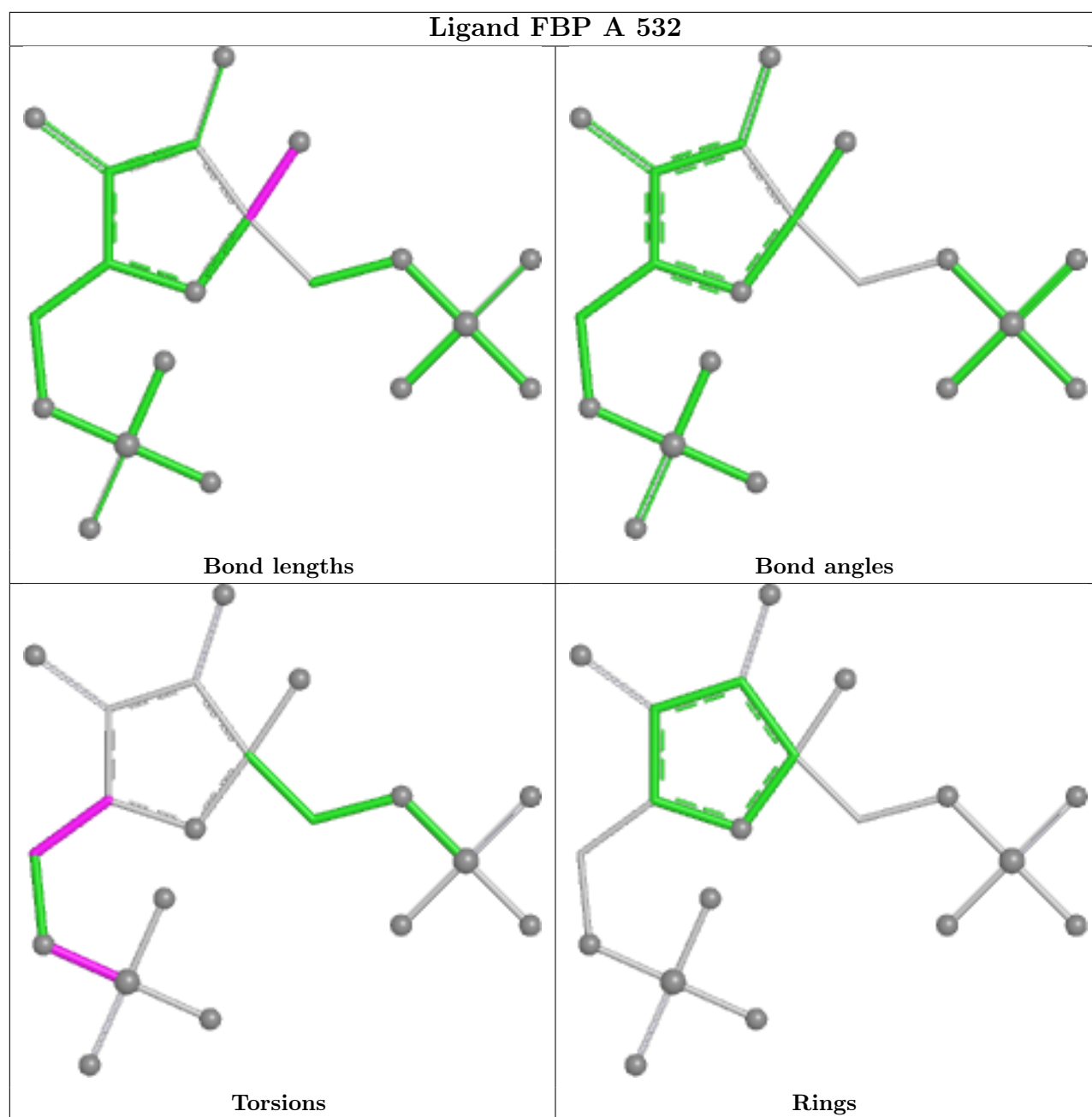


Ligand FBP D 532



Ligand FBP C 532





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	515/551 (93%)	0.45	16 (3%)	51	42	39, 71, 101, 149	0
1	B	512/551 (92%)	0.68	18 (3%)	47	38	48, 82, 127, 160	0
1	C	514/551 (93%)	0.50	13 (2%)	58	48	46, 77, 108, 161	0
1	D	515/551 (93%)	0.38	8 (1%)	70	62	38, 69, 107, 148	1 (0%)
All	All	2056/2204 (93%)	0.50	55 (2%)	56	47	38, 75, 114, 161	1 (0%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	18	LEU	3.5
1	C	17	GLN	3.3
1	B	134	LEU	3.1
1	B	139	THR	3.0
1	D	138	ALA	3.0
1	C	15	THR	3.0
1	B	17	GLN	3.0
1	D	404	ILE	3.0
1	A	126	GLY	2.8
1	D	143	THR	2.8
1	B	159	LEU	2.8
1	A	203	LEU	2.8
1	C	13	ILE	2.7
1	A	132	VAL	2.7
1	B	472	VAL	2.7
1	B	180	LEU	2.7
1	C	143	THR	2.7
1	B	203	LEU	2.7
1	C	134	LEU	2.7
1	A	134	LEU	2.6
1	C	440	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	440	GLN	2.5
1	A	147	ALA	2.5
1	C	168	VAL	2.5
1	A	15	THR	2.4
1	B	18	LEU	2.4
1	C	21	ALA	2.4
1	C	18	LEU	2.4
1	B	215	ALA	2.4
1	B	15	THR	2.4
1	A	156	ILE	2.4
1	B	470	PHE	2.3
1	A	478	VAL	2.3
1	B	157	LEU	2.3
1	A	40	ILE	2.3
1	D	278	ARG	2.3
1	A	124	ILE	2.3
1	B	60	THR	2.3
1	D	41	THR	2.3
1	C	470	PHE	2.2
1	A	150	GLU	2.2
1	C	26	PHE	2.2
1	B	471	PRO	2.2
1	A	13	ILE	2.2
1	B	16	GLN	2.1
1	A	528	VAL	2.1
1	C	240	VAL	2.1
1	A	506	GLY	2.1
1	A	123	LEU	2.1
1	B	76	PHE	2.1
1	D	157	LEU	2.1
1	D	35	ILE	2.1
1	C	82	GLU	2.1
1	B	47	ILE	2.0
1	B	143	THR	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

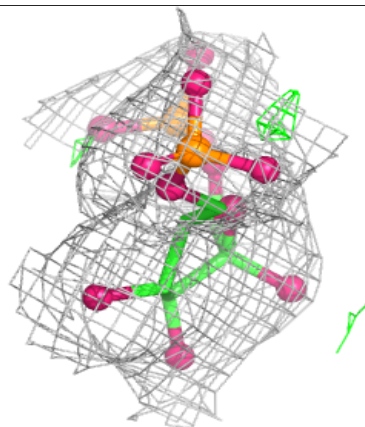
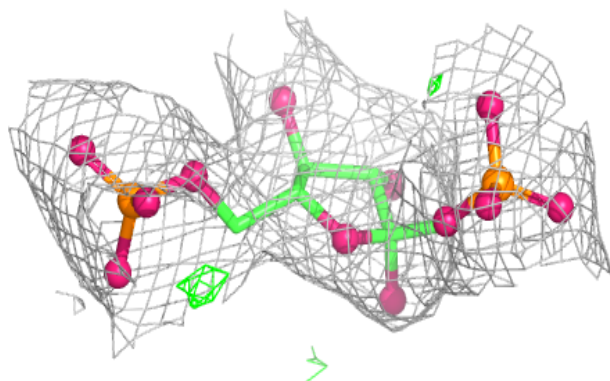
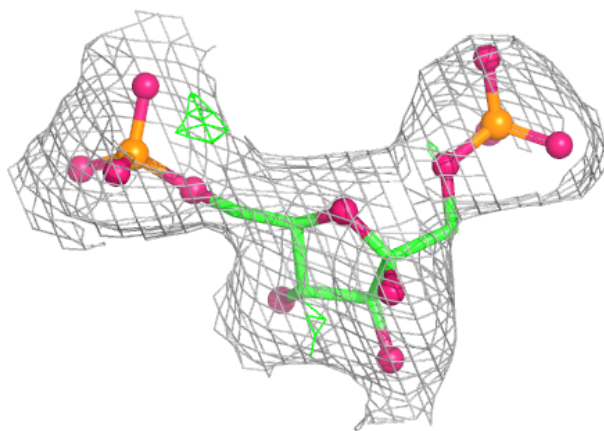
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MG	B	602	1/1	0.63	0.16	133,133,133,133	0
3	FBP	B	532	20/20	0.86	0.11	70,74,78,79	0
4	K	C	703	1/1	0.88	0.09	78,78,78,78	0
2	OXL	B	533	6/6	0.88	0.11	82,83,84,84	0
6	GOL	A	536	6/6	0.88	0.13	67,68,68,69	0
6	GOL	C	534	6/6	0.88	0.12	72,72,73,73	0
6	GOL	B	534	6/6	0.89	0.11	55,58,59,60	0
2	OXL	D	533	6/6	0.89	0.12	42,43,43,43	0
6	GOL	D	535	6/6	0.89	0.16	60,61,61,61	0
2	OXL	A	533	6/6	0.90	0.09	52,52,53,53	0
3	FBP	C	532	20/20	0.90	0.09	71,77,81,81	0
6	GOL	D	534	6/6	0.91	0.11	65,66,67,67	0
5	MG	D	604	1/1	0.91	0.09	53,53,53,53	0
4	K	D	704	1/1	0.92	0.07	64,64,64,64	0
3	FBP	A	532	20/20	0.92	0.08	71,72,76,76	0
2	OXL	C	533	6/6	0.93	0.09	66,66,66,66	0
3	FBP	D	532	20/20	0.95	0.07	62,63,66,66	0
5	MG	A	535	1/1	0.96	0.07	31,31,31,31	0
5	MG	C	603	1/1	0.97	0.06	50,50,50,50	0
4	K	A	534	1/1	0.99	0.02	56,56,56,56	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.

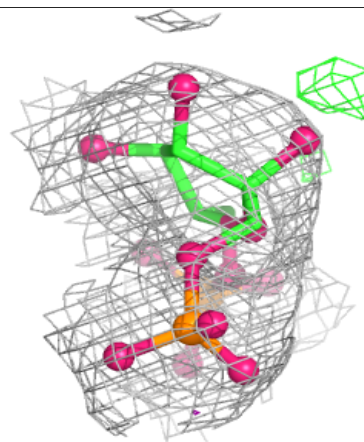
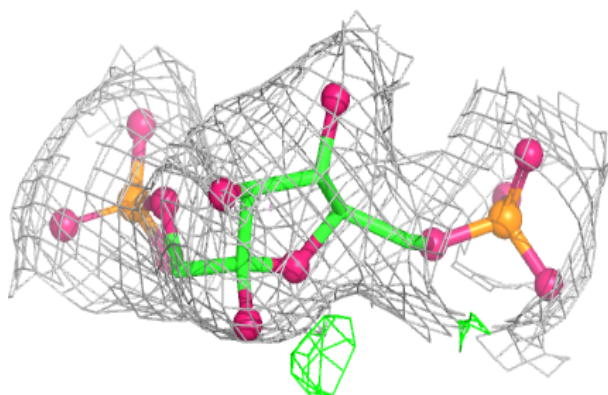
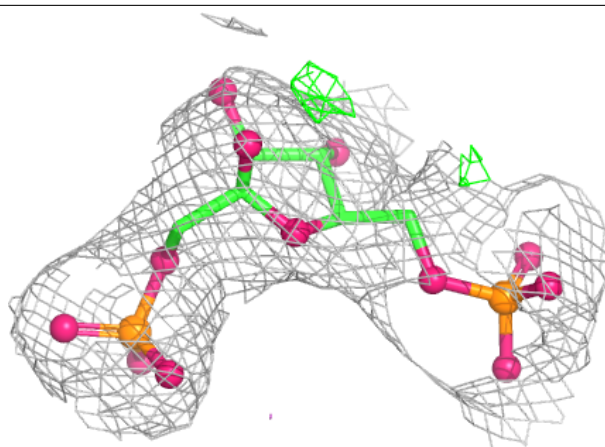
Electron density around FBP B 532:

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



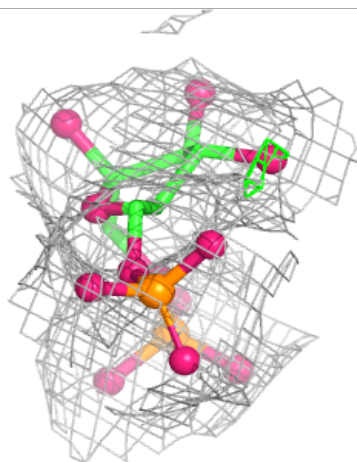
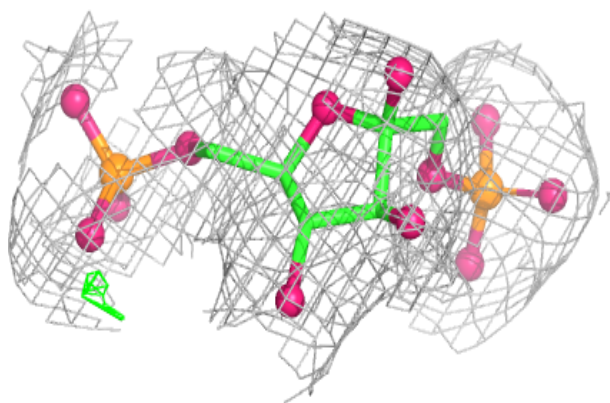
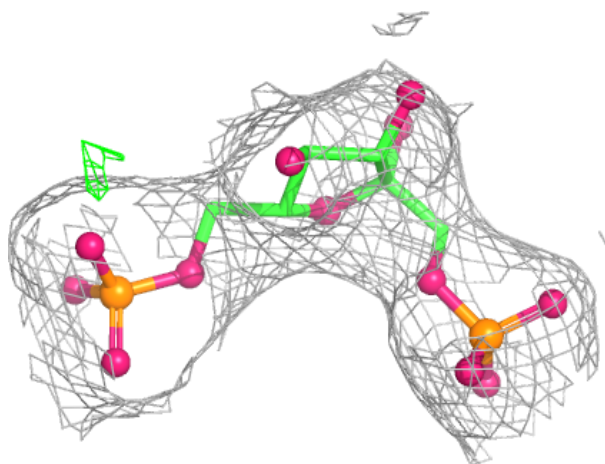
Electron density around FBP C 532:

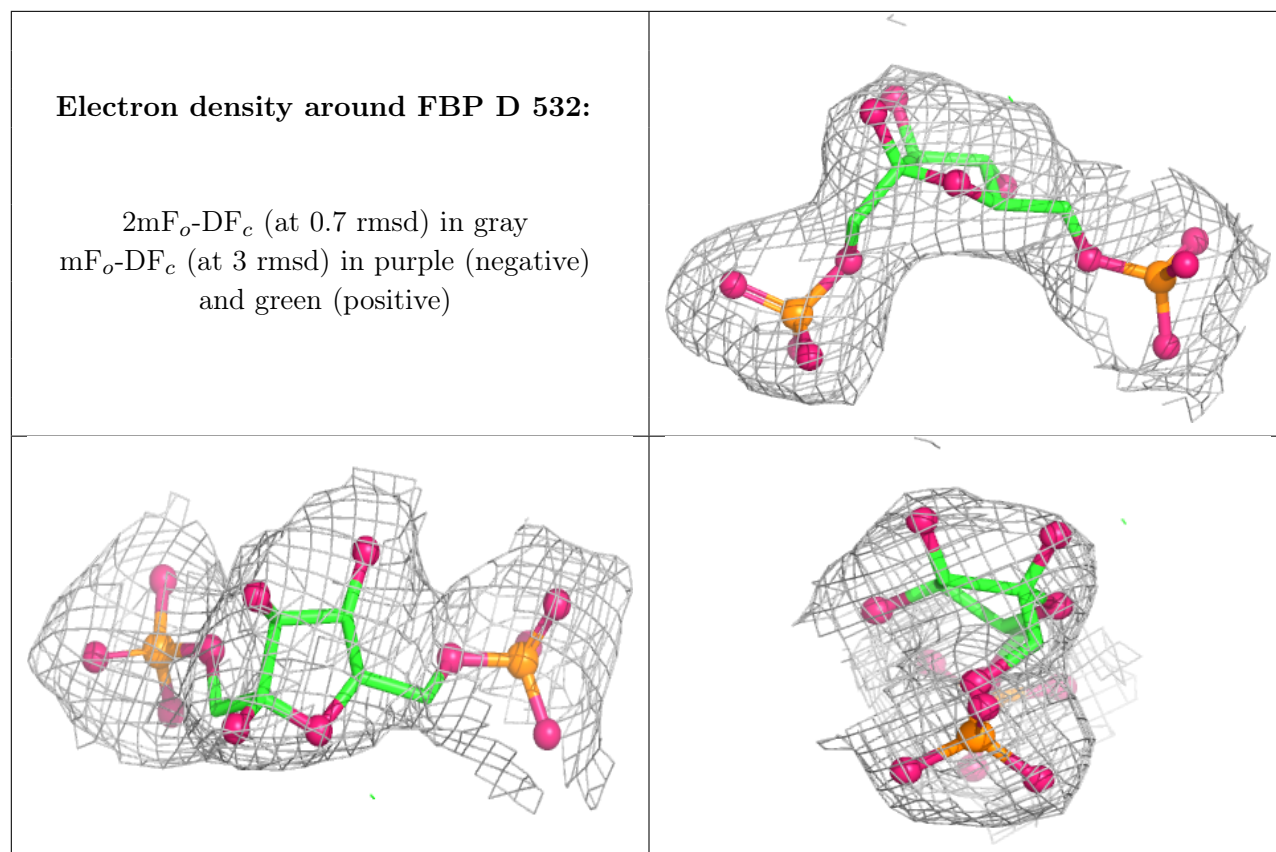
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FBP A 532:

$2mF_o-DF_c$ (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.