



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:32 PM UTC

PDB ID : 1T5A / pdb_00001t5a
Title : Human Pyruvate Kinase M2
Authors : Dombrauckas, J.D.; Santarsiero, B.D.; Mesecar, A.D.
Deposited on : 2004-05-03
Resolution : 2.80 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

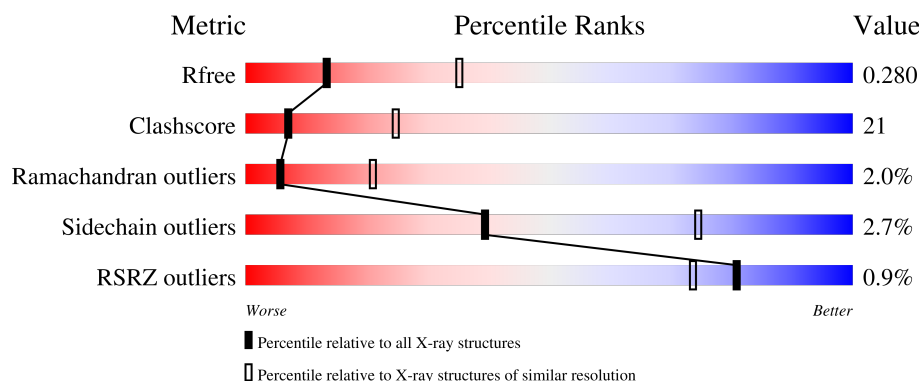
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	567	56% 32% • 8%
1	B	567	59% 29% • 8%
1	C	567	57% 31% • 8%
1	D	567	57% 31% • 8%

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
3	OXL	C	533	-	-	X	-
7	GOL	C	707	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 16271 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, M2 isozyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	519	Total	C	N	O	S	0	0	0
			3971	2496	704	746	25			
1	B	519	Total	C	N	O	S	0	0	0
			3971	2496	704	746	25			
1	C	519	Total	C	N	O	S	0	0	0
			3971	2496	704	746	25			
1	D	519	Total	C	N	O	S	0	0	0
			3971	2496	704	746	25			

There are 148 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-35	MET	-	cloning artifact	UNP P14618
A	-34	ARG	-	cloning artifact	UNP P14618
A	-33	GLY	-	cloning artifact	UNP P14618
A	-32	SER	-	cloning artifact	UNP P14618
A	-31	HIS	-	cloning artifact	UNP P14618
A	-30	HIS	-	cloning artifact	UNP P14618
A	-29	HIS	-	cloning artifact	UNP P14618
A	-28	HIS	-	cloning artifact	UNP P14618
A	-27	HIS	-	cloning artifact	UNP P14618
A	-26	HIS	-	cloning artifact	UNP P14618
A	-25	GLY	-	cloning artifact	UNP P14618
A	-24	MET	-	cloning artifact	UNP P14618
A	-23	ALA	-	cloning artifact	UNP P14618
A	-22	SER	-	cloning artifact	UNP P14618
A	-21	MET	-	cloning artifact	UNP P14618
A	-20	THR	-	cloning artifact	UNP P14618
A	-19	GLY	-	cloning artifact	UNP P14618
A	-18	GLY	-	cloning artifact	UNP P14618
A	-17	GLN	-	cloning artifact	UNP P14618
A	-16	GLN	-	cloning artifact	UNP P14618
A	-15	MET	-	cloning artifact	UNP P14618

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	GLY	-	cloning artifact	UNP P14618
A	-13	ARG	-	cloning artifact	UNP P14618
A	-12	ASP	-	cloning artifact	UNP P14618
A	-11	LEU	-	cloning artifact	UNP P14618
A	-10	TYR	-	cloning artifact	UNP P14618
A	-9	ASP	-	cloning artifact	UNP P14618
A	-8	ASP	-	cloning artifact	UNP P14618
A	-7	ASP	-	cloning artifact	UNP P14618
A	-6	ASP	-	cloning artifact	UNP P14618
A	-5	LYS	-	cloning artifact	UNP P14618
A	-4	ASP	-	cloning artifact	UNP P14618
A	-3	HIS	-	cloning artifact	UNP P14618
A	-2	PRO	-	cloning artifact	UNP P14618
A	-1	PHE	-	cloning artifact	UNP P14618
A	0	THR	-	cloning artifact	UNP P14618
A	1	MET	-	initiating methionine	UNP P14618
B	-35	MET	-	cloning artifact	UNP P14618
B	-34	ARG	-	cloning artifact	UNP P14618
B	-33	GLY	-	cloning artifact	UNP P14618
B	-32	SER	-	cloning artifact	UNP P14618
B	-31	HIS	-	cloning artifact	UNP P14618
B	-30	HIS	-	cloning artifact	UNP P14618
B	-29	HIS	-	cloning artifact	UNP P14618
B	-28	HIS	-	cloning artifact	UNP P14618
B	-27	HIS	-	cloning artifact	UNP P14618
B	-26	HIS	-	cloning artifact	UNP P14618
B	-25	GLY	-	cloning artifact	UNP P14618
B	-24	MET	-	cloning artifact	UNP P14618
B	-23	ALA	-	cloning artifact	UNP P14618
B	-22	SER	-	cloning artifact	UNP P14618
B	-21	MET	-	cloning artifact	UNP P14618
B	-20	THR	-	cloning artifact	UNP P14618
B	-19	GLY	-	cloning artifact	UNP P14618
B	-18	GLY	-	cloning artifact	UNP P14618
B	-17	GLN	-	cloning artifact	UNP P14618
B	-16	GLN	-	cloning artifact	UNP P14618
B	-15	MET	-	cloning artifact	UNP P14618
B	-14	GLY	-	cloning artifact	UNP P14618
B	-13	ARG	-	cloning artifact	UNP P14618
B	-12	ASP	-	cloning artifact	UNP P14618
B	-11	LEU	-	cloning artifact	UNP P14618
B	-10	TYR	-	cloning artifact	UNP P14618

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-9	ASP	-	cloning artifact	UNP P14618
B	-8	ASP	-	cloning artifact	UNP P14618
B	-7	ASP	-	cloning artifact	UNP P14618
B	-6	ASP	-	cloning artifact	UNP P14618
B	-5	LYS	-	cloning artifact	UNP P14618
B	-4	ASP	-	cloning artifact	UNP P14618
B	-3	HIS	-	cloning artifact	UNP P14618
B	-2	PRO	-	cloning artifact	UNP P14618
B	-1	PHE	-	cloning artifact	UNP P14618
B	0	THR	-	cloning artifact	UNP P14618
B	1	MET	-	initiating methionine	UNP P14618
C	-35	MET	-	cloning artifact	UNP P14618
C	-34	ARG	-	cloning artifact	UNP P14618
C	-33	GLY	-	cloning artifact	UNP P14618
C	-32	SER	-	cloning artifact	UNP P14618
C	-31	HIS	-	cloning artifact	UNP P14618
C	-30	HIS	-	cloning artifact	UNP P14618
C	-29	HIS	-	cloning artifact	UNP P14618
C	-28	HIS	-	cloning artifact	UNP P14618
C	-27	HIS	-	cloning artifact	UNP P14618
C	-26	HIS	-	cloning artifact	UNP P14618
C	-25	GLY	-	cloning artifact	UNP P14618
C	-24	MET	-	cloning artifact	UNP P14618
C	-23	ALA	-	cloning artifact	UNP P14618
C	-22	SER	-	cloning artifact	UNP P14618
C	-21	MET	-	cloning artifact	UNP P14618
C	-20	THR	-	cloning artifact	UNP P14618
C	-19	GLY	-	cloning artifact	UNP P14618
C	-18	GLY	-	cloning artifact	UNP P14618
C	-17	GLN	-	cloning artifact	UNP P14618
C	-16	GLN	-	cloning artifact	UNP P14618
C	-15	MET	-	cloning artifact	UNP P14618
C	-14	GLY	-	cloning artifact	UNP P14618
C	-13	ARG	-	cloning artifact	UNP P14618
C	-12	ASP	-	cloning artifact	UNP P14618
C	-11	LEU	-	cloning artifact	UNP P14618
C	-10	TYR	-	cloning artifact	UNP P14618
C	-9	ASP	-	cloning artifact	UNP P14618
C	-8	ASP	-	cloning artifact	UNP P14618
C	-7	ASP	-	cloning artifact	UNP P14618
C	-6	ASP	-	cloning artifact	UNP P14618
C	-5	LYS	-	cloning artifact	UNP P14618

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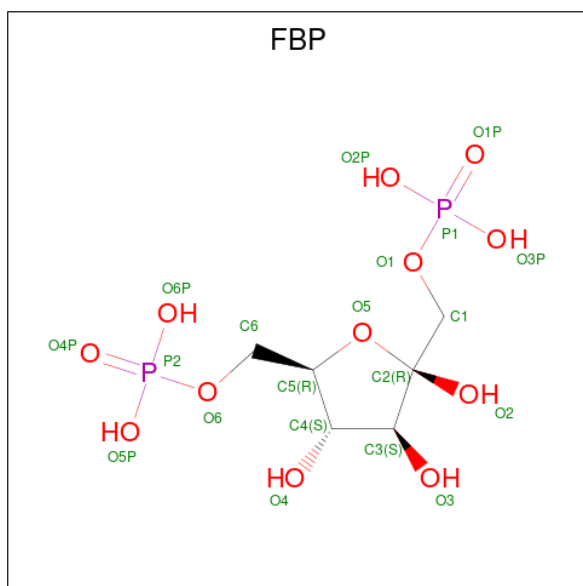
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C	-4	ASP	-	cloning artifact	UNP P14618
C	-3	HIS	-	cloning artifact	UNP P14618
C	-2	PRO	-	cloning artifact	UNP P14618
C	-1	PHE	-	cloning artifact	UNP P14618
C	0	THR	-	cloning artifact	UNP P14618
C	1	MET	-	initiating methionine	UNP P14618
D	-35	MET	-	cloning artifact	UNP P14618
D	-34	ARG	-	cloning artifact	UNP P14618
D	-33	GLY	-	cloning artifact	UNP P14618
D	-32	SER	-	cloning artifact	UNP P14618
D	-31	HIS	-	cloning artifact	UNP P14618
D	-30	HIS	-	cloning artifact	UNP P14618
D	-29	HIS	-	cloning artifact	UNP P14618
D	-28	HIS	-	cloning artifact	UNP P14618
D	-27	HIS	-	cloning artifact	UNP P14618
D	-26	HIS	-	cloning artifact	UNP P14618
D	-25	GLY	-	cloning artifact	UNP P14618
D	-24	MET	-	cloning artifact	UNP P14618
D	-23	ALA	-	cloning artifact	UNP P14618
D	-22	SER	-	cloning artifact	UNP P14618
D	-21	MET	-	cloning artifact	UNP P14618
D	-20	THR	-	cloning artifact	UNP P14618
D	-19	GLY	-	cloning artifact	UNP P14618
D	-18	GLY	-	cloning artifact	UNP P14618
D	-17	GLN	-	cloning artifact	UNP P14618
D	-16	GLN	-	cloning artifact	UNP P14618
D	-15	MET	-	cloning artifact	UNP P14618
D	-14	GLY	-	cloning artifact	UNP P14618
D	-13	ARG	-	cloning artifact	UNP P14618
D	-12	ASP	-	cloning artifact	UNP P14618
D	-11	LEU	-	cloning artifact	UNP P14618
D	-10	TYR	-	cloning artifact	UNP P14618
D	-9	ASP	-	cloning artifact	UNP P14618
D	-8	ASP	-	cloning artifact	UNP P14618
D	-7	ASP	-	cloning artifact	UNP P14618
D	-6	ASP	-	cloning artifact	UNP P14618
D	-5	LYS	-	cloning artifact	UNP P14618
D	-4	ASP	-	cloning artifact	UNP P14618
D	-3	HIS	-	cloning artifact	UNP P14618
D	-2	PRO	-	cloning artifact	UNP P14618
D	-1	PHE	-	cloning artifact	UNP P14618
D	0	THR	-	cloning artifact	UNP P14618

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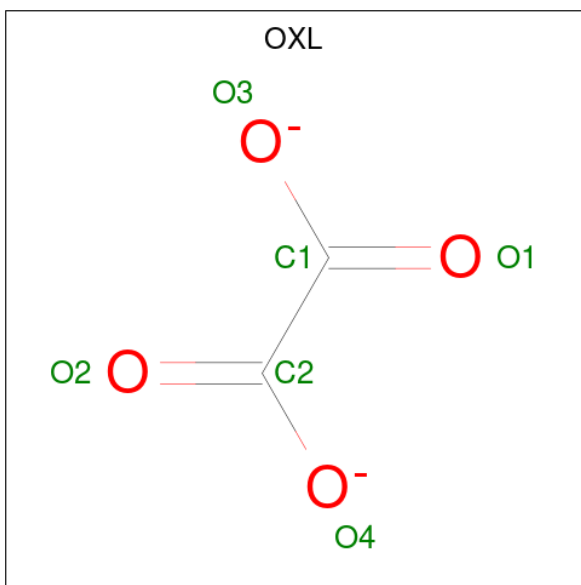
Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	-	initiating methionine	UNP P14618

- Molecule 2 is 1,6-di-O-phosphono-beta-D-fructofuranose (CCD ID: FBP) (formula: $C_6H_{14}O_{12}P_2$).



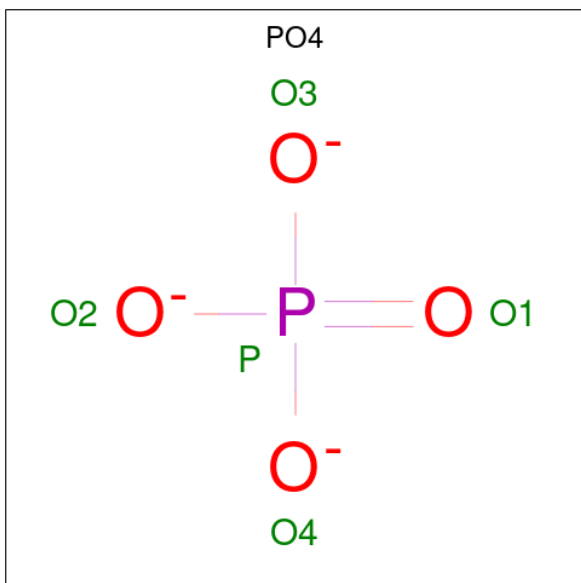
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			20	6	12	2		
2	B	1	Total	C	O	P	0	0
			20	6	12	2		
2	C	1	Total	C	O	P	0	0
			20	6	12	2		
2	D	1	Total	C	O	P	0	0
			20	6	12	2		

- Molecule 3 is OXALATE ION (CCD ID: OXL) (formula: C_2O_4).



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

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



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

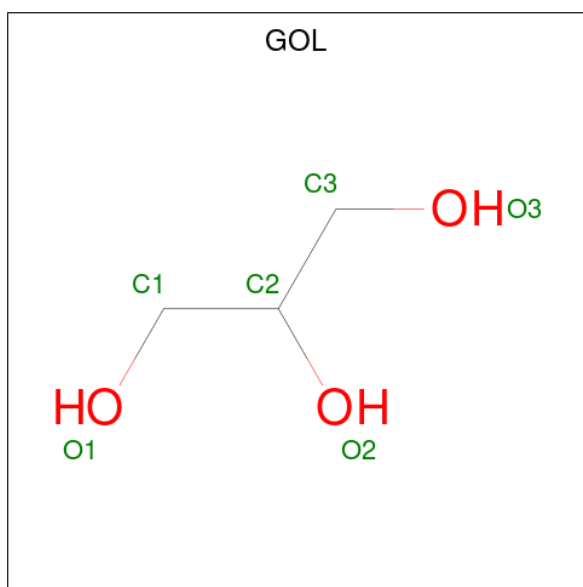
- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 6 is POTASSIUM ION (CCD ID: K) (formula: K).

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

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

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

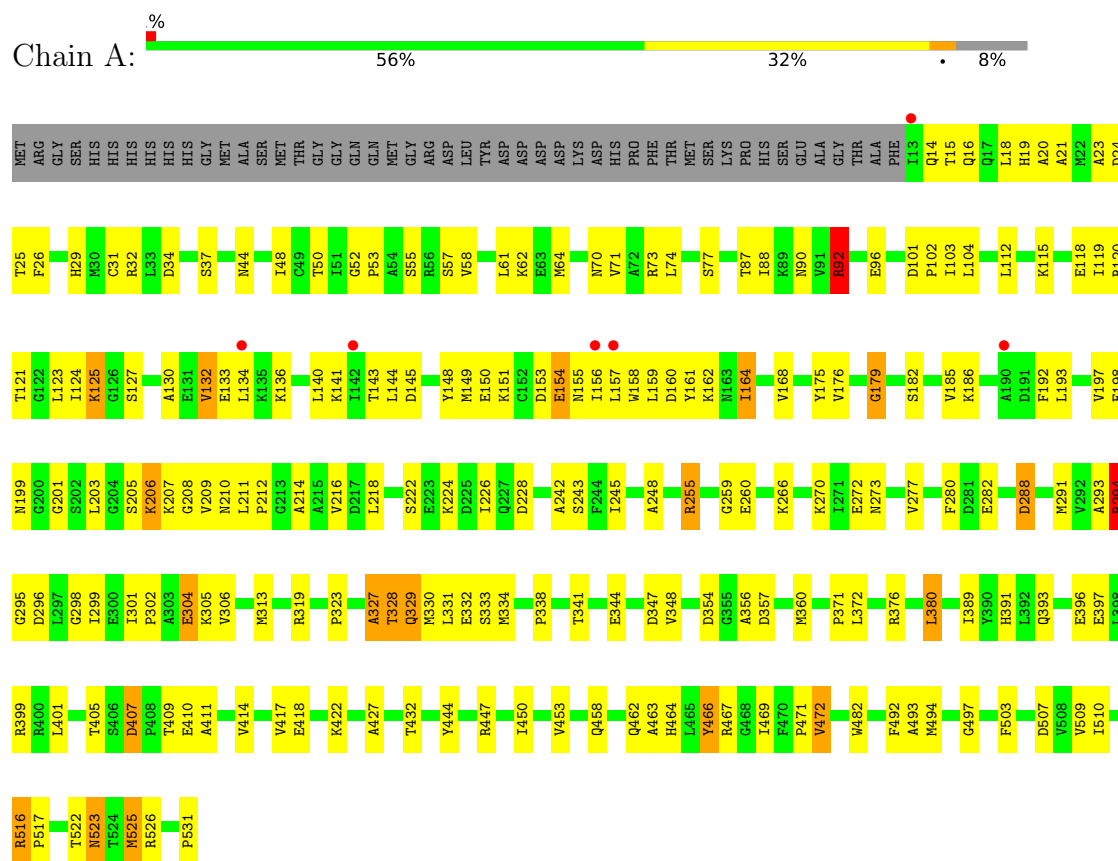
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	47	Total	O	0	0
			47	47		
8	B	28	Total	O	0	0
			28	28		
8	C	30	Total	O	0	0
			30	30		
8	D	30	Total	O	0	0
			30	30		

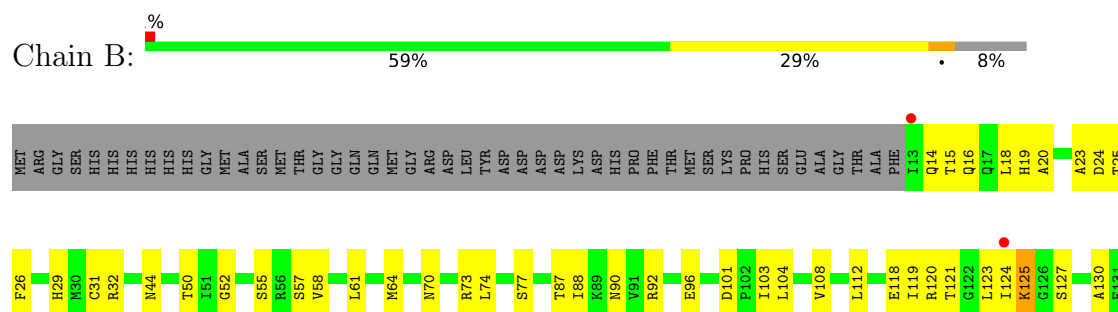
3 Residue-property plots

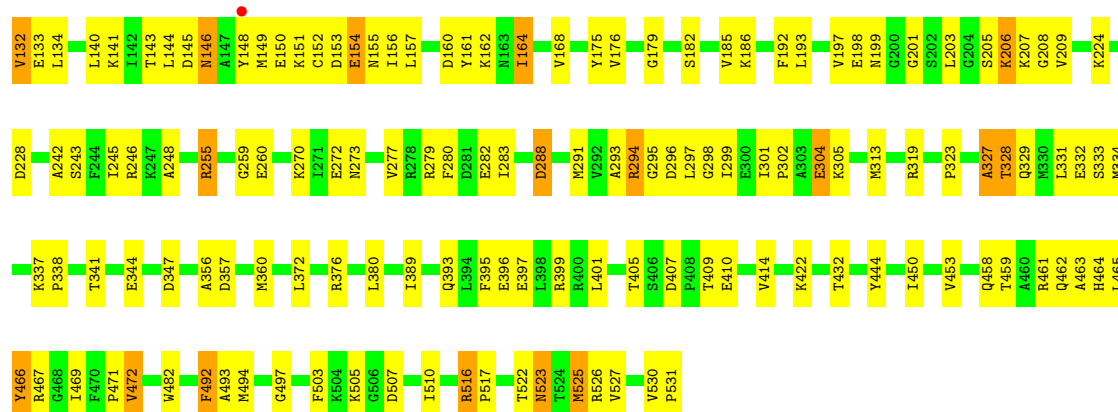
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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, M2 isozyme

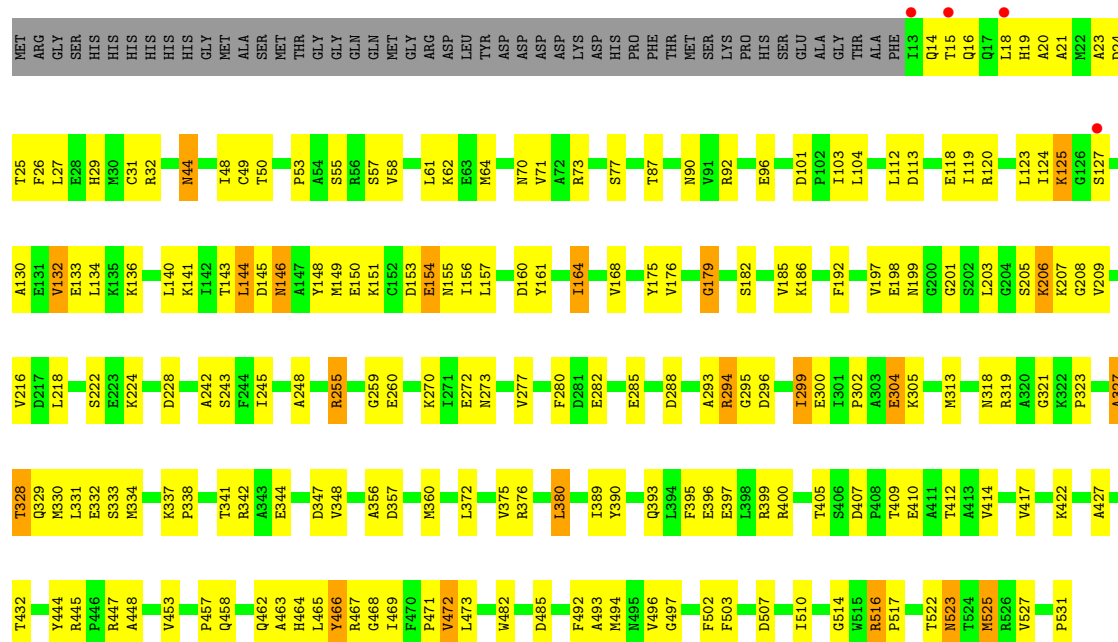


• Molecule 1: Pyruvate kinase, M2 isozyme

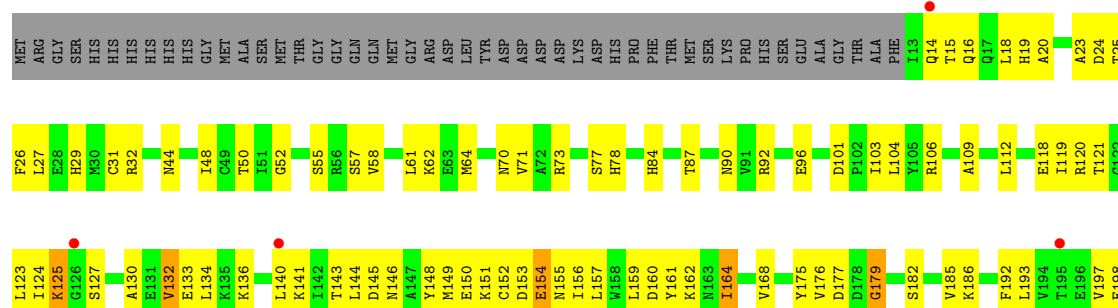


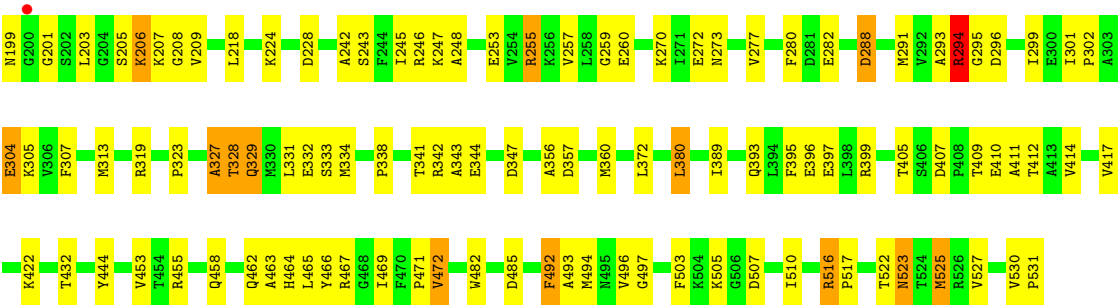


• Molecule 1: Pyruvate kinase, M2 isozyme



• Molecule 1: Pyruvate kinase, M2 isozyme





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	108.21Å 145.01Å 159.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80 20.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.4 (20.00-2.80) 96.2 (20.00-2.80)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.25 (at 2.81Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.231 , 0.278 0.235 , 0.280	Depositor DCC
R_{free} test set	3029 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	66.9	Xtriage
Anisotropy	0.328	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 49.4	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	16271	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% 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: GOL, OXL, FBP, K, MG, PO4

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.68	0/4034	1.05	26/5448 (0.5%)
1	B	0.64	0/4034	1.03	14/5448 (0.3%)
1	C	0.66	0/4034	1.03	17/5448 (0.3%)
1	D	0.62	0/4034	1.02	20/5448 (0.4%)
All	All	0.65	0/16136	1.03	77/21792 (0.4%)

There are no bond length outliers.

All (77) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	164	ILE	N-CA-C	8.62	119.41	110.36
1	A	92	ARG	NE-CZ-NH2	8.61	126.95	119.20
1	C	164	ILE	N-CA-C	8.37	119.15	110.36
1	D	164	ILE	N-CA-C	8.34	118.90	110.23
1	B	201	GLY	N-CA-C	-8.32	103.55	112.04
1	A	92	ARG	NE-CZ-NH1	-8.22	113.28	121.50
1	B	164	ILE	N-CA-C	8.03	118.79	110.36
1	C	77	SER	N-CA-C	-7.77	103.69	113.02
1	D	77	SER	N-CA-C	-7.73	103.74	113.02
1	A	201	GLY	N-CA-C	-7.48	104.41	112.04
1	B	77	SER	N-CA-C	-7.34	104.21	113.02
1	A	77	SER	N-CA-C	-7.31	104.25	113.02
1	A	92	ARG	CD-NE-CZ	6.88	134.04	124.40
1	C	327	ALA	N-CA-C	6.86	119.83	109.41
1	C	201	GLY	N-CA-C	-6.83	103.66	111.85
1	B	44	ASN	N-CA-C	6.59	120.53	112.23
1	D	294	ARG	N-CA-C	6.44	118.30	111.28
1	C	44	ASN	N-CA-C	6.33	120.20	112.23
1	A	44	ASN	N-CA-C	6.29	120.15	112.23
1	C	299	ILE	N-CA-C	-6.29	106.40	111.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	327	ALA	N-CA-C	6.26	118.93	109.41
1	C	294	ARG	N-CA-C	6.25	118.09	111.28
1	D	492	PHE	N-CA-C	-6.12	104.52	111.07
1	B	294	ARG	N-CA-C	6.08	117.91	111.28
1	A	87	THR	N-CA-C	-6.07	104.57	111.07
1	A	327	ALA	N-CA-C	6.00	118.54	109.41
1	B	492	PHE	N-CA-C	-6.00	104.65	111.07
1	B	87	THR	N-CA-C	-5.99	104.66	111.07
1	A	466	TYR	N-CA-C	5.97	118.68	109.07
1	D	24	ASP	N-CA-C	5.95	117.77	111.28
1	D	201	GLY	N-CA-C	-5.93	104.11	111.70
1	A	380	LEU	N-CA-C	5.79	117.27	111.07
1	A	52	GLY	CA-C-N	5.79	127.07	119.84
1	A	52	GLY	C-N-CA	5.79	127.07	119.84
1	C	218	LEU	CA-C-N	5.77	126.06	119.83
1	C	218	LEU	C-N-CA	5.77	126.06	119.83
1	B	52	GLY	CA-C-N	5.74	127.01	119.84
1	B	52	GLY	C-N-CA	5.74	127.01	119.84
1	B	144	LEU	N-CA-C	-5.70	106.31	113.72
1	D	218	LEU	CA-C-N	5.69	125.88	119.90
1	D	218	LEU	C-N-CA	5.69	125.88	119.90
1	A	24	ASP	N-CA-C	5.69	117.48	111.28
1	C	62	LYS	N-CA-C	-5.67	105.08	112.23
1	C	24	ASP	N-CA-C	5.65	117.43	111.28
1	B	327	ALA	N-CA-C	5.63	117.96	109.41
1	D	52	GLY	CA-C-N	5.57	126.80	119.84
1	D	52	GLY	C-N-CA	5.57	126.80	119.84
1	A	144	LEU	N-CA-C	-5.52	106.55	113.72
1	B	24	ASP	N-CA-C	5.50	117.28	111.28
1	D	44	ASN	N-CA-C	5.47	119.12	112.23
1	C	380	LEU	N-CA-C	5.43	116.88	111.07
1	C	87	THR	N-CA-C	-5.40	105.30	111.07
1	D	144	LEU	N-CA-C	-5.39	106.71	113.72
1	D	380	LEU	N-CA-C	5.39	116.83	111.07
1	A	288	ASP	N-CA-C	-5.38	106.89	113.50
1	A	294	ARG	N-CA-C	5.38	117.89	111.71
1	A	407	ASP	CA-C-N	5.36	125.43	119.32
1	A	407	ASP	C-N-CA	5.36	125.43	119.32
1	A	218	LEU	CA-C-N	5.33	125.49	119.90
1	A	218	LEU	C-N-CA	5.33	125.49	119.90
1	C	144	LEU	N-CA-C	-5.30	106.83	113.72
1	A	354	ASP	N-CA-C	-5.28	105.64	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	288	ASP	N-CA-C	-5.28	107.01	113.50
1	D	485	ASP	N-CA-C	-5.27	105.61	111.36
1	C	466	TYR	N-CA-C	5.25	117.53	109.07
1	A	201	GLY	CA-C-O	-5.15	118.74	122.45
1	C	20	ALA	N-CA-C	5.14	116.96	111.36
1	A	115	LYS	N-CA-C	-5.12	105.78	111.36
1	B	466	TYR	N-CA-C	5.12	117.31	109.07
1	A	329	GLN	N-CA-C	5.11	119.36	113.38
1	D	87	THR	N-CA-C	-5.10	105.61	111.07
1	D	329	GLN	N-CA-C	5.09	119.07	112.86
1	A	62	LYS	N-CA-C	-5.05	105.86	112.23
1	D	455	ARG	N-CA-C	-5.05	107.50	113.97
1	C	485	ASP	N-CA-C	-5.05	105.86	111.36
1	D	288	ASP	N-CA-C	-5.04	107.31	113.50
1	D	62	LYS	N-CA-C	-5.00	105.92	112.23

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	3971	0	4059	181	0
1	B	3971	0	4059	172	0
1	C	3971	0	4059	190	0
1	D	3971	0	4059	181	0
2	A	20	0	10	1	0
2	B	20	0	10	1	0
2	C	20	0	10	2	0
2	D	20	0	10	1	0
3	A	6	0	0	0	0
3	B	6	0	0	1	0
3	C	6	0	0	2	0
3	D	6	0	0	1	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	5	0	0	0	0
4	D	5	0	0	1	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	A	30	0	40	1	0
7	B	24	0	32	0	0
7	C	36	0	48	11	0
7	D	30	0	40	1	0
8	A	47	0	0	6	0
8	B	28	0	0	3	0
8	C	30	0	0	4	0
8	D	30	0	0	7	0
All	All	16271	0	16436	683	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 21.

All (683) 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:132:VAL:HG12	1:C:133:GLU:H	1.13	1.08
1:A:132:VAL:HG12	1:A:133:GLU:H	1.14	1.05
1:B:132:VAL:HG12	1:B:133:GLU:H	1.16	1.04
1:B:132:VAL:HG21	1:B:153:ASP:HA	1.42	1.01
1:D:132:VAL:HG12	1:D:133:GLU:H	1.19	1.00
1:D:132:VAL:HG21	1:D:153:ASP:HA	1.40	0.99
1:A:132:VAL:HG21	1:A:153:ASP:HA	1.47	0.97
1:D:510:ILE:HG23	1:D:525:MET:HE3	1.48	0.96
1:A:510:ILE:HG23	1:A:525:MET:HE3	1.45	0.96
1:B:380:LEU:HB3	1:D:304:GLU:HG2	1.49	0.94
1:B:248:ALA:HB2	1:B:282:GLU:HG2	1.51	0.93
1:C:132:VAL:HG21	1:C:153:ASP:HA	1.49	0.92
1:D:134:LEU:HD21	1:D:140:LEU:HD22	1.50	0.91
1:C:132:VAL:HG12	1:C:133:GLU:N	1.84	0.91
1:C:510:ILE:HG23	1:C:525:MET:HE3	1.51	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:134:LEU:HD21	1:B:140:LEU:HD22	1.54	0.90
1:B:132:VAL:HG12	1:B:133:GLU:N	1.87	0.89
1:A:248:ALA:HB2	1:A:282:GLU:HG2	1.54	0.88
1:A:132:VAL:HG12	1:A:133:GLU:N	1.89	0.88
1:B:304:GLU:HG2	1:D:380:LEU:HB3	1.55	0.88
1:C:494:MET:HG2	1:C:531:PRO:HD2	1.57	0.87
1:D:248:ALA:HB2	1:D:282:GLU:HG2	1.56	0.86
1:A:134:LEU:HD21	1:A:140:LEU:HD22	1.56	0.86
1:A:494:MET:HG2	1:A:531:PRO:HD2	1.58	0.85
1:B:494:MET:HG2	1:B:531:PRO:HD2	1.59	0.85
1:B:510:ILE:HG23	1:B:525:MET:HE3	1.56	0.85
1:D:494:MET:HG2	1:D:531:PRO:HD2	1.55	0.85
1:A:125:LYS:HE3	1:A:132:VAL:HG22	1.59	0.84
1:C:132:VAL:CG1	1:C:133:GLU:H	1.91	0.84
1:A:58:VAL:HG23	1:A:90:ASN:ND2	1.93	0.84
1:C:333:SER:HB3	1:C:344:GLU:OE1	1.77	0.84
1:C:248:ALA:HB2	1:C:282:GLU:HG2	1.61	0.82
1:D:132:VAL:HG12	1:D:133:GLU:N	1.90	0.82
1:C:445:ARG:HH22	7:C:707:GOL:H12	1.42	0.82
1:C:143:THR:HG22	1:C:145:ASP:H	1.45	0.81
1:D:127:SER:HB3	1:D:130:ALA:HB2	1.62	0.81
1:A:333:SER:HB3	1:A:344:GLU:OE1	1.81	0.80
1:B:333:SER:HB3	1:B:344:GLU:OE1	1.80	0.80
1:B:132:VAL:CG1	1:B:133:GLU:H	1.94	0.80
1:A:380:LEU:HB3	1:C:304:GLU:HG2	1.63	0.80
1:D:432:THR:HA	2:D:532:FBP:H61	1.63	0.80
1:A:127:SER:HB3	1:A:130:ALA:HB2	1.64	0.80
1:D:405:THR:HG21	1:D:410:GLU:HG2	1.64	0.80
1:C:134:LEU:HD21	1:C:140:LEU:HD22	1.62	0.79
1:D:132:VAL:HG11	1:D:154:GLU:N	1.97	0.79
1:A:132:VAL:CG1	1:A:133:GLU:H	1.93	0.79
1:B:58:VAL:HG23	1:B:90:ASN:ND2	1.97	0.79
1:B:143:THR:HG22	1:B:145:ASP:H	1.48	0.79
1:A:399:ARG:NH2	1:B:399:ARG:NH2	2.31	0.79
1:D:58:VAL:HG23	1:D:90:ASN:ND2	1.97	0.79
1:C:482:TRP:NE1	1:C:517:PRO:HG3	1.98	0.78
1:D:482:TRP:NE1	1:D:517:PRO:HG3	1.98	0.78
1:C:127:SER:HB3	1:C:130:ALA:HB2	1.66	0.78
1:A:327:ALA:HB1	1:A:360:MET:HE2	1.67	0.77
1:C:101:ASP:OD2	1:C:104:LEU:HD23	1.84	0.77
1:B:432:THR:HA	2:B:532:FBP:H61	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:ILE:HG23	1:B:132:VAL:HG23	1.65	0.77
1:A:124:ILE:HG23	1:A:132:VAL:HG23	1.66	0.77
1:C:58:VAL:HG23	1:C:90:ASN:ND2	2.00	0.77
1:D:125:LYS:HE3	1:D:132:VAL:HG22	1.67	0.77
1:A:132:VAL:HG11	1:A:154:GLU:N	1.99	0.77
1:B:132:VAL:HG11	1:B:154:GLU:N	1.98	0.77
1:D:143:THR:HG22	1:D:145:ASP:H	1.47	0.77
1:B:494:MET:CG	1:B:531:PRO:HD2	2.15	0.76
1:A:143:THR:HG22	1:A:145:ASP:H	1.50	0.76
1:C:124:ILE:HG23	1:C:132:VAL:HG23	1.68	0.76
1:C:132:VAL:HG11	1:C:154:GLU:N	2.00	0.76
1:C:399:ARG:NH2	1:D:399:ARG:NH2	2.32	0.76
1:D:124:ILE:HG23	1:D:132:VAL:HG23	1.66	0.76
1:A:101:ASP:OD2	1:A:104:LEU:HD23	1.85	0.76
1:B:127:SER:HB3	1:B:130:ALA:HB2	1.68	0.75
1:B:179:GLY:HA3	1:B:299:ILE:HD12	1.69	0.74
1:A:182:SER:OG	1:A:198:GLU:HB2	1.87	0.74
1:D:179:GLY:HA3	1:D:299:ILE:HD12	1.69	0.74
1:B:101:ASP:OD2	1:B:104:LEU:HD23	1.87	0.74
1:B:482:TRP:NE1	1:B:517:PRO:HG3	2.03	0.74
1:D:132:VAL:CG1	1:D:133:GLU:H	1.97	0.74
1:C:125:LYS:HE3	1:C:132:VAL:HG22	1.69	0.73
1:D:494:MET:CG	1:D:531:PRO:HD2	2.17	0.73
1:C:222:SER:HB3	8:C:710:HOH:O	1.88	0.73
1:D:333:SER:HB3	1:D:344:GLU:OE1	1.88	0.73
1:C:516:ARG:HG3	1:C:516:ARG:HH11	1.53	0.73
1:A:494:MET:CG	1:A:531:PRO:HD2	2.18	0.73
1:B:405:THR:HG21	1:B:410:GLU:HG2	1.71	0.73
1:C:445:ARG:HH12	7:C:707:GOL:H31	1.54	0.72
1:B:125:LYS:HE3	1:B:132:VAL:HG22	1.69	0.72
1:A:432:THR:HA	2:A:532:FBP:H61	1.71	0.72
1:A:175:TYR:HB3	1:A:179:GLY:HA2	1.71	0.72
1:A:399:ARG:NH2	1:B:399:ARG:HH21	1.88	0.72
1:C:179:GLY:HA3	1:C:299:ILE:HD12	1.71	0.72
1:C:405:THR:HG21	1:C:410:GLU:HG2	1.71	0.72
1:D:175:TYR:HB3	1:D:179:GLY:HA2	1.71	0.71
1:C:132:VAL:HG11	1:C:154:GLU:H	1.55	0.71
1:C:494:MET:CG	1:C:531:PRO:HD2	2.20	0.71
1:B:132:VAL:HG11	1:B:154:GLU:H	1.55	0.70
1:B:175:TYR:HB3	1:B:179:GLY:HA2	1.73	0.70
1:B:453:VAL:HG21	1:B:493:ALA:HB2	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:422:LYS:HE3	1:D:405:THR:HG22	1.72	0.70
1:A:132:VAL:HG11	1:A:154:GLU:H	1.56	0.70
1:D:132:VAL:HG11	1:D:154:GLU:H	1.56	0.70
1:D:482:TRP:CD1	1:D:517:PRO:HG3	2.26	0.70
1:C:399:ARG:HH21	1:D:399:ARG:NH2	1.88	0.69
1:C:482:TRP:CD1	1:C:517:PRO:HG3	2.27	0.69
1:A:482:TRP:NE1	1:A:517:PRO:HG3	2.06	0.69
1:A:164:ILE:O	1:A:168:VAL:HG12	1.92	0.69
1:A:179:GLY:HA3	1:A:299:ILE:HD12	1.73	0.69
1:D:101:ASP:OD2	1:D:104:LEU:HD23	1.92	0.69
1:A:19:HIS:ND1	1:A:32:ARG:HD3	2.07	0.69
1:A:21:ALA:HB1	8:A:723:HOH:O	1.91	0.69
1:D:103:ILE:HG22	1:D:104:LEU:HD22	1.75	0.69
1:C:164:ILE:O	1:C:168:VAL:HG12	1.93	0.69
1:A:304:GLU:HG2	1:C:380:LEU:HB3	1.75	0.68
1:D:516:ARG:HG3	1:D:516:ARG:HH11	1.58	0.68
1:A:497:GLY:HA3	1:A:503:PHE:CZ	2.29	0.68
1:C:399:ARG:NH2	1:D:399:ARG:HH21	1.91	0.68
1:C:19:HIS:ND1	1:C:32:ARG:HD3	2.09	0.68
1:B:453:VAL:CG2	1:B:493:ALA:HB2	2.24	0.68
1:A:399:ARG:HH21	1:B:399:ARG:NH2	1.92	0.68
1:D:182:SER:OG	1:D:198:GLU:HB2	1.94	0.67
1:A:405:THR:HG22	1:B:422:LYS:HE3	1.77	0.67
1:D:327:ALA:HB1	1:D:360:MET:HE2	1.77	0.67
1:C:243:SER:OG	1:C:270:LYS:HE2	1.95	0.67
1:D:255:ARG:HH11	1:D:255:ARG:HG3	1.59	0.67
1:A:141:LYS:HE3	1:A:192:PHE:CD2	2.30	0.67
1:A:482:TRP:CD1	1:A:517:PRO:HG3	2.29	0.67
1:C:175:TYR:HB3	1:C:179:GLY:HA2	1.77	0.66
1:A:255:ARG:HG3	1:A:255:ARG:HH11	1.60	0.66
1:D:329:GLN:HG2	1:D:332:GLU:CG	2.25	0.66
1:C:21:ALA:HB1	8:C:724:HOH:O	1.94	0.66
1:A:64:MET:CE	1:A:372:LEU:HD23	2.26	0.66
1:B:482:TRP:CD1	1:B:517:PRO:HG3	2.31	0.65
1:B:15:THR:HG22	1:B:16:GLN:HG2	1.78	0.65
1:C:453:VAL:HG21	1:C:493:ALA:HB2	1.77	0.65
1:C:516:ARG:HG3	1:C:516:ARG:NH1	2.11	0.65
1:A:405:THR:HG21	1:A:410:GLU:HG2	1.76	0.65
1:C:103:ILE:HG22	1:C:104:LEU:HD22	1.78	0.65
1:B:331:LEU:HD23	1:B:344:GLU:HB3	1.79	0.65
1:C:182:SER:OG	1:C:198:GLU:HB2	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:331:LEU:HD23	1:C:344:GLU:HB3	1.79	0.64
1:B:516:ARG:HG3	1:B:516:ARG:HH11	1.61	0.64
1:B:143:THR:CG2	1:B:145:ASP:HB3	2.28	0.64
1:B:182:SER:OG	1:B:198:GLU:HB2	1.97	0.64
1:C:153:ASP:O	1:C:155:ASN:N	2.31	0.64
1:A:143:THR:CG2	1:A:145:ASP:HB3	2.28	0.64
1:B:327:ALA:HB1	1:B:360:MET:HE2	1.79	0.64
1:D:331:LEU:HD23	1:D:344:GLU:HB3	1.80	0.64
1:C:327:ALA:HB1	1:C:360:MET:HE2	1.79	0.63
1:D:143:THR:CG2	1:D:145:ASP:HB3	2.29	0.63
1:A:298:GLY:HA3	1:C:342:ARG:NE	2.13	0.63
1:B:494:MET:HG2	1:B:531:PRO:CD	2.27	0.63
1:D:494:MET:HG2	1:D:531:PRO:CD	2.28	0.63
1:B:19:HIS:ND1	1:B:32:ARG:HD3	2.13	0.63
1:A:141:LYS:HE3	1:A:192:PHE:CG	2.34	0.63
1:B:15:THR:O	1:B:18:LEU:HG	1.99	0.62
1:B:64:MET:CE	1:B:372:LEU:HD23	2.28	0.62
1:A:329:GLN:HG2	1:A:332:GLU:CG	2.29	0.62
1:D:134:LEU:CD2	1:D:140:LEU:HD22	2.25	0.62
1:D:516:ARG:HG3	1:D:516:ARG:NH1	2.14	0.62
1:D:466:TYR:HB2	1:D:469:ILE:HD12	1.82	0.62
1:C:422:LYS:HE3	1:D:405:THR:CG2	2.30	0.62
1:D:19:HIS:ND1	1:D:32:ARG:HD3	2.14	0.62
1:C:280:PHE:CE1	1:C:313:MET:HG2	2.34	0.62
1:D:319:ARG:NH2	8:D:710:HOH:O	2.30	0.62
1:C:294:ARG:HH22	1:C:347:ASP:CG	2.06	0.61
1:B:164:ILE:O	1:B:168:VAL:HG12	1.99	0.61
1:D:164:ILE:O	1:D:168:VAL:HG12	2.00	0.61
1:D:389:ILE:HD11	1:D:467:ARG:HH21	1.64	0.61
1:A:134:LEU:CD2	1:A:140:LEU:HD22	2.30	0.61
1:C:143:THR:CG2	1:C:145:ASP:HB3	2.30	0.61
1:C:64:MET:CE	1:C:372:LEU:HD23	2.31	0.61
1:C:405:THR:HG22	1:D:422:LYS:HE3	1.82	0.61
1:D:294:ARG:HH22	1:D:347:ASP:CG	2.09	0.61
1:A:294:ARG:HH22	1:A:347:ASP:CG	2.08	0.61
1:A:389:ILE:HD11	1:A:467:ARG:HH21	1.66	0.61
1:B:466:TYR:HB2	1:B:469:ILE:HD12	1.82	0.61
1:B:329:GLN:HG2	1:B:332:GLU:CG	2.31	0.61
1:A:15:THR:O	1:A:18:LEU:HG	2.00	0.60
1:C:255:ARG:HG3	1:C:255:ARG:HH11	1.64	0.60
1:D:119:ILE:HG12	1:D:161:TYR:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:64:MET:CE	1:D:372:LEU:HD23	2.31	0.60
1:C:15:THR:O	1:C:18:LEU:HG	2.02	0.60
1:A:302:PRO:HG2	1:A:305:LYS:HD2	1.83	0.60
1:D:302:PRO:HG2	1:D:305:LYS:HD2	1.82	0.60
1:C:494:MET:HG2	1:C:531:PRO:CD	2.30	0.59
1:C:120:ARG:HA	1:C:207:LYS:O	2.02	0.59
1:B:153:ASP:O	1:B:155:ASN:N	2.35	0.59
1:B:302:PRO:HG2	1:B:305:LYS:HD2	1.84	0.59
1:D:453:VAL:HG21	1:D:493:ALA:HB2	1.82	0.59
1:A:242:ALA:HB1	1:A:245:ILE:HD11	1.84	0.59
1:A:453:VAL:HG21	1:A:493:ALA:HB2	1.85	0.59
1:A:15:THR:HG22	1:A:16:GLN:HG2	1.84	0.59
1:C:453:VAL:CG2	1:C:493:ALA:HB2	2.32	0.59
1:D:64:MET:HE2	1:D:372:LEU:HD23	1.83	0.58
1:D:15:THR:O	1:D:18:LEU:HG	2.03	0.58
1:B:255:ARG:HG3	1:B:255:ARG:HH11	1.67	0.58
1:D:141:LYS:HE3	1:D:192:PHE:CD2	2.38	0.58
1:A:472:VAL:HG13	1:A:492:PHE:CE2	2.39	0.58
1:A:329:GLN:HG2	1:A:332:GLU:HG3	1.85	0.58
1:B:516:ARG:HG3	1:B:516:ARG:NH1	2.19	0.58
1:C:389:ILE:HD11	1:C:467:ARG:HH21	1.69	0.58
1:A:120:ARG:HA	1:A:207:LYS:O	2.04	0.58
1:D:118:GLU:OE2	1:D:120:ARG:NH1	2.35	0.58
1:B:92:ARG:O	1:B:96:GLU:HG2	2.03	0.58
1:B:389:ILE:HD11	1:B:467:ARG:HH21	1.67	0.58
1:C:482:TRP:CE2	1:C:517:PRO:HG3	2.39	0.58
1:A:153:ASP:O	1:A:155:ASN:N	2.37	0.58
1:B:141:LYS:HE3	1:B:192:PHE:CG	2.39	0.58
1:C:329:GLN:HG2	1:C:332:GLU:CG	2.34	0.58
1:D:148:TYR:HD2	1:D:151:LYS:HD2	1.69	0.58
1:B:294:ARG:HH22	1:B:347:ASP:CG	2.12	0.57
1:C:445:ARG:HH12	7:C:707:GOL:C3	2.17	0.57
1:B:472:VAL:HG13	1:B:492:PHE:CE2	2.39	0.57
1:C:321:GLY:HA2	7:C:707:GOL:O2	2.04	0.57
1:D:15:THR:HG22	1:D:16:GLN:HG2	1.86	0.57
1:A:447:ARG:HD3	8:A:753:HOH:O	2.03	0.57
1:A:64:MET:HE2	1:A:372:LEU:HD23	1.87	0.57
1:C:466:TYR:HB2	1:C:469:ILE:HD12	1.86	0.57
1:D:482:TRP:CE2	1:D:517:PRO:HG3	2.39	0.57
1:A:176:VAL:HA	1:A:208:GLY:O	2.05	0.57
1:C:148:TYR:HD2	1:C:151:LYS:HD2	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:141:LYS:HE3	1:D:192:PHE:CG	2.40	0.57
1:A:298:GLY:HA3	1:C:342:ARG:HE	1.68	0.57
1:A:140:LEU:HD21	1:A:157:LEU:HD22	1.85	0.56
1:A:280:PHE:CE1	1:A:313:MET:HG2	2.40	0.56
1:B:176:VAL:HA	1:B:208:GLY:O	2.04	0.56
1:C:118:GLU:OE2	1:C:120:ARG:NH1	2.34	0.56
1:B:140:LEU:HD21	1:B:157:LEU:HD22	1.87	0.56
1:B:148:TYR:HD2	1:B:151:LYS:HD2	1.68	0.56
1:B:482:TRP:CE2	1:B:517:PRO:HG3	2.40	0.56
1:C:294:ARG:NH2	1:C:347:ASP:OD1	2.33	0.56
1:D:463:ALA:HB3	1:D:471:PRO:HG3	1.87	0.56
1:A:453:VAL:CG2	1:A:493:ALA:HB2	2.34	0.56
1:B:70:ASN:HD22	1:B:464:HIS:CE1	2.24	0.56
1:C:15:THR:HG22	1:C:16:GLN:HG2	1.87	0.56
1:D:255:ARG:HH11	1:D:255:ARG:CG	2.16	0.56
1:D:395:PHE:CZ	1:D:399:ARG:HD3	2.40	0.56
1:D:92:ARG:O	1:D:96:GLU:HG2	2.05	0.56
1:A:186:LYS:HE2	1:A:186:LYS:HA	1.88	0.56
1:A:331:LEU:HD23	1:A:344:GLU:HB3	1.87	0.56
1:C:92:ARG:O	1:C:96:GLU:HG2	2.06	0.56
1:D:323:PRO:HB3	1:D:465:LEU:O	2.06	0.56
1:C:333:SER:CB	1:C:344:GLU:OE1	2.52	0.56
1:A:148:TYR:HD2	1:A:151:LYS:HD2	1.69	0.56
1:A:319:ARG:HH21	1:C:31:CYS:HB3	1.70	0.56
1:B:134:LEU:CD2	1:B:140:LEU:HD22	2.31	0.56
1:D:242:ALA:HB1	1:D:245:ILE:HD11	1.88	0.56
1:B:186:LYS:HA	1:B:186:LYS:HE2	1.87	0.56
1:B:463:ALA:HB3	1:B:471:PRO:HG3	1.88	0.56
1:A:143:THR:HG22	1:A:145:ASP:HB3	1.87	0.56
1:A:494:MET:HG2	1:A:531:PRO:CD	2.32	0.56
1:B:372:LEU:O	1:B:376:ARG:HG3	2.05	0.56
1:C:472:VAL:HG13	1:C:492:PHE:CE2	2.40	0.55
1:D:120:ARG:HA	1:D:207:LYS:O	2.07	0.55
1:D:134:LEU:HB3	1:D:197:VAL:HG21	1.88	0.55
1:B:280:PHE:CE1	1:B:313:MET:HG2	2.41	0.55
1:C:432:THR:HA	2:C:532:FBP:H61	1.88	0.55
1:D:356:ALA:O	1:D:467:ARG:NH1	2.39	0.55
1:D:453:VAL:CG2	1:D:493:ALA:HB2	2.36	0.55
1:D:472:VAL:HG13	1:D:492:PHE:CE2	2.41	0.55
1:D:329:GLN:HG2	1:D:332:GLU:HG3	1.87	0.55
1:A:255:ARG:HH11	1:A:255:ARG:CG	2.19	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:141:LYS:HE3	1:B:192:PHE:CD2	2.41	0.55
1:B:143:THR:HG22	1:B:145:ASP:HB3	1.88	0.55
1:C:514:GLY:HA3	2:C:532:FBP:O3	2.06	0.55
1:B:157:LEU:HD13	1:B:203:LEU:HD21	1.89	0.54
1:D:140:LEU:HD21	1:D:157:LEU:HD22	1.90	0.54
1:D:497:GLY:HA3	1:D:503:PHE:CZ	2.41	0.54
1:A:103:ILE:HG22	1:A:104:LEU:HD22	1.90	0.54
1:B:175:TYR:O	1:B:209:VAL:HA	2.07	0.54
1:C:302:PRO:HG2	1:C:305:LYS:HD2	1.89	0.54
1:D:143:THR:HG22	1:D:145:ASP:HB3	1.89	0.54
1:D:280:PHE:CE1	1:D:313:MET:HG2	2.43	0.54
1:D:393:GLN:O	1:D:397:GLU:HG3	2.08	0.54
1:D:153:ASP:O	1:D:155:ASN:N	2.40	0.54
1:D:157:LEU:HD13	1:D:203:LEU:HD21	1.89	0.54
1:A:466:TYR:HB2	1:A:469:ILE:HD12	1.90	0.54
1:B:243:SER:OG	1:B:270:LYS:HE2	2.08	0.54
1:D:224:LYS:HG2	1:D:228:ASP:OD2	2.07	0.54
1:B:333:SER:CB	1:B:344:GLU:OE1	2.52	0.54
1:B:120:ARG:HA	1:B:207:LYS:O	2.07	0.54
1:C:176:VAL:HA	1:C:208:GLY:O	2.08	0.54
1:C:255:ARG:HH11	1:C:255:ARG:CG	2.20	0.54
1:D:84:HIS:HD2	8:D:723:HOH:O	1.90	0.54
1:D:176:VAL:HA	1:D:208:GLY:O	2.07	0.54
1:B:295:GLY:CA	1:B:328:THR:HG21	2.38	0.54
1:D:294:ARG:NH2	1:D:347:ASP:OD1	2.40	0.54
1:A:157:LEU:HD13	1:A:203:LEU:HD21	1.89	0.54
1:B:294:ARG:NH2	1:B:347:ASP:OD1	2.40	0.54
1:C:516:ARG:NH1	1:C:517:PRO:O	2.41	0.54
1:C:157:LEU:HD13	1:C:203:LEU:HD21	1.91	0.53
1:D:153:ASP:HB2	1:D:154:GLU:OE1	2.09	0.53
1:C:516:ARG:HH11	1:C:516:ARG:CG	2.20	0.53
1:B:242:ALA:HB1	1:B:245:ILE:HD11	1.90	0.53
1:A:319:ARG:HH21	1:C:31:CYS:CB	2.22	0.53
1:A:405:THR:CG2	1:B:422:LYS:HE3	2.38	0.53
1:C:175:TYR:O	1:C:209:VAL:HA	2.08	0.53
1:A:92:ARG:O	1:A:96:GLU:HG2	2.08	0.53
1:B:305:LYS:NZ	8:B:718:HOH:O	2.41	0.53
1:B:409:THR:HG22	1:B:522:THR:HB	1.90	0.53
1:C:119:ILE:HG12	1:C:161:TYR:HB2	1.89	0.53
1:C:393:GLN:O	1:C:397:GLU:HG3	2.09	0.53
1:A:294:ARG:NH2	1:A:347:ASP:OD1	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:327:ALA:O	1:D:328:THR:HB	2.07	0.53
1:A:118:GLU:OE2	1:A:120:ARG:NH1	2.37	0.53
1:B:124:ILE:CG2	1:B:132:VAL:HG23	2.37	0.53
1:B:329:GLN:HG2	1:B:332:GLU:HG3	1.91	0.53
1:D:186:LYS:HA	1:D:186:LYS:HE2	1.90	0.53
1:D:295:GLY:CA	1:D:328:THR:HG21	2.39	0.53
1:A:134:LEU:HB3	1:A:197:VAL:HG21	1.90	0.53
1:D:26:PHE:O	1:D:29:HIS:HB3	2.09	0.53
1:B:64:MET:HE3	1:B:372:LEU:HD23	1.89	0.53
1:C:143:THR:HG21	1:C:145:ASP:HB3	1.89	0.53
1:A:175:TYR:O	1:A:209:VAL:HA	2.09	0.52
1:C:134:LEU:CD2	1:C:140:LEU:HD22	2.36	0.52
1:B:123:LEU:HB2	1:B:150:GLU:HA	1.91	0.52
1:D:243:SER:OG	1:D:270:LYS:HE2	2.09	0.52
1:A:119:ILE:HG12	1:A:161:TYR:HB2	1.90	0.52
1:A:341:THR:OG1	1:A:344:GLU:HG3	2.09	0.52
1:C:389:ILE:HD11	1:C:467:ARG:NH2	2.24	0.52
1:B:327:ALA:O	1:B:328:THR:HB	2.08	0.52
1:D:78:HIS:ND1	7:D:705:GOL:H2	2.24	0.52
1:A:153:ASP:HB2	1:A:154:GLU:OE1	2.10	0.52
1:B:356:ALA:O	1:B:467:ARG:NH1	2.43	0.52
1:C:140:LEU:HD21	1:C:157:LEU:HD22	1.91	0.52
1:D:323:PRO:HA	1:D:357:ASP:OD1	2.09	0.52
1:A:26:PHE:O	1:A:29:HIS:HB3	2.10	0.52
1:B:143:THR:HG21	1:B:145:ASP:HB3	1.92	0.52
1:B:494:MET:HE3	1:B:531:PRO:HD3	1.92	0.52
1:C:327:ALA:O	1:C:328:THR:HB	2.10	0.52
1:D:120:ARG:N	1:D:160:ASP:OD2	2.41	0.51
1:B:334:MET:HE3	1:B:338:PRO:O	2.09	0.51
1:C:64:MET:HE2	1:C:372:LEU:HD23	1.92	0.51
1:C:123:LEU:HB2	1:C:150:GLU:HA	1.91	0.51
1:C:186:LYS:HE2	1:C:186:LYS:HA	1.92	0.51
1:B:31:CYS:CB	1:D:319:ARG:HH21	2.23	0.51
1:D:389:ILE:HD11	1:D:467:ARG:NH2	2.25	0.51
1:A:243:SER:OG	1:A:270:LYS:HE2	2.11	0.51
1:C:26:PHE:O	1:C:29:HIS:HB3	2.10	0.51
1:C:70:ASN:HD22	1:C:464:HIS:CE1	2.28	0.51
1:D:175:TYR:O	1:D:209:VAL:HA	2.10	0.51
1:B:26:PHE:O	1:B:29:HIS:HB3	2.10	0.51
1:C:124:ILE:CG2	1:C:132:VAL:HG23	2.39	0.51
1:C:356:ALA:O	1:C:467:ARG:NH1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:395:PHE:CZ	1:C:399:ARG:HD3	2.45	0.51
1:C:463:ALA:HB3	1:C:471:PRO:HG3	1.93	0.51
1:D:23:ALA:HB2	1:D:32:ARG:NH1	2.25	0.51
1:B:103:ILE:HG22	1:B:104:LEU:HD22	1.90	0.51
1:D:516:ARG:HH11	1:D:516:ARG:CG	2.23	0.51
1:A:64:MET:HE3	1:A:372:LEU:HD23	1.92	0.51
1:C:255:ARG:NH2	1:C:288:ASP:OD1	2.44	0.51
1:A:463:ALA:HB3	1:A:471:PRO:HG3	1.93	0.51
1:C:141:LYS:HE3	1:C:192:PHE:CG	2.46	0.51
1:A:134:LEU:N	1:A:134:LEU:HD12	2.27	0.50
1:B:458:GLN:O	1:B:462:GLN:HG3	2.11	0.50
1:C:372:LEU:O	1:C:376:ARG:HG3	2.11	0.50
1:B:329:GLN:HA	1:B:332:GLU:HG2	1.94	0.50
1:B:389:ILE:HD11	1:B:467:ARG:NH2	2.26	0.50
1:D:124:ILE:CG2	1:D:132:VAL:HG23	2.40	0.50
1:A:123:LEU:HB2	1:A:150:GLU:HA	1.93	0.50
1:D:409:THR:HG22	1:D:522:THR:HB	1.93	0.50
1:A:333:SER:CB	1:A:344:GLU:OE1	2.55	0.50
1:B:255:ARG:HH11	1:B:255:ARG:CG	2.25	0.50
1:C:136:LYS:HE2	1:C:198:GLU:O	2.12	0.50
1:D:270:LYS:HD2	1:D:291:MET:SD	2.51	0.50
1:A:414:VAL:HG22	1:A:444:TYR:CZ	2.46	0.50
1:B:395:PHE:CZ	1:B:399:ARG:HD3	2.47	0.50
1:C:205:SER:O	1:C:206:LYS:C	2.54	0.50
1:A:291:MET:HE2	1:A:360:MET:SD	2.52	0.50
1:C:285:GLU:O	7:C:709:GOL:H32	2.11	0.50
1:D:270:LYS:NZ	3:D:533:OXL:O4	2.42	0.50
1:A:242:ALA:O	1:A:270:LYS:HG3	2.11	0.49
1:B:134:LEU:HB3	1:B:197:VAL:HG21	1.93	0.49
1:C:23:ALA:HB2	1:C:32:ARG:NH1	2.27	0.49
1:A:143:THR:HG21	1:A:145:ASP:HB3	1.94	0.49
1:A:306:VAL:HB	8:A:719:HOH:O	2.11	0.49
1:B:323:PRO:HB3	1:B:465:LEU:O	2.12	0.49
1:B:516:ARG:HH11	1:B:516:ARG:CG	2.25	0.49
1:D:143:THR:HG21	1:D:145:ASP:HB3	1.93	0.49
1:A:222:SER:O	1:A:226:ILE:HG13	2.11	0.49
1:B:31:CYS:HB3	1:D:319:ARG:HH21	1.77	0.49
1:B:393:GLN:O	1:B:397:GLU:HG3	2.12	0.49
1:A:124:ILE:CG2	1:A:132:VAL:HG23	2.39	0.49
1:D:463:ALA:HB1	1:D:469:ILE:HG21	1.93	0.49
1:A:327:ALA:O	1:A:328:THR:HB	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:GLN:O	1:A:397:GLU:HG3	2.12	0.49
1:B:319:ARG:HH21	1:D:31:CYS:HB3	1.77	0.49
1:B:108:VAL:O	1:B:461:ARG:HG2	2.13	0.49
1:B:319:ARG:HH21	1:D:31:CYS:CB	2.25	0.49
1:D:55:SER:O	1:D:61:LEU:HD13	2.13	0.49
1:B:407:ASP:C	1:B:407:ASP:OD2	2.56	0.49
1:A:389:ILE:HD11	1:A:467:ARG:NH2	2.26	0.49
1:C:323:PRO:HB3	1:C:465:LEU:O	2.13	0.49
1:D:253:GLU:O	1:D:257:VAL:HG23	2.13	0.49
1:A:295:GLY:CA	1:A:328:THR:HG21	2.43	0.48
1:A:329:GLN:HA	1:A:332:GLU:HG2	1.94	0.48
1:B:55:SER:O	1:B:61:LEU:HD13	2.12	0.48
1:B:119:ILE:HG12	1:B:161:TYR:HB2	1.96	0.48
1:A:411:ALA:HA	1:B:422:LYS:HG2	1.96	0.48
1:A:526:ARG:HA	1:B:523:ASN:O	2.13	0.48
1:B:341:THR:HB	1:D:329:GLN:OE1	2.13	0.48
1:C:141:LYS:HE3	1:C:192:PHE:CD2	2.49	0.48
1:D:112:LEU:C	1:D:112:LEU:HD23	2.38	0.48
1:B:134:LEU:N	1:B:134:LEU:HD12	2.29	0.48
1:C:329:GLN:HG2	1:C:332:GLU:HG3	1.94	0.48
1:D:341:THR:OG1	1:D:344:GLU:HG3	2.13	0.48
1:A:121:THR:O	1:A:206:LYS:HA	2.14	0.48
1:A:272:GLU:OE2	1:A:296:ASP:OD2	2.30	0.48
1:C:405:THR:CG2	1:D:422:LYS:HE3	2.43	0.48
1:C:206:LYS:HZ3	7:C:704:GOL:H32	1.78	0.48
1:D:70:ASN:HD22	1:D:464:HIS:CE1	2.32	0.48
1:B:134:LEU:HD23	1:B:197:VAL:HG22	1.96	0.48
1:C:64:MET:HE3	1:C:372:LEU:HD23	1.96	0.47
1:C:132:VAL:CG1	1:C:133:GLU:N	2.56	0.47
1:C:146:ASN:O	1:C:149:MET:HG2	2.14	0.47
1:D:329:GLN:HA	1:D:332:GLU:HG2	1.95	0.47
1:B:153:ASP:HB2	1:B:154:GLU:OE1	2.13	0.47
1:C:143:THR:HG22	1:C:145:ASP:HB3	1.95	0.47
1:D:255:ARG:CG	1:D:255:ARG:NH1	2.74	0.47
1:D:255:ARG:NH2	1:D:288:ASP:OD1	2.47	0.47
1:A:401:LEU:HD12	1:C:27:LEU:HD23	1.96	0.47
1:B:118:GLU:OE2	1:B:120:ARG:HD2	2.15	0.47
1:D:121:THR:O	1:D:206:LYS:HA	2.14	0.47
1:A:422:LYS:HE3	1:B:405:THR:HG22	1.97	0.47
1:A:516:ARG:HG3	1:A:516:ARG:HH11	1.79	0.47
1:B:64:MET:HE2	1:B:372:LEU:HD23	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:380:LEU:CB	1:D:304:GLU:HG2	2.33	0.47
1:C:118:GLU:OE2	1:C:120:ARG:HD2	2.14	0.47
1:A:224:LYS:HG2	1:A:228:ASP:OD2	2.14	0.47
1:A:272:GLU:HG3	1:A:293:ALA:HB3	1.96	0.47
1:A:329:GLN:OE1	1:C:341:THR:HB	2.15	0.47
1:C:497:GLY:HA3	1:C:503:PHE:CZ	2.49	0.47
1:D:123:LEU:O	1:D:152:CYS:HB2	2.15	0.47
1:A:216:VAL:HG23	1:A:216:VAL:O	2.14	0.47
1:B:31:CYS:HB3	1:D:319:ARG:NH2	2.30	0.47
1:B:120:ARG:N	1:B:160:ASP:OD2	2.46	0.47
1:A:168:VAL:CG2	1:A:185:VAL:HG21	2.44	0.47
1:B:118:GLU:OE2	1:B:120:ARG:NH1	2.40	0.47
1:C:272:GLU:CG	1:C:293:ALA:HB3	2.44	0.47
1:C:458:GLN:O	1:C:462:GLN:HG3	2.14	0.47
1:C:494:MET:HE3	1:C:531:PRO:HD3	1.96	0.47
1:D:134:LEU:N	1:D:134:LEU:HD12	2.30	0.47
1:D:343:ALA:HB3	8:D:728:HOH:O	2.13	0.47
1:A:205:SER:O	1:A:206:LYS:C	2.57	0.47
1:B:23:ALA:HB2	1:B:32:ARG:NH1	2.30	0.47
1:C:44:ASN:OD1	1:C:468:GLY:HA2	2.15	0.47
1:A:57:SER:O	1:A:58:VAL:C	2.58	0.47
1:B:121:THR:O	1:B:206:LYS:HA	2.15	0.47
1:B:497:GLY:HA3	1:B:503:PHE:CZ	2.50	0.47
1:B:516:ARG:NH1	1:B:517:PRO:O	2.48	0.47
1:C:16:GLN:OE1	1:C:447:ARG:HD2	2.15	0.47
1:D:50:THR:HA	1:D:73:ARG:HB3	1.96	0.47
1:D:123:LEU:HB2	1:D:150:GLU:HA	1.95	0.47
1:C:300:GLU:OE2	7:C:706:GOL:H11	2.15	0.47
1:C:134:LEU:HD12	1:C:134:LEU:N	2.30	0.46
1:A:48:ILE:HG12	1:A:71:VAL:HB	1.98	0.46
1:C:457:PRO:HB3	1:C:473:LEU:HD21	1.97	0.46
1:D:71:VAL:HG22	1:D:109:ALA:HB3	1.97	0.46
1:D:205:SER:O	1:D:206:LYS:C	2.56	0.46
1:A:255:ARG:CG	1:A:255:ARG:NH1	2.76	0.46
1:B:74:LEU:HD11	1:B:88:ILE:HG12	1.96	0.46
1:B:323:PRO:HA	1:B:357:ASP:OD1	2.15	0.46
1:C:330:MET:HE2	1:C:348:VAL:HG22	1.98	0.46
1:A:523:ASN:O	1:B:526:ARG:HA	2.15	0.46
1:C:295:GLY:CA	1:C:328:THR:HG21	2.46	0.46
1:C:329:GLN:HA	1:C:332:GLU:HG2	1.96	0.46
1:D:333:SER:CB	1:D:344:GLU:OE1	2.60	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:482:TRP:CE2	1:A:517:PRO:HG3	2.49	0.46
1:B:293:ALA:HB1	3:B:533:OXL:C2	2.46	0.46
1:D:405:THR:HG23	8:D:725:HOH:O	2.16	0.46
1:C:55:SER:O	1:C:61:LEU:HD13	2.15	0.46
1:D:516:ARG:NH1	1:D:517:PRO:O	2.49	0.46
1:A:70:ASN:HD22	1:A:464:HIS:CE1	2.33	0.46
1:B:205:SER:O	1:B:206:LYS:C	2.58	0.46
1:C:242:ALA:O	1:C:270:LYS:HG3	2.16	0.46
1:D:407:ASP:C	1:D:407:ASP:OD2	2.59	0.46
1:B:123:LEU:O	1:B:152:CYS:HB2	2.16	0.45
1:C:323:PRO:HA	1:C:357:ASP:OD1	2.16	0.45
1:C:445:ARG:HH22	7:C:707:GOL:C1	2.19	0.45
1:A:120:ARG:N	1:A:160:ASP:OD2	2.45	0.45
1:C:333:SER:HB2	1:C:341:THR:HG23	1.97	0.45
1:C:422:LYS:HG2	1:D:411:ALA:HA	1.98	0.45
1:D:106:ARG:HG2	8:D:721:HOH:O	2.14	0.45
1:B:57:SER:O	1:B:58:VAL:C	2.59	0.45
1:B:273:ASN:O	1:B:277:VAL:HG23	2.17	0.45
1:C:525:MET:HE1	1:C:527:VAL:HG23	1.99	0.45
1:B:333:SER:HB2	1:B:341:THR:HG23	1.99	0.45
1:C:49:CYS:SG	1:C:375:VAL:HG22	2.56	0.45
1:C:134:LEU:HB3	1:C:197:VAL:HG21	1.97	0.45
1:C:224:LYS:HG2	1:C:228:ASP:OD2	2.16	0.45
1:D:48:ILE:HG12	1:D:71:VAL:HB	1.99	0.45
1:D:168:VAL:CG2	1:D:185:VAL:HG21	2.46	0.45
1:A:20:ALA:C	1:A:29:HIS:HD1	2.25	0.45
1:A:334:MET:HE3	1:A:338:PRO:O	2.15	0.45
1:C:414:VAL:HG22	1:C:444:TYR:CZ	2.51	0.45
1:D:272:GLU:HG3	1:D:293:ALA:HB3	1.99	0.45
1:A:516:ARG:HG3	1:A:516:ARG:NH1	2.31	0.45
1:C:153:ASP:HB2	1:C:154:GLU:OE1	2.16	0.45
1:C:255:ARG:CG	1:C:255:ARG:NH1	2.79	0.45
1:D:417:VAL:HG21	1:D:444:TYR:HB2	1.98	0.45
1:A:55:SER:O	1:A:61:LEU:HD13	2.17	0.45
1:A:132:VAL:CG1	1:A:133:GLU:N	2.61	0.45
1:A:216:VAL:HG21	7:A:704:GOL:O2	2.17	0.45
1:A:409:THR:HG22	1:A:522:THR:HB	1.97	0.45
1:C:120:ARG:N	1:C:160:ASP:OD2	2.48	0.45
1:C:127:SER:HB3	1:C:130:ALA:CB	2.43	0.45
1:D:332:GLU:O	1:D:333:SER:C	2.60	0.45
1:A:21:ALA:HB2	8:A:728:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:272:GLU:OE2	1:D:296:ASP:OD2	2.35	0.45
1:C:216:VAL:HG23	1:C:216:VAL:O	2.16	0.45
1:A:301:ILE:HB	1:A:302:PRO:HD2	1.99	0.44
1:A:319:ARG:NH2	1:C:31:CYS:HB3	2.31	0.44
1:A:494:MET:HE3	1:A:531:PRO:HD3	1.99	0.44
1:C:318:ASN:HA	7:C:707:GOL:H11	1.99	0.44
1:D:458:GLN:O	1:D:462:GLN:HG3	2.17	0.44
1:A:34:ASP:HB3	1:A:37:SER:HB2	1.99	0.44
1:B:50:THR:HA	1:B:73:ARG:HB3	1.99	0.44
1:B:168:VAL:CG2	1:B:185:VAL:HG21	2.48	0.44
1:D:168:VAL:HG21	1:D:185:VAL:HG21	2.00	0.44
1:D:525:MET:HE1	1:D:527:VAL:HG23	1.99	0.44
1:A:356:ALA:O	1:A:467:ARG:NH1	2.50	0.44
1:B:224:LYS:HG2	1:B:228:ASP:OD2	2.17	0.44
1:D:414:VAL:HG22	1:D:444:TYR:CZ	2.52	0.44
1:A:50:THR:HA	1:A:73:ARG:HB3	2.00	0.44
1:D:157:LEU:CD1	1:D:203:LEU:HD21	2.47	0.44
1:A:16:GLN:OE1	1:A:447:ARG:HD2	2.18	0.44
1:A:136:LYS:HE2	1:A:198:GLU:O	2.17	0.44
1:B:15:THR:C	1:B:16:GLN:HG2	2.43	0.44
1:B:279:ARG:O	1:B:283:ILE:HG13	2.17	0.44
1:B:26:PHE:C	1:B:26:PHE:CD2	2.96	0.44
1:A:134:LEU:HD23	1:A:197:VAL:HG22	1.99	0.44
1:A:458:GLN:O	1:A:462:GLN:HG3	2.17	0.44
1:B:123:LEU:HD23	1:B:205:SER:HB3	2.00	0.44
1:C:123:LEU:HD23	1:C:205:SER:HB3	2.00	0.44
1:C:409:THR:HG22	1:C:522:THR:HB	2.00	0.44
1:B:255:ARG:NH2	1:B:288:ASP:OD1	2.51	0.44
1:D:159:LEU:HD22	1:D:209:VAL:HG21	2.00	0.44
1:A:168:VAL:HG21	1:A:185:VAL:HG21	1.99	0.43
1:A:270:LYS:HD2	1:A:291:MET:SD	2.58	0.43
1:C:153:ASP:C	1:C:155:ASN:H	2.26	0.43
1:D:20:ALA:C	1:D:29:HIS:HD1	2.25	0.43
1:D:272:GLU:CG	1:D:293:ALA:HB3	2.48	0.43
1:A:157:LEU:CD1	1:A:203:LEU:HD21	2.48	0.43
1:B:334:MET:HA	1:B:337:LYS:O	2.18	0.43
1:C:242:ALA:HB1	1:C:245:ILE:HD11	1.99	0.43
1:A:158:TRP:O	1:A:159:LEU:HD23	2.18	0.43
1:B:414:VAL:HG22	1:B:444:TYR:CZ	2.53	0.43
1:D:305:LYS:NZ	8:D:736:HOH:O	2.51	0.43
1:A:450:ILE:HB	1:A:469:ILE:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:ALA:C	1:B:29:HIS:HD1	2.26	0.43
1:A:211:LEU:O	1:A:214:ALA:HB3	2.19	0.43
1:C:270:LYS:NZ	3:C:533:OXL:O3	2.45	0.43
1:C:272:GLU:HG3	1:C:293:ALA:HB3	2.00	0.43
1:C:417:VAL:HG21	1:C:444:TYR:HB2	2.00	0.43
1:D:120:ARG:NH2	4:D:534:PO4:O2	2.38	0.43
1:A:273:ASN:O	1:A:277:VAL:HG23	2.19	0.43
1:B:148:TYR:CD2	1:B:151:LYS:HD2	2.52	0.43
1:D:333:SER:HB2	1:D:341:THR:HG23	1.99	0.43
1:C:48:ILE:HG12	1:C:71:VAL:HB	2.01	0.43
1:D:78:HIS:O	1:D:84:HIS:HE1	2.02	0.43
1:D:148:TYR:CD2	1:D:151:LYS:HD2	2.52	0.43
1:A:372:LEU:O	1:A:376:ARG:HG3	2.19	0.43
1:B:157:LEU:CD1	1:B:203:LEU:HD21	2.48	0.43
1:C:26:PHE:C	1:C:26:PHE:CD2	2.97	0.43
1:C:243:SER:OG	1:C:270:LYS:CE	2.65	0.43
1:C:285:GLU:O	7:C:709:GOL:C3	2.66	0.43
1:D:246:ARG:HG3	1:D:246:ARG:HH11	1.84	0.43
1:B:459:THR:HG22	8:B:720:HOH:O	2.19	0.43
1:A:31:CYS:CB	1:C:319:ARG:HH21	2.32	0.43
1:A:112:LEU:C	1:A:112:LEU:HD23	2.44	0.43
1:B:248:ALA:HB2	1:B:282:GLU:CG	2.36	0.43
1:B:272:GLU:HG3	1:B:293:ALA:HB3	2.00	0.43
1:C:50:THR:HA	1:C:73:ARG:HB3	2.01	0.43
1:C:272:GLU:OE2	1:C:296:ASP:OD2	2.37	0.43
1:A:102:PRO:HA	8:A:712:HOH:O	2.18	0.42
1:A:330:MET:HE2	1:A:348:VAL:HG22	2.00	0.42
1:B:401:LEU:HD12	1:D:27:LEU:HD23	2.00	0.42
1:C:334:MET:HE3	1:C:338:PRO:O	2.19	0.42
1:D:136:LYS:HE2	1:D:198:GLU:O	2.18	0.42
1:D:412:THR:OG1	1:D:523:ASN:HA	2.18	0.42
1:A:427:ALA:O	1:A:509:VAL:HG13	2.19	0.42
1:B:298:GLY:HA3	1:D:342:ARG:NE	2.34	0.42
1:B:304:GLU:CD	1:B:304:GLU:H	2.27	0.42
1:B:450:ILE:HB	1:B:469:ILE:HA	2.00	0.42
1:C:400:ARG:NH1	8:C:728:HOH:O	2.50	0.42
1:A:210:ASN:C	1:A:212:PRO:HD3	2.44	0.42
1:A:371:PRO:HG2	1:A:372:LEU:H	1.85	0.42
1:B:270:LYS:HD2	1:B:291:MET:SD	2.59	0.42
1:D:177:ASP:OD1	1:D:207:LYS:HD2	2.19	0.42
1:A:168:VAL:HG11	1:A:193:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:509:VAL:HG12	1:A:510:ILE:N	2.35	0.42
1:B:395:PHE:O	1:B:399:ARG:HG3	2.18	0.42
1:B:525:MET:HE1	1:B:527:VAL:HG23	2.01	0.42
1:C:407:ASP:OD2	1:C:407:ASP:C	2.62	0.42
1:D:57:SER:O	1:D:58:VAL:C	2.62	0.42
1:D:149:MET:HG3	1:D:150:GLU:HG3	2.01	0.42
1:B:168:VAL:HG21	1:B:185:VAL:HG21	2.01	0.42
1:C:390:TYR:CE2	1:C:393:GLN:HB2	2.54	0.42
1:A:272:GLU:CG	1:A:293:ALA:HB3	2.49	0.42
1:C:273:ASN:HA	1:C:300:GLU:HG2	2.02	0.42
1:D:26:PHE:C	1:D:26:PHE:CD2	2.98	0.42
1:A:23:ALA:HB2	1:A:32:ARG:NH1	2.34	0.42
1:A:418:GLU:OE1	1:B:399:ARG:NH1	2.53	0.42
1:D:132:VAL:HG11	1:D:154:GLU:CA	2.50	0.42
1:D:243:SER:HA	1:D:270:LYS:HE2	2.00	0.42
1:D:494:MET:HE3	1:D:531:PRO:HD3	2.02	0.42
1:B:319:ARG:NH2	1:D:31:CYS:HB3	2.35	0.42
1:D:118:GLU:OE2	1:D:120:ARG:HD2	2.19	0.42
1:A:31:CYS:HB3	1:C:319:ARG:HH21	1.85	0.42
1:A:175:TYR:CE2	1:A:212:PRO:HG2	2.55	0.42
1:C:273:ASN:O	1:C:277:VAL:HG23	2.20	0.42
1:C:341:THR:OG1	1:C:344:GLU:HG3	2.20	0.42
1:C:463:ALA:HB1	1:C:469:ILE:HG21	2.02	0.41
1:A:74:LEU:HD11	1:A:88:ILE:HG12	2.02	0.41
1:B:272:GLU:OE2	1:B:296:ASP:OD2	2.37	0.41
1:C:15:THR:C	1:C:16:GLN:HG2	2.44	0.41
1:A:266:LYS:HA	1:A:266:LYS:HD3	1.88	0.41
1:A:407:ASP:OD2	1:A:407:ASP:C	2.64	0.41
1:B:297:LEU:O	1:B:301:ILE:HG12	2.20	0.41
1:C:112:LEU:C	1:C:112:LEU:HD23	2.44	0.41
1:D:472:VAL:HG21	1:D:496:VAL:HG11	2.01	0.41
1:C:168:VAL:HG21	1:C:185:VAL:HG21	2.02	0.41
1:D:134:LEU:HD23	1:D:197:VAL:HG22	2.02	0.41
1:A:123:LEU:HD23	1:A:205:SER:HB3	2.01	0.41
1:A:124:ILE:O	1:A:125:LYS:C	2.63	0.41
1:A:149:MET:HG3	1:A:150:GLU:HG3	2.03	0.41
1:B:242:ALA:O	1:B:270:LYS:HG3	2.20	0.41
1:C:26:PHE:C	1:C:26:PHE:HD2	2.29	0.41
1:A:15:THR:C	1:A:16:GLN:HG2	2.45	0.41
1:A:280:PHE:CD1	1:A:313:MET:HG2	2.55	0.41
1:A:288:ASP:O	1:A:323:PRO:HD2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:PRO:HA	1:A:357:ASP:OD1	2.20	0.41
1:A:332:GLU:O	1:A:333:SER:C	2.62	0.41
1:A:391:HIS:HB2	8:A:723:HOH:O	2.21	0.41
1:B:246:ARG:HG3	1:B:246:ARG:HH11	1.85	0.41
1:D:472:VAL:CG2	1:D:496:VAL:HG11	2.50	0.41
1:A:162:LYS:C	1:A:164:ILE:H	2.27	0.41
1:A:417:VAL:HG21	1:A:444:TYR:HB2	2.03	0.41
1:B:132:VAL:HG11	1:B:154:GLU:CA	2.50	0.41
1:D:334:MET:HE3	1:D:338:PRO:O	2.21	0.41
1:A:118:GLU:OE2	1:A:120:ARG:HD2	2.20	0.41
1:B:26:PHE:C	1:B:26:PHE:HD2	2.27	0.41
1:B:162:LYS:C	1:B:164:ILE:H	2.28	0.41
1:C:57:SER:O	1:C:58:VAL:C	2.64	0.41
1:C:57:SER:OG	8:C:737:HOH:O	2.22	0.41
1:C:148:TYR:CD2	1:C:151:LYS:HD2	2.53	0.41
1:D:15:THR:C	1:D:16:GLN:HG2	2.45	0.41
1:A:132:VAL:HG11	1:A:154:GLU:CA	2.49	0.41
1:A:509:VAL:CG1	1:A:510:ILE:N	2.84	0.41
1:C:73:ARG:HH11	1:C:113:ASP:CG	2.28	0.41
1:C:296:ASP:OD2	3:C:533:OXL:O2	2.39	0.41
1:C:334:MET:HA	1:C:337:LYS:O	2.21	0.41
1:C:390:TYR:CD2	1:C:393:GLN:HB3	2.56	0.41
1:C:445:ARG:NH2	7:C:707:GOL:H12	2.23	0.41
1:C:502:PHE:N	1:C:502:PHE:CD1	2.89	0.41
1:D:242:ALA:O	1:D:270:LYS:HG3	2.21	0.41
1:D:273:ASN:O	1:D:277:VAL:HG23	2.21	0.41
1:A:333:SER:HB2	1:A:341:THR:HG23	2.03	0.41
1:B:505:LYS:O	1:B:530:VAL:HB	2.21	0.41
1:D:123:LEU:HD23	1:D:205:SER:HB3	2.03	0.41
1:D:301:ILE:HB	1:D:302:PRO:HD2	2.03	0.41
1:B:272:GLU:CG	1:B:293:ALA:HB3	2.51	0.40
1:B:409:THR:HG21	8:B:711:HOH:O	2.21	0.40
1:C:132:VAL:HG11	1:C:154:GLU:CA	2.50	0.40
1:C:332:GLU:O	1:C:333:SER:C	2.64	0.40
1:C:412:THR:OG1	1:C:523:ASN:HA	2.21	0.40
1:D:307:PHE:HA	8:D:722:HOH:O	2.20	0.40
1:A:127:SER:HB3	1:A:130:ALA:CB	2.42	0.40
1:C:134:LEU:HD23	1:C:197:VAL:HG22	2.03	0.40
1:C:168:VAL:CG2	1:C:185:VAL:HG21	2.51	0.40
1:D:78:HIS:O	1:D:84:HIS:CE1	2.74	0.40
1:B:332:GLU:O	1:B:333:SER:C	2.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:427:ALA:HA	1:C:448:ALA:HB1	2.02	0.40
1:C:472:VAL:CG2	1:C:496:VAL:HG11	2.52	0.40
1:D:168:VAL:HG11	1:D:193:LEU:HD11	2.02	0.40
1:B:112:LEU:C	1:B:112:LEU:HD23	2.46	0.40
1:C:143:THR:C	1:C:144:LEU:HD12	2.47	0.40
1:D:136:LYS:HB2	1:D:136:LYS:HE3	1.89	0.40
1:D:162:LYS:C	1:D:164:ILE:H	2.29	0.40
1:D:505:LYS:O	1:D:530:VAL:HB	2.21	0.40
1:A:153:ASP:C	1:A:155:ASN:H	2.29	0.40
1:B:146:ASN:O	1:B:149:MET:HG2	2.22	0.40
1:B:153:ASP:C	1:B:155:ASN:H	2.30	0.40
1:B:168:VAL:HG11	1:B:193:LEU:HD11	2.04	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	517/567 (91%)	479 (93%)	28 (5%)	10 (2%)	6	22
1	B	517/567 (91%)	477 (92%)	30 (6%)	10 (2%)	6	22
1	C	517/567 (91%)	482 (93%)	24 (5%)	11 (2%)	5	20
1	D	517/567 (91%)	479 (93%)	27 (5%)	11 (2%)	5	20
All	All	2068/2268 (91%)	1917 (93%)	109 (5%)	42 (2%)	6	21

All (42) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	154	GLU
1	B	154	GLU
1	C	154	GLU

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Mol	Chain	Res	Type
1	D	154	GLU
1	A	125	LYS
1	A	132	VAL
1	A	523	ASN
1	B	125	LYS
1	B	132	VAL
1	B	523	ASN
1	C	125	LYS
1	C	259	GLY
1	C	523	ASN
1	D	125	LYS
1	D	132	VAL
1	D	523	ASN
1	A	179	GLY
1	A	206	LYS
1	A	507	ASP
1	B	206	LYS
1	B	259	GLY
1	C	132	VAL
1	C	146	ASN
1	C	206	LYS
1	C	507	ASP
1	D	206	LYS
1	D	507	ASP
1	A	259	GLY
1	B	146	ASN
1	B	507	ASP
1	D	259	GLY
1	A	14	GLN
1	A	328	THR
1	B	14	GLN
1	C	14	GLN
1	D	14	GLN
1	D	146	ASN
1	D	328	THR
1	B	328	THR
1	C	328	THR
1	C	179	GLY
1	D	179	GLY

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	427/466 (92%)	414 (97%)	13 (3%)	36	72
1	B	427/466 (92%)	417 (98%)	10 (2%)	44	78
1	C	427/466 (92%)	416 (97%)	11 (3%)	40	75
1	D	427/466 (92%)	415 (97%)	12 (3%)	38	73
All	All	1708/1864 (92%)	1662 (97%)	46 (3%)	39	74

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	THR
1	A	53	PRO
1	A	92	ARG
1	A	156	ILE
1	A	199	ASN
1	A	255	ARG
1	A	260	GLU
1	A	294	ARG
1	A	304	GLU
1	A	396	GLU
1	A	472	VAL
1	A	516	ARG
1	A	525	MET
1	B	25	THR
1	B	156	ILE
1	B	199	ASN
1	B	255	ARG
1	B	260	GLU
1	B	304	GLU
1	B	396	GLU
1	B	472	VAL
1	B	516	ARG
1	B	525	MET
1	C	25	THR

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Mol	Chain	Res	Type
1	C	53	PRO
1	C	156	ILE
1	C	199	ASN
1	C	255	ARG
1	C	260	GLU
1	C	304	GLU
1	C	396	GLU
1	C	472	VAL
1	C	516	ARG
1	C	525	MET
1	D	25	THR
1	D	156	ILE
1	D	199	ASN
1	D	247	LYS
1	D	255	ARG
1	D	260	GLU
1	D	294	ARG
1	D	304	GLU
1	D	396	GLU
1	D	472	VAL
1	D	516	ARG
1	D	525	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	ASN
1	A	146	ASN
1	A	184	GLN
1	A	252	HIS
1	A	391	HIS
1	A	393	GLN
1	A	439	HIS
1	A	462	GLN
1	B	70	ASN
1	B	146	ASN
1	B	252	HIS
1	B	393	GLN
1	B	439	HIS
1	B	462	GLN
1	C	70	ASN
1	C	252	HIS

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Mol	Chain	Res	Type
1	C	393	GLN
1	C	439	HIS
1	C	462	GLN
1	C	491	ASN
1	D	70	ASN
1	D	84	HIS
1	D	155	ASN
1	D	184	GLN
1	D	252	HIS
1	D	393	GLN
1	D	439	HIS
1	D	462	GLN
1	D	491	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 40 ligands modelled in this entry, 8 are monoatomic - leaving 32 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	$\# Z > 2$
7	GOL	B	704	-	5,5,5	0.99	0	5,5,5	0.24	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	GOL	A	704	-	5,5,5	0.86	0	5,5,5	0.44	0
7	GOL	C	709	-	5,5,5	0.71	0	5,5,5	0.34	0
7	GOL	B	706	-	5,5,5	1.03	0	5,5,5	0.19	0
4	PO4	B	534	-	4,4,4	2.69	2 (50%)	6,6,6	0.95	0
7	GOL	A	705	-	5,5,5	0.86	0	5,5,5	0.13	0
7	GOL	D	706	-	5,5,5	1.21	0	5,5,5	0.41	0
3	OXL	A	533	5	5,5,5	1.46	1 (20%)	6,6,6	2.28	2 (33%)
7	GOL	A	703	-	5,5,5	0.81	0	5,5,5	0.18	0
7	GOL	B	705	-	5,5,5	0.85	0	5,5,5	0.30	0
7	GOL	C	708	-	5,5,5	0.85	0	5,5,5	0.21	0
7	GOL	D	707	-	5,5,5	0.65	0	5,5,5	0.27	0
2	FBP	B	532	-	18,20,20	1.56	5 (27%)	21,32,32	0.97	2 (9%)
3	OXL	D	533	5	5,5,5	1.60	2 (40%)	6,6,6	2.14	2 (33%)
2	FBP	A	532	-	18,20,20	1.49	3 (16%)	21,32,32	0.89	0
7	GOL	C	704	-	5,5,5	0.81	0	5,5,5	0.28	0
7	GOL	C	705	-	5,5,5	1.02	0	5,5,5	0.27	0
4	PO4	A	534	-	4,4,4	2.23	2 (50%)	6,6,6	1.00	0
7	GOL	D	705	-	5,5,5	0.80	0	5,5,5	0.27	0
7	GOL	D	709	-	5,5,5	1.22	0	5,5,5	0.38	0
7	GOL	A	702	-	5,5,5	0.63	0	5,5,5	0.25	0
7	GOL	C	706	-	5,5,5	0.45	0	5,5,5	0.58	0
7	GOL	D	708	-	5,5,5	1.09	0	5,5,5	0.35	0
4	PO4	C	534	-	4,4,4	1.94	1 (25%)	6,6,6	1.25	0
2	FBP	C	532	-	18,20,20	1.54	4 (22%)	21,32,32	0.87	1 (4%)
7	GOL	A	706	-	5,5,5	0.97	0	5,5,5	0.50	0
7	GOL	B	703	-	5,5,5	0.67	0	5,5,5	0.31	0
3	OXL	B	533	5	5,5,5	1.36	1 (20%)	6,6,6	2.35	2 (33%)
7	GOL	C	707	-	5,5,5	0.69	0	5,5,5	0.40	0
3	OXL	C	533	5	5,5,5	1.46	1 (20%)	6,6,6	2.28	2 (33%)
4	PO4	D	534	-	4,4,4	2.56	1 (25%)	6,6,6	0.86	0
2	FBP	D	532	-	18,20,20	1.48	3 (16%)	21,32,32	0.84	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
7	GOL	B	704	-	-	4/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	GOL	A	704	-	-	3/4/4/4	-
7	GOL	C	709	-	-	4/4/4/4	-
7	GOL	B	706	-	-	4/4/4/4	-
7	GOL	A	705	-	-	0/4/4/4	-
7	GOL	D	706	-	-	2/4/4/4	-
3	OXL	A	533	5	-	0/4/4/4	-
7	GOL	A	703	-	-	4/4/4/4	-
7	GOL	B	705	-	-	2/4/4/4	-
7	GOL	C	708	-	-	2/4/4/4	-
7	GOL	D	707	-	-	1/4/4/4	-
2	FBP	B	532	-	-	1/13/32/32	0/1/1/1
3	OXL	D	533	5	-	0/4/4/4	-
2	FBP	A	532	-	-	1/13/32/32	0/1/1/1
7	GOL	C	704	-	-	4/4/4/4	-
7	GOL	C	705	-	-	2/4/4/4	-
7	GOL	D	705	-	-	4/4/4/4	-
7	GOL	D	709	-	-	2/4/4/4	-
7	GOL	A	702	-	-	3/4/4/4	-
7	GOL	C	706	-	-	3/4/4/4	-
7	GOL	D	708	-	-	0/4/4/4	-
2	FBP	C	532	-	-	1/13/32/32	0/1/1/1
7	GOL	A	706	-	-	4/4/4/4	-
7	GOL	B	703	-	-	2/4/4/4	-
3	OXL	B	533	5	-	0/4/4/4	-
7	GOL	C	707	-	-	2/4/4/4	-
3	OXL	C	533	5	-	0/4/4/4	-
2	FBP	D	532	-	-	1/13/32/32	0/1/1/1

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	534	PO4	P-O1	4.73	1.61	1.50
4	D	534	PO4	P-O1	4.53	1.61	1.50
2	B	532	FBP	P1-O3P	-3.70	1.41	1.54
4	C	534	PO4	P-O1	3.66	1.59	1.50
4	A	534	PO4	P-O1	3.66	1.59	1.50
2	A	532	FBP	P1-O3P	-3.45	1.42	1.54
2	C	532	FBP	P1-O3P	-3.33	1.42	1.54
2	D	532	FBP	P1-O3P	-3.25	1.42	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	532	FBP	O2-C2	3.24	1.46	1.40
2	B	532	FBP	O5-C2	2.69	1.47	1.43
2	B	532	FBP	P1-O2P	-2.53	1.45	1.54
2	A	532	FBP	P2-O5P	-2.50	1.45	1.54
2	D	532	FBP	O5-C2	2.47	1.47	1.43
2	D	532	FBP	P2-O5P	-2.43	1.45	1.54
2	C	532	FBP	O5-C2	2.24	1.47	1.43
4	B	534	PO4	P-O3	2.24	1.61	1.54
2	C	532	FBP	O3-C3	-2.23	1.38	1.42
3	B	533	OXL	O4-C2	-2.23	1.24	1.30
4	A	534	PO4	P-O3	2.22	1.61	1.54
3	D	533	OXL	O2-C2	2.15	1.27	1.22
3	A	533	OXL	O2-C2	2.13	1.27	1.22
2	A	532	FBP	P1-O2P	-2.13	1.46	1.54
2	B	532	FBP	P2-O5P	-2.06	1.47	1.54
3	C	533	OXL	O4-C2	-2.05	1.25	1.30
3	D	533	OXL	O4-C2	-2.02	1.25	1.30
2	B	532	FBP	O3-C3	-2.00	1.38	1.42

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	533	OXL	O3-C1-C2	4.14	120.87	112.83
3	B	533	OXL	O3-C1-C2	4.09	120.77	112.83
3	D	533	OXL	O3-C1-C2	3.96	120.51	112.83
3	C	533	OXL	O3-C1-C2	3.67	119.95	112.83
3	B	533	OXL	O1-C1-C2	-3.59	113.15	120.63
3	C	533	OXL	O1-C1-C2	-3.31	113.73	120.63
3	A	533	OXL	O1-C1-C2	-3.30	113.75	120.63
3	D	533	OXL	O1-C1-C2	-3.04	114.30	120.63
2	B	532	FBP	O2-C2-O5	2.34	113.82	109.33
2	B	532	FBP	O2P-P1-O1	2.11	112.16	106.67
2	C	532	FBP	O2P-P1-O1	2.11	112.16	106.67

There are no chirality outliers.

All (56) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	703	GOL	C1-C2-C3-O3
7	A	706	GOL	O1-C1-C2-C3
7	A	706	GOL	C1-C2-C3-O3
7	B	703	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
7	B	704	GOL	O1-C1-C2-C3
7	B	704	GOL	C1-C2-C3-O3
7	B	705	GOL	O1-C1-C2-O2
7	B	705	GOL	O1-C1-C2-C3
7	B	706	GOL	C1-C2-C3-O3
7	B	706	GOL	O2-C2-C3-O3
7	C	704	GOL	C1-C2-C3-O3
7	C	707	GOL	O1-C1-C2-O2
7	C	707	GOL	O1-C1-C2-C3
7	C	709	GOL	C1-C2-C3-O3
7	D	705	GOL	O1-C1-C2-O2
7	D	709	GOL	O1-C1-C2-C3
7	A	704	GOL	O1-C1-C2-O2
7	A	702	GOL	C1-C2-C3-O3
7	A	703	GOL	O1-C1-C2-C3
7	A	704	GOL	O1-C1-C2-C3
7	B	706	GOL	O1-C1-C2-C3
7	C	705	GOL	C1-C2-C3-O3
7	C	708	GOL	O1-C1-C2-C3
7	C	709	GOL	O1-C1-C2-C3
7	D	705	GOL	O1-C1-C2-C3
7	D	705	GOL	C1-C2-C3-O3
7	D	706	GOL	C1-C2-C3-O3
7	A	702	GOL	O2-C2-C3-O3
7	A	703	GOL	O2-C2-C3-O3
7	A	706	GOL	O2-C2-C3-O3
7	B	703	GOL	O2-C2-C3-O3
7	B	704	GOL	O2-C2-C3-O3
7	C	704	GOL	O2-C2-C3-O3
7	C	708	GOL	O1-C1-C2-O2
7	C	709	GOL	O1-C1-C2-O2
7	C	709	GOL	O2-C2-C3-O3
7	D	705	GOL	O2-C2-C3-O3
7	D	709	GOL	O1-C1-C2-O2
7	A	706	GOL	O1-C1-C2-O2
7	C	705	GOL	O2-C2-C3-O3
7	A	704	GOL	O2-C2-C3-O3
7	B	704	GOL	O1-C1-C2-O2
7	C	706	GOL	O2-C2-C3-O3
7	C	706	GOL	O1-C1-C2-C3
7	B	706	GOL	O1-C1-C2-O2
7	D	706	GOL	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
2	A	532	FBP	O5-C5-C6-O6
2	D	532	FBP	O5-C5-C6-O6
7	C	704	GOL	O1-C1-C2-C3
7	C	704	GOL	O1-C1-C2-O2
2	B	532	FBP	O5-C5-C6-O6
7	C	706	GOL	O1-C1-C2-O2
2	C	532	FBP	O5-C5-C6-O6
7	A	702	GOL	O1-C1-C2-C3
7	A	703	GOL	O1-C1-C2-O2
7	D	707	GOL	O1-C1-C2-O2

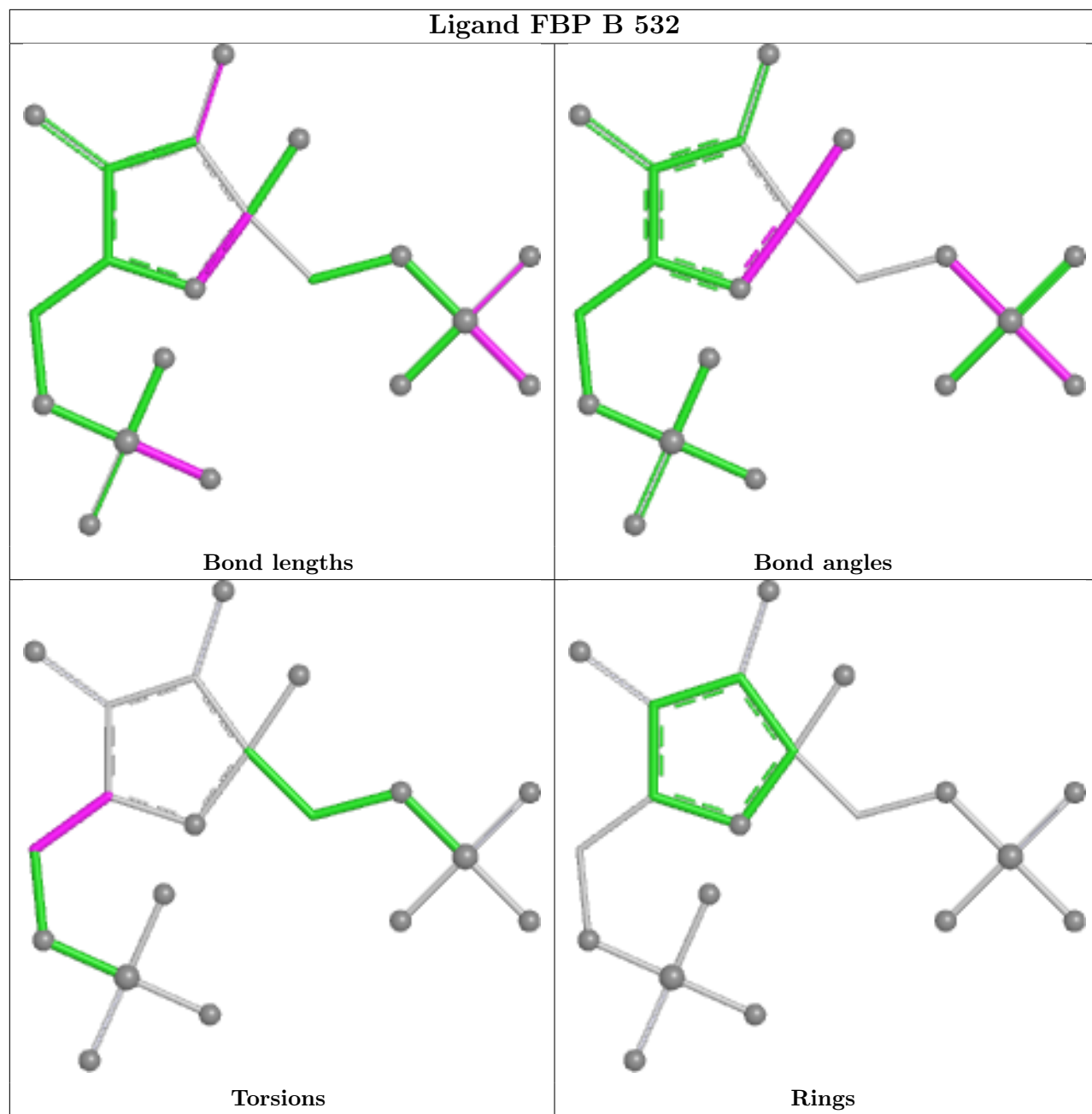
There are no ring outliers.

14 monomers are involved in 23 short contacts:

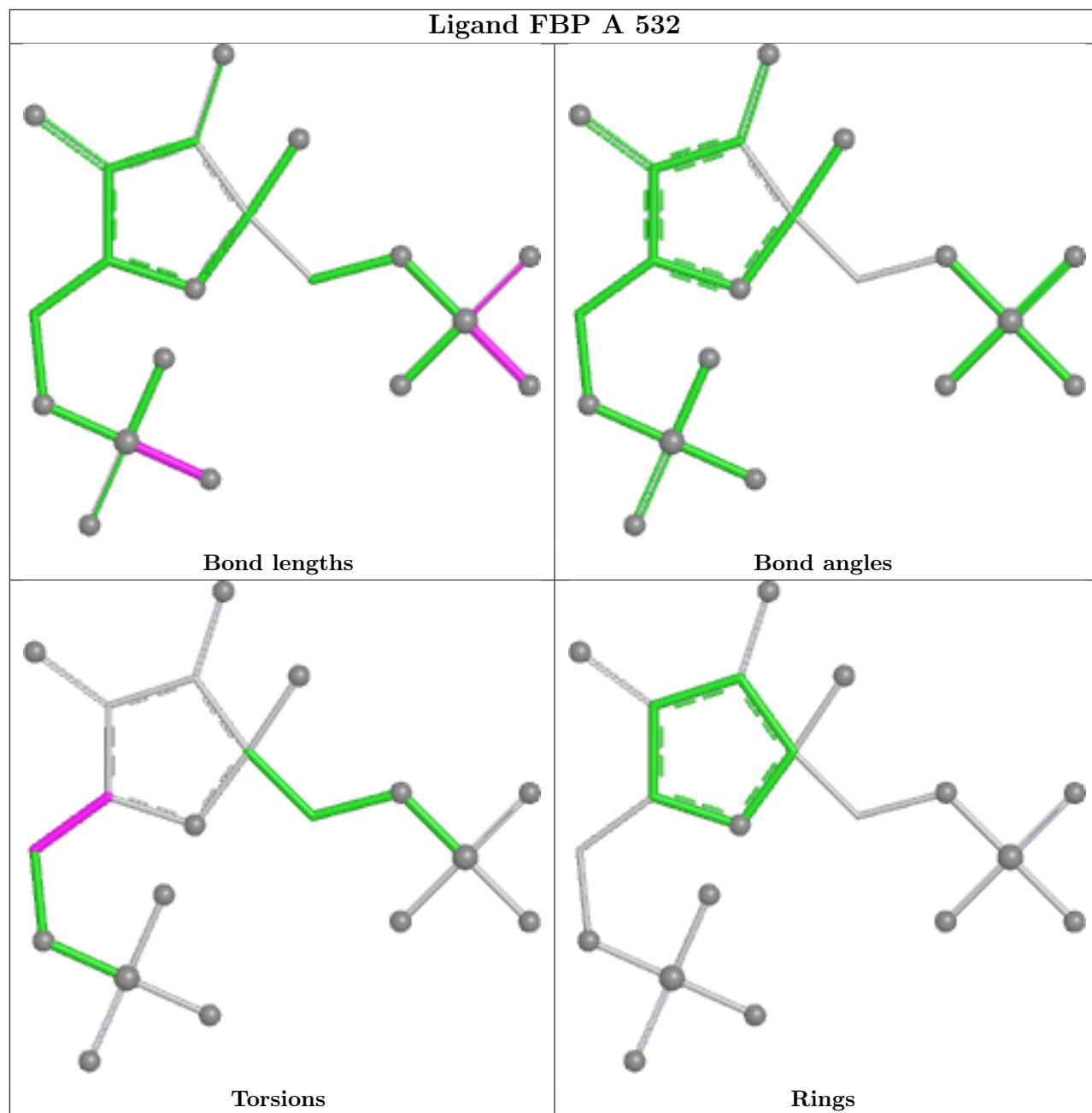
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	704	GOL	1	0
7	C	709	GOL	2	0
2	B	532	FBP	1	0
3	D	533	OXL	1	0
2	A	532	FBP	1	0
7	C	704	GOL	1	0
7	D	705	GOL	1	0
7	C	706	GOL	1	0
2	C	532	FBP	2	0
3	B	533	OXL	1	0
7	C	707	GOL	7	0
3	C	533	OXL	2	0
4	D	534	PO4	1	0
2	D	532	FBP	1	0

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.

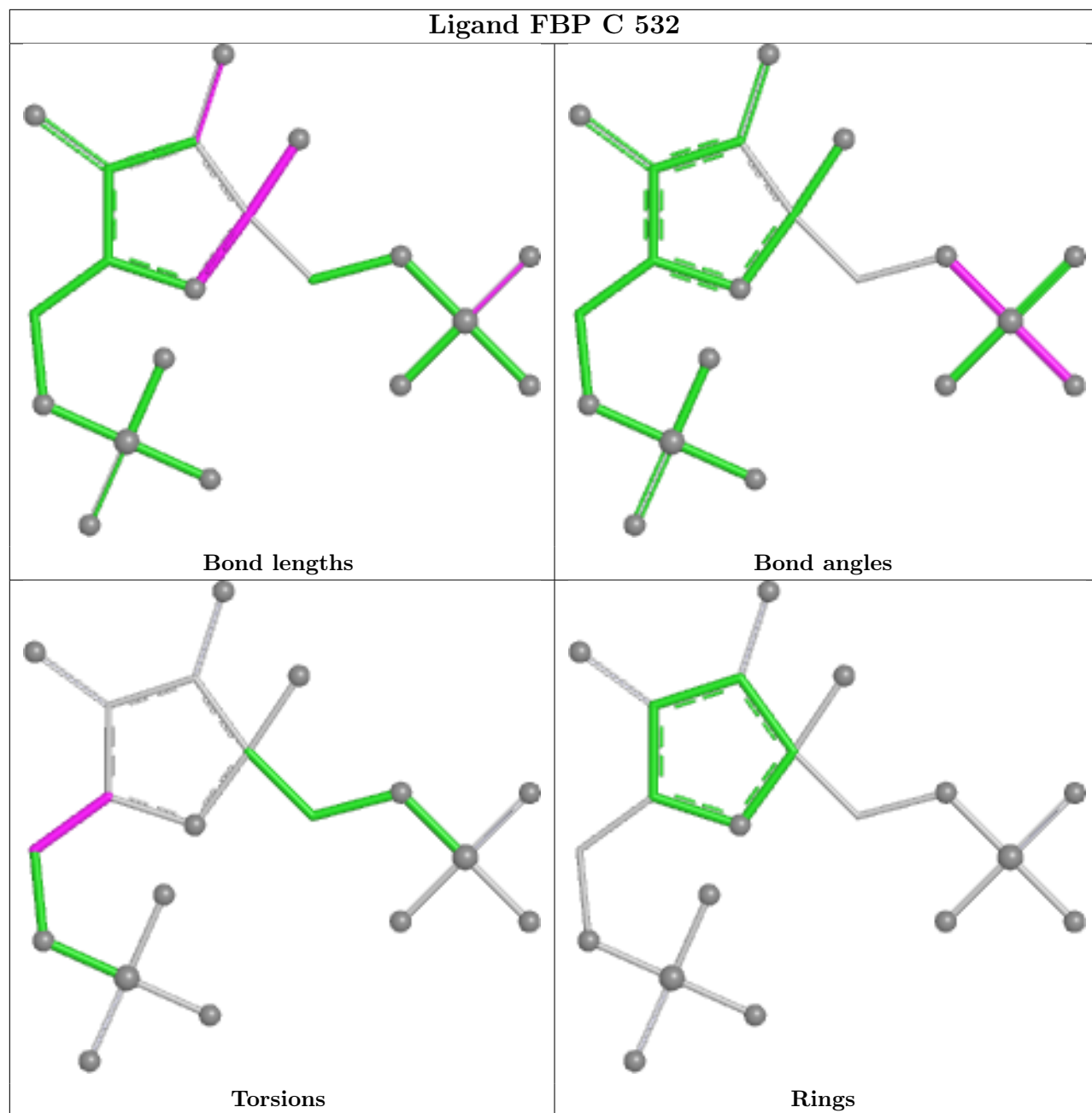
Ligand FBP B 532

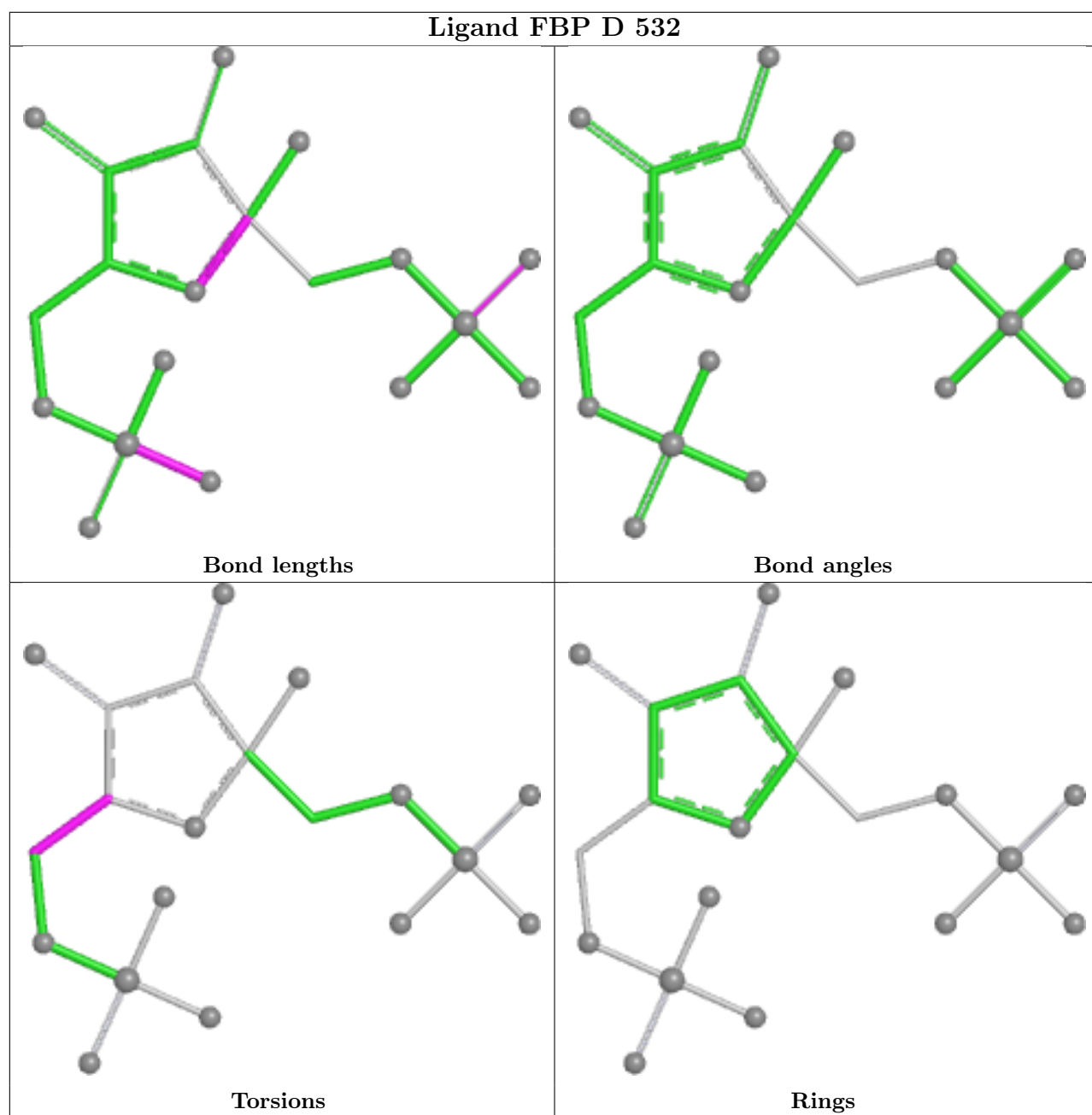


Ligand FBP A 532



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	519/567 (91%)	-0.21	6 (1%) 76 68	23, 60, 99, 99	0
1	B	519/567 (91%)	-0.25	3 (0%) 85 80	29, 65, 99, 99	0
1	C	519/567 (91%)	-0.14	4 (0%) 82 75	26, 65, 97, 99	0
1	D	519/567 (91%)	-0.16	5 (0%) 79 72	34, 69, 99, 99	0
All	All	2076/2268 (91%)	-0.19	18 (0%) 81 74	23, 65, 99, 99	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	142	ILE	3.2
1	D	14	GLN	3.2
1	C	15	THR	3.1
1	D	140	LEU	3.1
1	C	127	SER	3.1
1	D	195	THR	2.9
1	A	157	LEU	2.9
1	A	156	ILE	2.6
1	A	13	ILE	2.5
1	D	126	GLY	2.5
1	B	148	TYR	2.5
1	D	200	GLY	2.4
1	A	134	LEU	2.3
1	B	13	ILE	2.3
1	A	190	ALA	2.3
1	B	124	ILE	2.1
1	C	18	LEU	2.1
1	C	13	ILE	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
7	GOL	A	706	6/6	0.68	0.19	42,42,42,42	0
7	GOL	D	706	6/6	0.68	0.12	66,66,66,66	0
7	GOL	B	703	6/6	0.76	0.12	66,66,66,66	0
7	GOL	B	705	6/6	0.78	0.11	66,66,66,66	0
7	GOL	C	705	6/6	0.80	0.13	66,66,66,66	0
7	GOL	C	707	6/6	0.80	0.22	66,66,66,66	0
7	GOL	C	704	6/6	0.80	0.14	66,66,66,66	0
7	GOL	B	704	6/6	0.81	0.11	66,66,66,66	0
7	GOL	A	702	6/6	0.81	0.10	66,66,66,66	0
7	GOL	C	708	6/6	0.82	0.11	66,66,66,66	0
4	PO4	B	534	5/5	0.82	0.18	66,66,66,66	0
6	K	C	703	1/1	0.83	0.17	66,66,66,66	0
6	K	A	701	1/1	0.84	0.17	66,66,66,66	0
7	GOL	D	709	6/6	0.84	0.14	42,42,42,42	0
4	PO4	C	534	5/5	0.85	0.15	66,66,66,66	0
7	GOL	D	708	6/6	0.85	0.10	66,66,66,66	0
7	GOL	A	703	6/6	0.85	0.09	66,66,66,66	0
7	GOL	B	706	6/6	0.86	0.10	42,42,42,42	0
7	GOL	A	704	6/6	0.86	0.12	66,66,66,66	0
7	GOL	A	705	6/6	0.88	0.09	66,66,66,66	0
2	FBP	C	532	20/20	0.88	0.10	66,66,66,66	0
7	GOL	C	709	6/6	0.88	0.10	42,42,42,42	0
2	FBP	D	532	20/20	0.89	0.10	66,66,66,66	0
4	PO4	D	534	5/5	0.89	0.14	66,66,66,66	0
7	GOL	D	705	6/6	0.89	0.09	66,66,66,66	0
7	GOL	C	706	6/6	0.90	0.12	66,66,66,66	0
3	OXL	C	533	6/6	0.90	0.12	66,66,66,66	0

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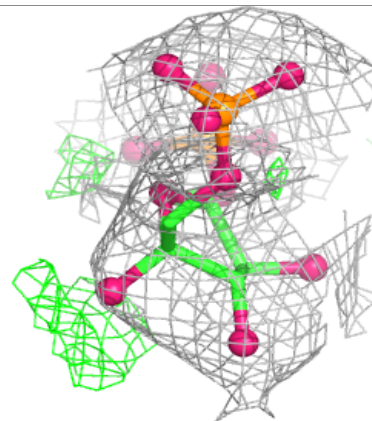
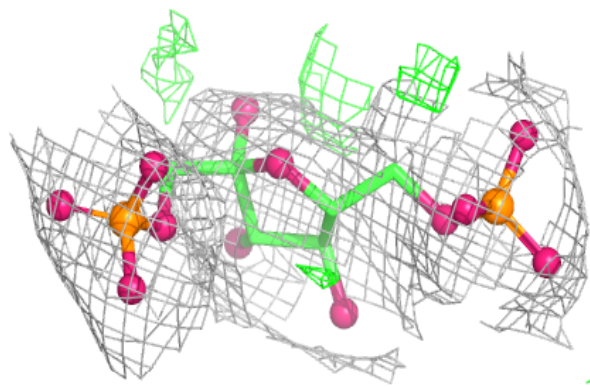
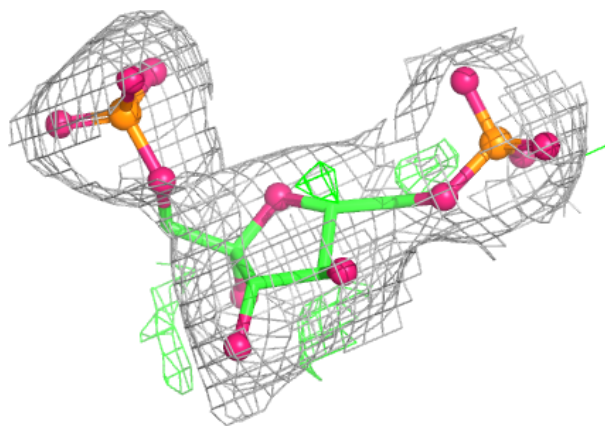
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	PO4	A	534	5/5	0.90	0.17	66,66,66,66	0
6	K	B	702	1/1	0.90	0.14	66,66,66,66	0
6	K	D	704	1/1	0.91	0.11	66,66,66,66	0
3	OXL	A	533	6/6	0.91	0.09	66,66,66,66	0
7	GOL	D	707	6/6	0.92	0.08	66,66,66,66	0
2	FBP	B	532	20/20	0.93	0.10	66,66,66,66	0
3	OXL	D	533	6/6	0.93	0.08	66,66,66,66	0
5	MG	A	601	1/1	0.94	0.12	66,66,66,66	0
5	MG	C	603	1/1	0.94	0.19	66,66,66,66	0
3	OXL	B	533	6/6	0.95	0.06	66,66,66,66	0
5	MG	D	604	1/1	0.95	0.06	66,66,66,66	0
2	FBP	A	532	20/20	0.96	0.07	66,66,66,66	0
5	MG	B	602	1/1	0.96	0.12	66,66,66,66	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.

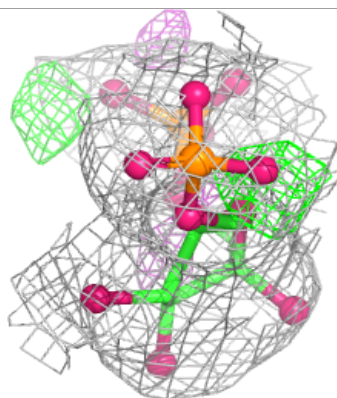
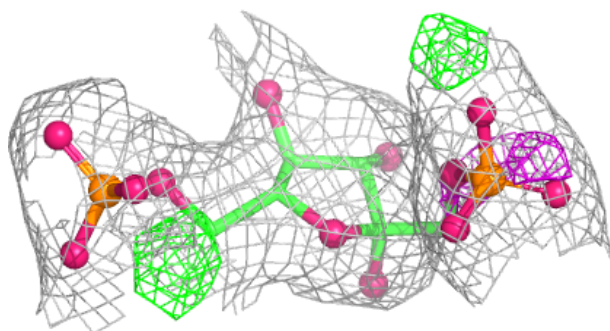
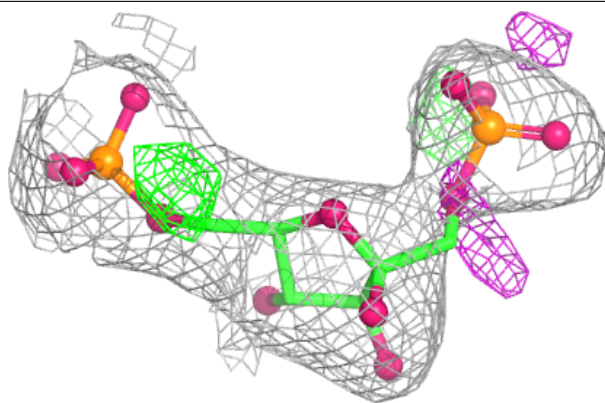
Electron density around FBP C 532:

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

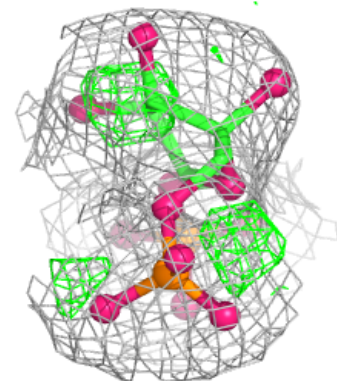
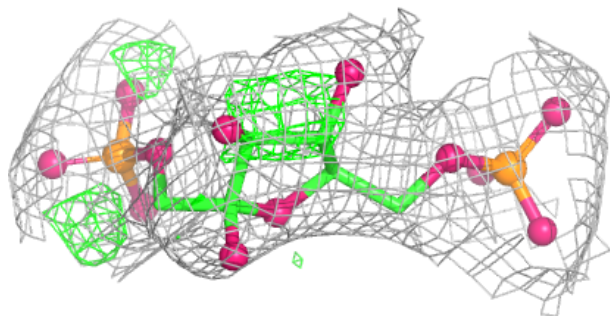
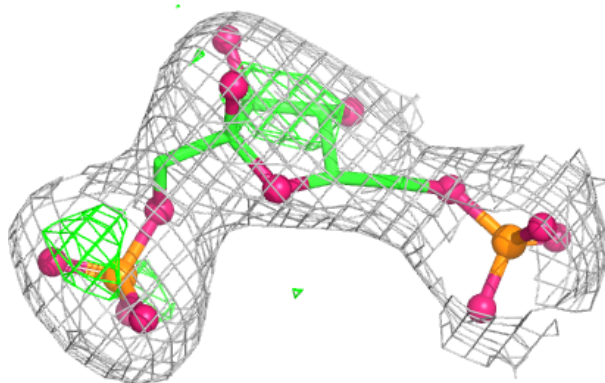


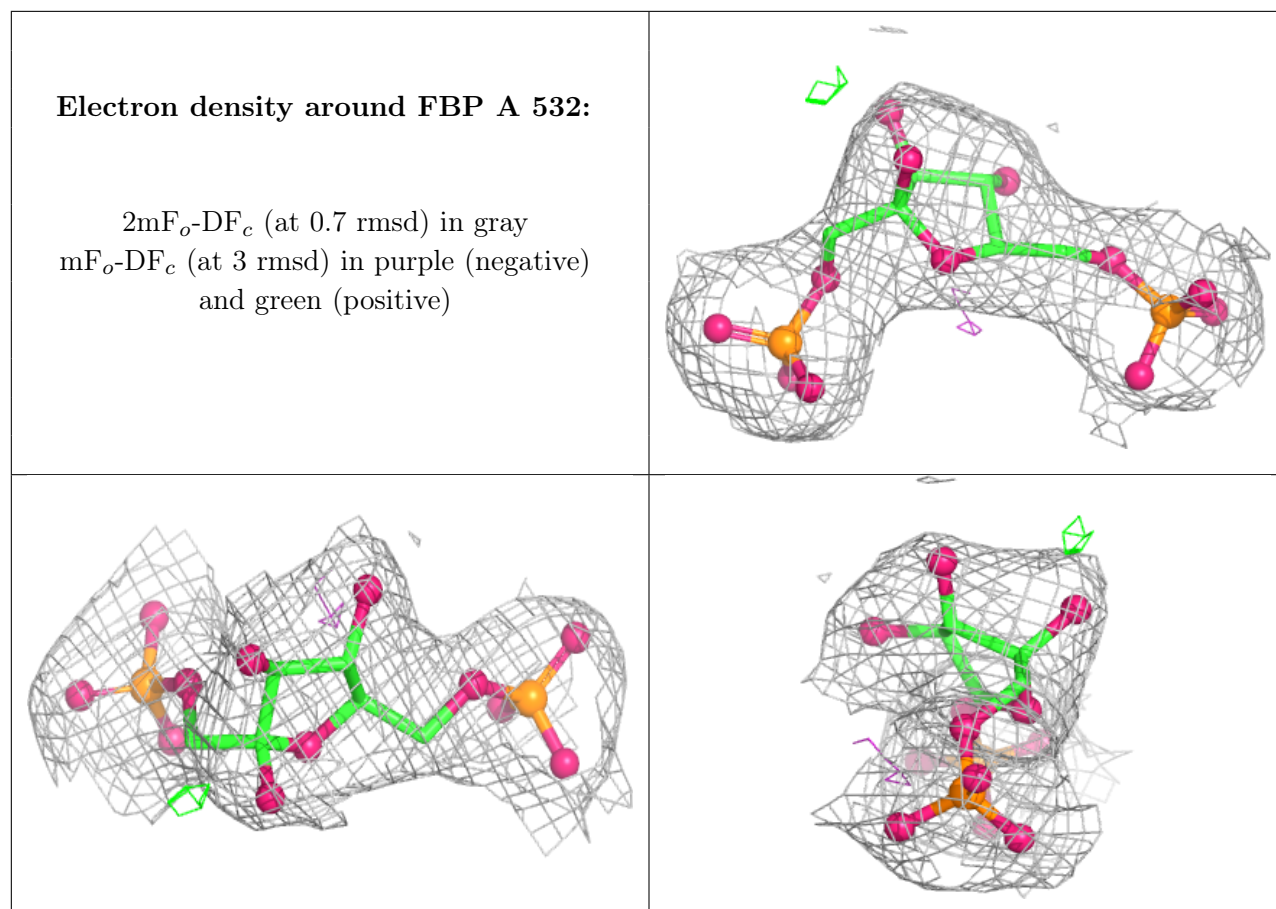
Electron density around FBP D 532:

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

**Electron density around FBP 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)





6.5 Other polymers ⓘ

There are no such residues in this entry.