



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 03:32 am GMT

PDB ID : 1T5A
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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

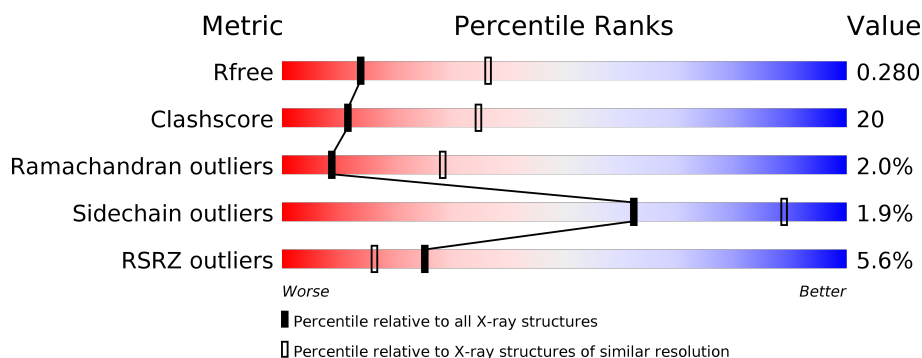
1 Overall quality at a glance

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}	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>7%</div> <div> <div></div> <div>60%</div> <div>29%</div> <div>8%</div> </div> </div>
1	B	567	<div> <div>6%</div> <div> <div></div> <div>62%</div> <div>27%</div> <div>8%</div> </div> </div>
1	C	567	<div> <div>2%</div> <div> <div></div> <div>60%</div> <div>29%</div> <div>8%</div> </div> </div>
1	D	567	<div> <div>6%</div> <div> <div></div> <div>61%</div> <div>28%</div> <div>8%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	OXL	C	533	-	-	X	X
3	OXL	D	533	-	-	-	X
7	GOL	A	703	-	-	-	X
7	GOL	B	704	-	-	-	X
7	GOL	B	705	-	-	-	X
7	GOL	C	705	-	-	-	X
7	GOL	C	707	-	-	X	X
7	GOL	C	709	-	-	-	X
7	GOL	D	708	-	-	-	X
7	GOL	D	709	-	-	-	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 MET	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 MET	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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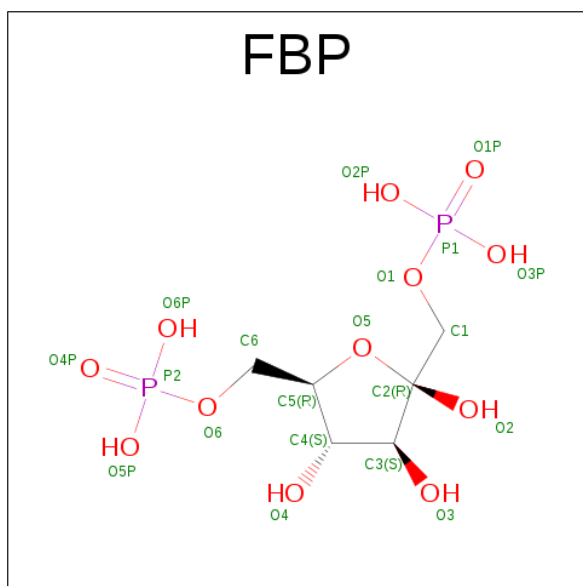
Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	ASP	-	CLONING ARTIFACT	UNP P14618
C	-3	HIS	-	CLONING ARTIFACT	UNP P14618
C	-2	PRO	-	CLONING ARTIFACT	UNP P14618
C	-1	PHE	-	CLONING ARTIFACT	UNP P14618
C	0	THR	-	CLONING ARTIFACT	UNP P14618
C	1	MET	-	INITIATING MET	UNP P14618
D	-35	MET	-	CLONING ARTIFACT	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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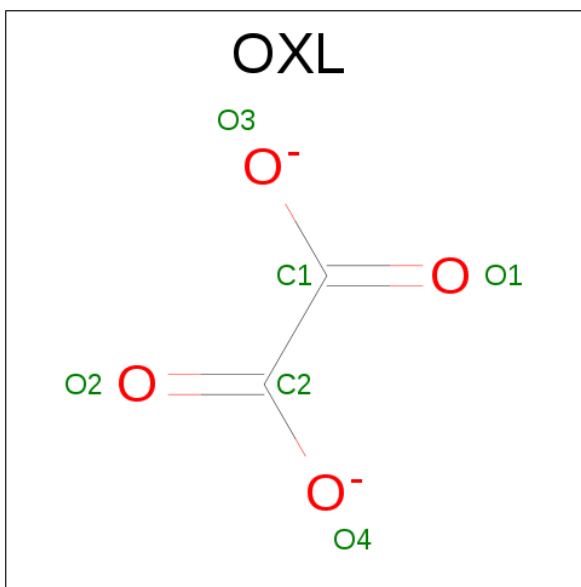
Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	-	INITIATING MET	UNP P14618

- Molecule 2 is SUGAR (FRUCTOSE-1,6-DIPHOSPHATE) (three-letter code: FBP) (formula: $C_6H_{14}O_{12}P_2$).



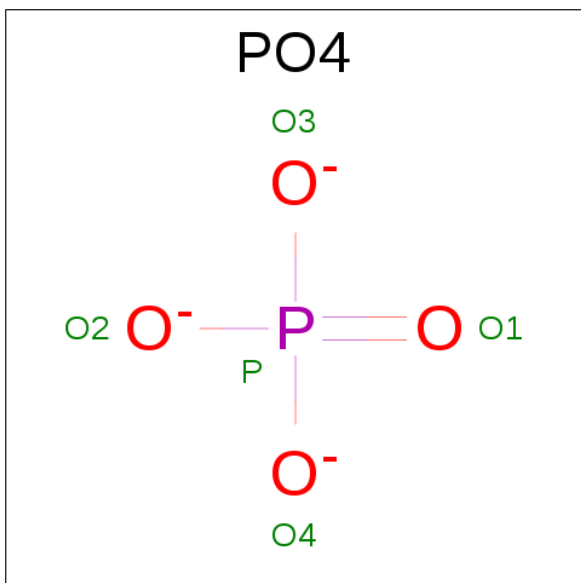
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			20	6	12	2		
2	B	1	Total	C	O	P	0	0
			20	6	12	2		
2	C	1	Total	C	O	P	0	0
			20	6	12	2		
2	D	1	Total	C	O	P	0	0
			20	6	12	2		

- Molecule 3 is OXALATE ION (three-letter code: 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 (three-letter code: PO4) (formula: O₄P).



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

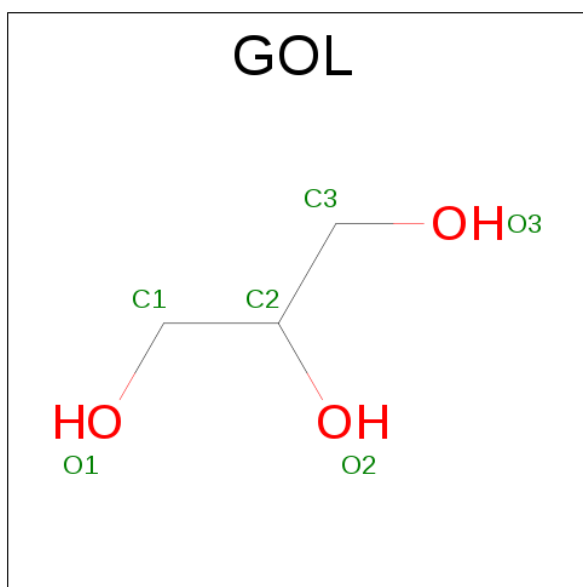
- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

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

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

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

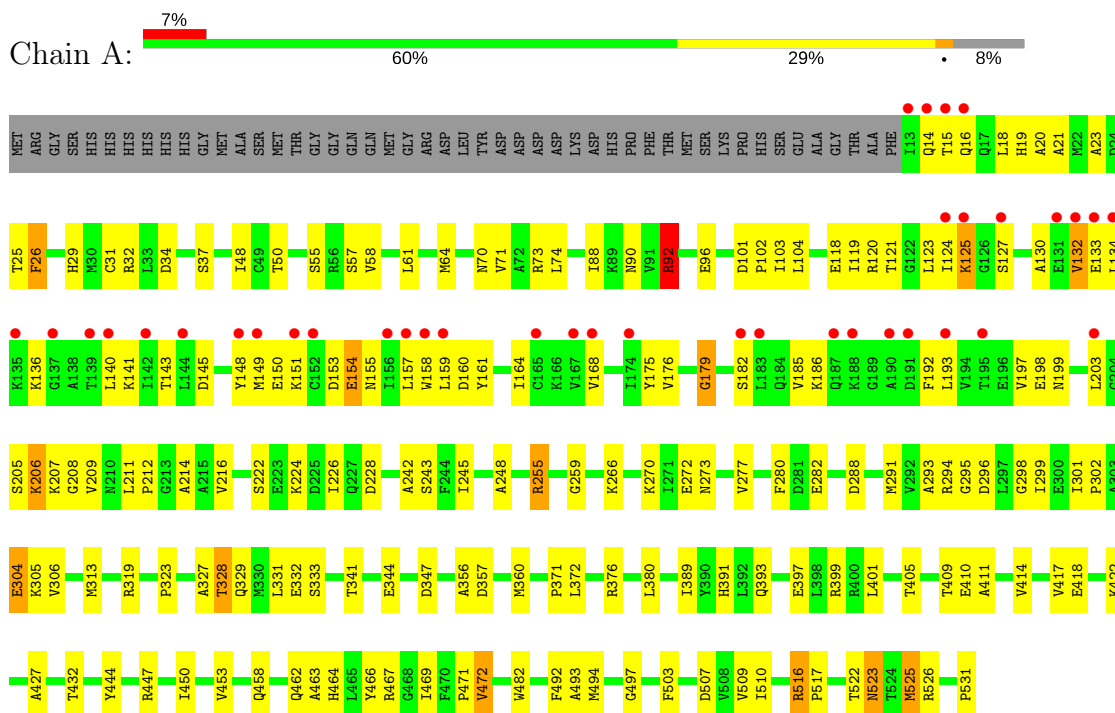
- Molecule 8 is water.

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

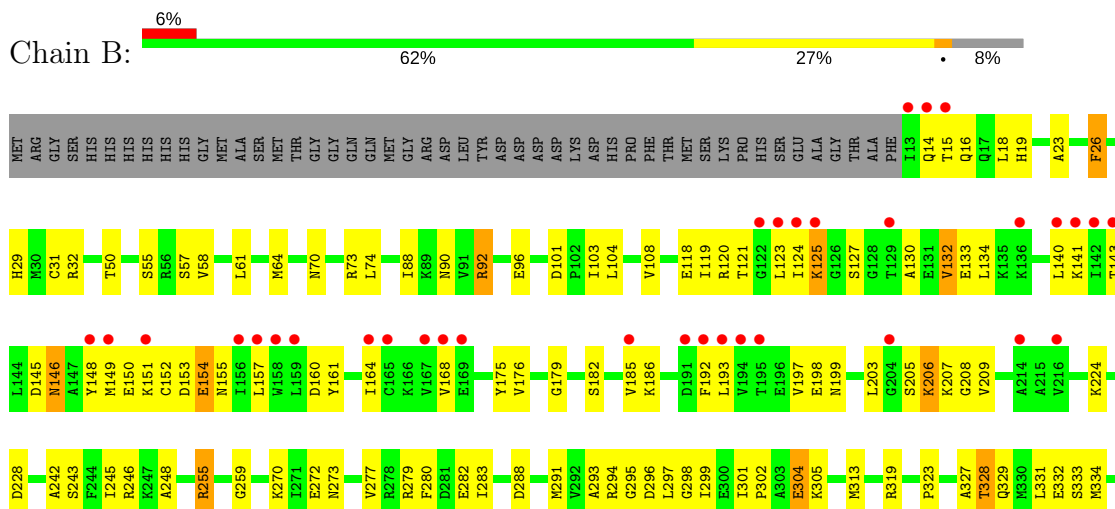
3 Residue-property plots

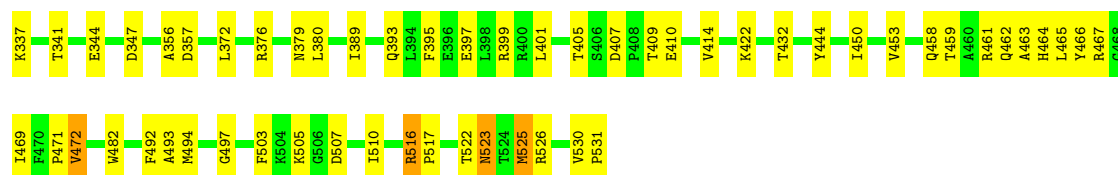
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

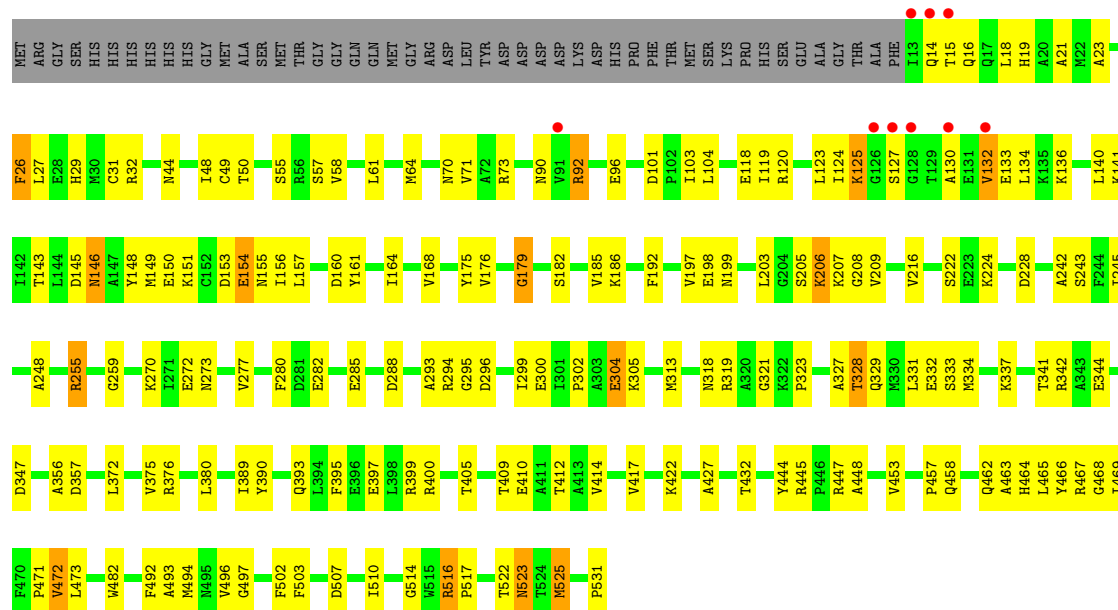


- Molecule 1: Pyruvate kinase, M2 isozyme

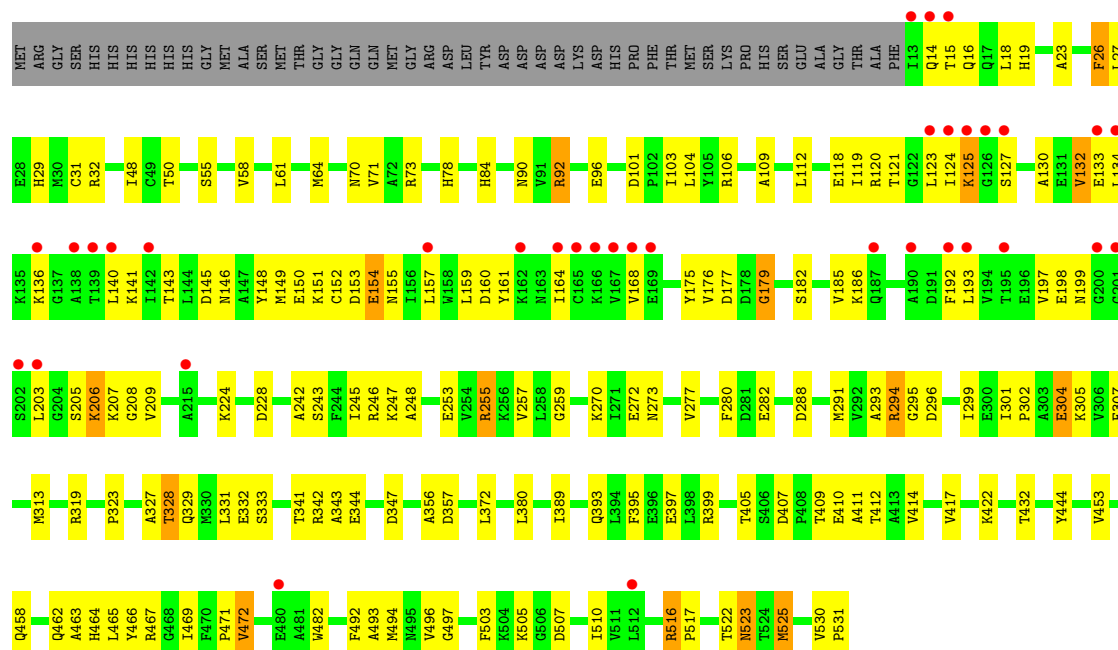




• Molecule 1: Pyruvate kinase, M2 isozyme



• 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 48.30 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.4 (20.00-2.80) 96.4 (48.30-2.80)	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	3022 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	66.9	Xtriage
Anisotropy	0.328	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 55.0	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	0.93	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, MG, FBP, K, OXL, 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	0.53	0/4034	0.74	3/5448 (0.1%)
1	B	0.51	1/4034 (0.0%)	0.69	2/5448 (0.0%)
1	C	0.52	0/4034	0.69	2/5448 (0.0%)
1	D	0.50	0/4034	0.68	2/5448 (0.0%)
All	All	0.51	1/16136 (0.0%)	0.70	9/21792 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	379	ASN	CB-CG	5.22	1.63	1.51

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	92	ARG	NE-CZ-NH1	-14.04	113.28	120.30
1	A	92	ARG	NE-CZ-NH2	13.29	126.95	120.30
1	D	92	ARG	NE-CZ-NH1	7.58	124.09	120.30
1	A	92	ARG	CD-NE-CZ	7.46	134.04	123.60
1	B	92	ARG	NE-CZ-NH2	-6.94	116.83	120.30
1	D	92	ARG	NE-CZ-NH2	-5.87	117.36	120.30
1	B	92	ARG	NE-CZ-NH1	5.79	123.20	120.30
1	C	92	ARG	NE-CZ-NH1	5.39	122.99	120.30
1	C	92	ARG	NE-CZ-NH2	-5.31	117.64	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3971	0	4059	170	0
1	B	3971	0	4059	160	0
1	C	3971	0	4059	175	0
1	D	3971	0	4059	172	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
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	636	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 20.

All (636) 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: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: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:132:VAL:HG12	1:D:133:GLU:N	1.90	0.86
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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:VAL:CG1	1:A:133:GLU:H	1.93	0.79
1:B:143:THR:HG22	1:B:145:ASP:H	1.48	0.79
1:B:58:VAL:HG23	1:B:90:ASN:ND2	1.97	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: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:HH11	1:D:516:ARG:HG3	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:510:ILE:HG23	1:D:525:MET:HE2	1.78	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
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:D:331:LEU:HD23	1:D:344:GLU:HB3	1.80	0.64
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:NH1	1:D:516:ARG:HG3	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: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:A:389:ILE:HD11	1:A:467:ARG:HH21	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:64:MET:HE2	1:C:372:LEU:HD23	1.81	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
1:D:64:MET:HE2	1:D:372:LEU:HD23	1.81	0.60
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: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:C:510:ILE:HG23	1:C:525:MET:HE2	1.85	0.58
1:A:329:GLN:HG2	1:A:332:GLU:HG3	1.85	0.58
1:B:516:ARG:NH1	1:B:516:ARG:HG3	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:389:ILE:HD11	1:B:467:ARG:HH21	1.67	0.58
1:B:92:ARG:O	1:B:96:GLU:HG2	2.03	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:294:ARG:HH22	1:C:347:ASP:CG	2.06	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
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: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:C:15:THR:HG22	1:C:16:GLN:HG2	1.87	0.56
1:D:294:ARG:HH22	1:D:347:ASP:CG	2.09	0.56
1:D:92:ARG:O	1:D:96:GLU:HG2	2.05	0.56
1:A:186:LYS:HA	1:A:186:LYS:HE2	1.88	0.56
1:A:331:LEU:HD23	1:A:344:GLU:HB3	1.87	0.56
1:A:294:ARG:HH22	1:A:347:ASP:CG	2.08	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:HE2	1:B:186:LYS:HA	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:A:510:ILE:HG23	1:A:525:MET:HE2	1.86	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:472:VAL:HG13	1:C:492:PHE:CE2	2.40	0.55
1:D:134:LEU:HB3	1:D:197:VAL:HG21	1.88	0.55
1:D:120:ARG:HA	1:D:207:LYS:O	2.07	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:472:VAL:HG13	1:D:492:PHE:CE2	2.41	0.55
1:D:453:VAL:CG2	1:D:493:ALA:HB2	2.36	0.55
1:D:329:GLN:HG2	1:D:332:GLU:HG3	1.87	0.55
1:A:255:ARG:CG	1:A:255:ARG:HH11	2.19	0.55
1:B:143:THR:HG22	1:B:145:ASP:HB3	1.88	0.55
1:B:141:LYS:HE3	1:B:192:PHE:CD2	2.41	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:CG	1:C:255:ARG:HH11	2.20	0.54
1:D:176:VAL:HA	1:D:208:GLY:O	2.07	0.54
1:D:84:HIS:HD2	8:D:723:HOH:O	1.90	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:B:327:ALA:O	1:B:328:THR:HB	2.08	0.53
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:516:ARG:CG	1:C:516:ARG:HH11	2.20	0.53
1:A:510:ILE:HG23	1:A:525:MET:CE	2.38	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: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
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:B:294:ARG:HH22	1:B:347:ASP:CG	2.12	0.53
1:D:186:LYS:HE2	1:D:186:LYS:HA	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: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: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:64:MET:HE3	1:B:372:LEU:HD23	1.90	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:C:123:LEU:HB2	1:C:150:GLU:HA	1.91	0.51
1:C:186:LYS:HA	1:C:186:LYS:HE2	1.92	0.51
1:B:31:CYS:CB	1:D:319:ARG:HH21	2.23	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:C:356:ALA:O	1:C:467:ARG:NH1	2.43	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:CG	1:D:516:ARG:HH11	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:305:LYS:NZ	8:B:718:HOH:O	2.41	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:CG	1:B:255:ARG:HH11	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:285:GLU:O	7:C:709:GOL:H32	2.11	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:CG	1:B:516:ARG:HH11	2.25	0.49
1:D:143:THR:HG21	1:D:145:ASP:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:319:ARG:HH21	1:D:31:CYS:CB	2.25	0.49
1:B:108:VAL:O	1:B:461:ARG:HG2	2.13	0.49
1:D:55:SER:O	1:D:61:LEU:HD13	2.13	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:64:MET:HE2	1:B:372:LEU:HD23	1.94	0.48
1:B:119:ILE:HG12	1:B:161:TYR:HB2	1.96	0.48
1:B:55:SER:O	1:B:61:LEU:HD13	2.12	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:A:411:ALA:HA	1:B:422:LYS:HG2	1.96	0.48
1:B:510:ILE:HG23	1:B:525:MET:HE2	1.95	0.48
1:C:141:LYS:HE3	1:C:192:PHE:CD2	2.49	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:D:510:ILE:HG23	1:D:525:MET:CE	2.42	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: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:NH1	1:D:255:ARG:CG	2.74	0.47
1:D:255:ARG:NH2	1:D:288:ASP:OD1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:516:ARG:HG3	1:A:516:ARG:HH11	1.79	0.47
1:A:422:LYS:HE3	1:B:405:THR:HG22	1.97	0.47
1:C:118:GLU:OE2	1:C:120:ARG:HD2	2.14	0.47
1:B:380:LEU:CB	1:D:304:GLU:HG2	2.33	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:120:ARG:N	1:B:160:ASP:OD2	2.46	0.47
1:B:31:CYS:HB3	1:D:319:ARG:NH2	2.30	0.47
1:A:168:VAL:CG2	1:A:185:VAL:HG21	2.44	0.47
1:C:458:GLN:O	1:C:462:GLN:HG3	2.14	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: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: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: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:123:LEU:HB2	1:D:150:GLU:HA	1.95	0.47
1:D:50:THR:HA	1:D:73:ARG:HB3	1.96	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:C:510:ILE:HG23	1:C:525:MET:CE	2.45	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:333:SER:CB	1:D:344:GLU:OE1	2.60	0.46
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:C:242:ALA:O	1:C:270:LYS:HG3	2.16	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:273:ASN:O	1:B:277:VAL:HG23	2.17	0.45
1:B:333:SER:HB2	1:B:341:THR:HG23	1.99	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:C:49:CYS:SG	1:C:375:VAL:HG22	2.56	0.45
1:D:168:VAL:CG2	1:D:185:VAL:HG21	2.46	0.45
1:D:48:ILE:HG12	1:D:71:VAL:HB	1.99	0.45
1:C:205:SER:O	1:C:206:LYS:C	2.54	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:327:ALA:HB1	1:A:360:MET:CE	2.45	0.45
1:A:516:ARG:NH1	1:A:516:ARG:HG3	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:409:THR:HG22	1:A:522:THR:HB	1.97	0.45
1:A:216:VAL:HG21	7:A:704:GOL:O2	2.17	0.45
1:C:127:SER:HB3	1:C:130:ALA:CB	2.43	0.45
1:C:120:ARG:N	1:C:160:ASP:OD2	2.48	0.45
1:A:21:ALA:HB2	8:A:728:HOH:O	2.16	0.45
1:D:272:GLU:OE2	1:D:296:ASP:OD2	2.35	0.45
1:C:216:VAL:O	1:C:216:VAL:HG23	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:168:VAL:CG2	1:B:185:VAL:HG21	2.48	0.44
1:B:50:THR:HA	1:B:73:ARG:HB3	1.99	0.44
1:D:168:VAL:HG21	1:D:185:VAL:HG21	2.00	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:B:407:ASP:C	1:B:407:ASP:OD2	2.56	0.44
1:D:157:LEU:CD1	1:D:203:LEU:HD21	2.47	0.44
1:A:136:LYS:HE2	1:A:198:GLU:O	2.17	0.44
1:A:16:GLN:OE1	1:A:447:ARG:HD2	2.18	0.44
1:B:279:ARG:O	1:B:283:ILE:HG13	2.17	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:D:112:LEU:HD23	1:D:112:LEU:C	2.38	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
1:A:211:LEU:O	1:A:214:ALA:HB3	2.19	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:C:270:LYS:NZ	3:C:533:OXL:O3	2.45	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:48:ILE:HG12	1:C:71:VAL:HB	2.01	0.43
1:D:148:TYR:CD2	1:D:151:LYS:HD2	2.52	0.43
1:D:78:HIS:O	1:D:84:HIS:HE1	2.02	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: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: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:272:GLU:OE2	1:C:296:ASP:OD2	2.37	0.43
1:C:50:THR:HA	1:C:73:ARG:HB3	2.01	0.43
1:A:102:PRO:HA	8:A:712:HOH:O	2.18	0.42
1:D:136:LYS:HE2	1:D:198:GLU:O	2.18	0.42
1:B:401:LEU:HD12	1:D:27:LEU:HD23	2.00	0.42
1:D:412:THR:OG1	1:D:523:ASN:HA	2.18	0.42
1:D:270:LYS:NZ	3:D:533:OXL:O4	2.42	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: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: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
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: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:205:SER:O	1:A:206:LYS:C	2.57	0.42
1:A:272:GLU:CG	1:A:293:ALA:HB3	2.49	0.42
1:A:57:SER:O	1:A:58:VAL:C	2.58	0.42
1:C:273:ASN:HA	1:C:300:GLU:HG2	2.02	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:B:510:ILE:HG23	1:B:525:MET:CE	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:118:GLU:OE2	1:D:120:ARG:HD2	2.19	0.42
1:B:319:ARG:NH2	1:D:31:CYS:HB3	2.35	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:A:31:CYS:HB3	1:C:319:ARG:HH21	1.85	0.42
1:C:341:THR:OG1	1:C:344:GLU:HG3	2.20	0.42
1:D:205:SER:O	1:D:206:LYS:C	2.56	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:A:266:LYS:HD3	1:A:266:LYS:HA	1.88	0.41
1:B:297:LEU:O	1:B:301:ILE:HG12	2.20	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: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:A:288:ASP:O	1:A:323:PRO:HD2	2.19	0.41
1:A:280:PHE:CD1	1:A:313:MET:HG2	2.55	0.41
1:A:323:PRO:HA	1:A:357:ASP:OD1	2.20	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: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:B:205:SER:O	1:B:206:LYS:C	2.58	0.41
1:A:118:GLU:OE2	1:A:120:ARG:HD2	2.20	0.41
1:C:148:TYR:CD2	1:C:151:LYS:HD2	2.53	0.41
1:C:57:SER:OG	8:C:737:HOH:O	2.22	0.41
1:D:407:ASP:C	1:D:407:ASP:OD2	2.59	0.41
1:C:390:TYR:CD2	1:C:393:GLN:HB3	2.56	0.41
1:C:296:ASP:OD2	3:C:533:OXL:O2	2.39	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: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:334:MET:HA	1:C:337:LYS:O	2.21	0.41
1:C:502:PHE:CD1	1:C:502:PHE:N	2.89	0.41
1:C:445:ARG:NH2	7:C:707:GOL:H12	2.23	0.41
1:A:333:SER:HB2	1:A:341:THR:HG23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:505:LYS:O	1:B:530:VAL:HB	2.21	0.41
1:B:57:SER:O	1:B:58:VAL:C	2.59	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: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:A:20:ALA:C	1:A:29:HIS:HD1	2.25	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: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:D:136:LYS:HB2	1:D:136:LYS:HE3	1.89	0.40
1:D:505:LYS:O	1:D:530:VAL:HB	2.21	0.40
1:B:146:ASN:O	1:B:149:MET:HG2	2.22	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%)	9	30
1	B	517/567 (91%)	477 (92%)	30 (6%)	10 (2%)	9	30
1	C	517/567 (91%)	482 (93%)	24 (5%)	11 (2%)	8	27
1	D	517/567 (91%)	479 (93%)	27 (5%)	11 (2%)	8	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2068/2268 (91%)	1917 (93%)	109 (5%)	42 (2%)	9	28

All (42) Ramachandran outliers are listed below:

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

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Mol	Chain	Res	Type
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%)	418 (98%)	9 (2%)	59	88
1	B	427/466 (92%)	420 (98%)	7 (2%)	68	91
1	C	427/466 (92%)	419 (98%)	8 (2%)	62	89
1	D	427/466 (92%)	418 (98%)	9 (2%)	59	88
All	All	1708/1864 (92%)	1675 (98%)	33 (2%)	62	89

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	THR
1	A	26	PHE
1	A	92	ARG
1	A	199	ASN
1	A	255	ARG
1	A	304	GLU
1	A	472	VAL
1	A	516	ARG
1	A	525	MET
1	B	26	PHE
1	B	199	ASN
1	B	255	ARG
1	B	304	GLU
1	B	472	VAL
1	B	516	ARG
1	B	525	MET

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Mol	Chain	Res	Type
1	C	26	PHE
1	C	156	ILE
1	C	199	ASN
1	C	255	ARG
1	C	304	GLU
1	C	472	VAL
1	C	516	ARG
1	C	525	MET
1	D	26	PHE
1	D	199	ASN
1	D	247	LYS
1	D	255	ARG
1	D	294	ARG
1	D	304	GLU
1	D	472	VAL
1	D	516	ARG
1	D	525	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	84	HIS
1	A	90	ASN
1	A	393	GLN
1	A	439	HIS
1	A	464	HIS
1	B	14	GLN
1	B	90	ASN
1	B	393	GLN
1	C	14	GLN
1	C	70	ASN
1	C	84	HIS
1	C	90	ASN
1	C	393	GLN
1	C	439	HIS
1	D	84	HIS
1	D	90	ASN
1	D	393	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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$
2	FBP	A	532	-	18,20,20	1.40	3 (16%)	23,32,32	0.91	0
3	OXL	A	533	5	0,5,5	0.00	-	0,6,6	0.00	-
4	PO4	A	534	-	4,4,4	2.28	1 (25%)	6,6,6	0.84	0
7	GOL	A	702	-	5,5,5	0.58	0	5,5,5	0.21	0
7	GOL	A	703	-	5,5,5	0.76	0	5,5,5	0.16	0
7	GOL	A	704	-	5,5,5	0.81	0	5,5,5	0.40	0
7	GOL	A	705	-	5,5,5	0.80	0	5,5,5	0.14	0
7	GOL	A	706	-	5,5,5	0.93	0	5,5,5	0.44	0
2	FBP	B	532	-	18,20,20	1.50	3 (16%)	23,32,32	1.01	3 (13%)
3	OXL	B	533	5	0,5,5	0.00	-	0,6,6	0.00	-
4	PO4	B	534	-	4,4,4	2.80	1 (25%)	6,6,6	0.80	0
7	GOL	B	703	-	5,5,5	0.61	0	5,5,5	0.28	0
7	GOL	B	704	-	5,5,5	0.93	0	5,5,5	0.22	0
7	GOL	B	705	-	5,5,5	0.79	0	5,5,5	0.28	0
7	GOL	B	706	-	5,5,5	0.99	0	5,5,5	0.15	0
2	FBP	C	532	-	18,20,20	1.49	4 (22%)	23,32,32	0.90	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	OXL	C	533	5	0,5,5	0.00	-	0,6,6	0.00	-
4	PO4	C	534	-	4,4,4	2.08	1 (25%)	6,6,6	1.05	0
7	GOL	C	704	-	5,5,5	0.75	0	5,5,5	0.26	0
7	GOL	C	705	-	5,5,5	0.96	0	5,5,5	0.26	0
7	GOL	C	706	-	5,5,5	0.39	0	5,5,5	0.51	0
7	GOL	C	707	-	5,5,5	0.63	0	5,5,5	0.35	0
7	GOL	C	708	-	5,5,5	0.79	0	5,5,5	0.18	0
7	GOL	C	709	-	5,5,5	0.67	0	5,5,5	0.29	0
2	FBP	D	532	-	18,20,20	1.42	3 (16%)	23,32,32	0.87	0
3	OXL	D	533	5	0,5,5	0.00	-	0,6,6	0.00	-
4	PO4	D	534	-	4,4,4	2.67	1 (25%)	6,6,6	0.73	0
7	GOL	D	705	-	5,5,5	0.76	0	5,5,5	0.24	0
7	GOL	D	706	-	5,5,5	1.16	0	5,5,5	0.39	0
7	GOL	D	707	-	5,5,5	0.59	0	5,5,5	0.23	0
7	GOL	D	708	-	5,5,5	1.03	0	5,5,5	0.34	0
7	GOL	D	709	-	5,5,5	1.17	0	5,5,5	0.33	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
2	FBP	A	532	-	-	0/13/32/32	0/1/1/1
3	OXL	A	533	5	-	0/0/4/4	0/0/0/0
4	PO4	A	534	-	-	0/0/0/0	0/0/0/0
7	GOL	A	702	-	-	0/4/4/4	0/0/0/0
7	GOL	A	703	-	-	0/4/4/4	0/0/0/0
7	GOL	A	704	-	-	0/4/4/4	0/0/0/0
7	GOL	A	705	-	-	0/4/4/4	0/0/0/0
7	GOL	A	706	-	-	0/4/4/4	0/0/0/0
2	FBP	B	532	-	-	0/13/32/32	0/1/1/1
3	OXL	B	533	5	-	0/0/4/4	0/0/0/0
4	PO4	B	534	-	-	0/0/0/0	0/0/0/0
7	GOL	B	703	-	-	0/4/4/4	0/0/0/0
7	GOL	B	704	-	-	0/4/4/4	0/0/0/0
7	GOL	B	705	-	-	0/4/4/4	0/0/0/0
7	GOL	B	706	-	-	0/4/4/4	0/0/0/0
2	FBP	C	532	-	-	0/13/32/32	0/1/1/1
3	OXL	C	533	5	-	0/0/4/4	0/0/0/0
4	PO4	C	534	-	-	0/0/0/0	0/0/0/0
7	GOL	C	704	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	GOL	C	705	-	-	0/4/4/4	0/0/0/0
7	GOL	C	706	-	-	0/4/4/4	0/0/0/0
7	GOL	C	707	-	-	0/4/4/4	0/0/0/0
7	GOL	C	708	-	-	0/4/4/4	0/0/0/0
7	GOL	C	709	-	-	0/4/4/4	0/0/0/0
2	FBP	D	532	-	-	0/13/32/32	0/1/1/1
3	OXL	D	533	5	-	0/0/4/4	0/0/0/0
4	PO4	D	534	-	-	0/0/0/0	0/0/0/0
7	GOL	D	705	-	-	0/4/4/4	0/0/0/0
7	GOL	D	706	-	-	0/4/4/4	0/0/0/0
7	GOL	D	707	-	-	0/4/4/4	0/0/0/0
7	GOL	D	708	-	-	0/4/4/4	0/0/0/0
7	GOL	D	709	-	-	0/4/4/4	0/0/0/0

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	532	FBP	P1-O3P	-3.35	1.41	1.54
2	A	532	FBP	P1-O3P	-3.13	1.42	1.54
2	C	532	FBP	P1-O3P	-3.01	1.42	1.54
2	D	532	FBP	P1-O3P	-2.94	1.42	1.54
2	B	532	FBP	P1-O2P	-2.29	1.45	1.54
2	A	532	FBP	P2-O5P	-2.26	1.45	1.54
2	D	532	FBP	P2-O5P	-2.20	1.45	1.54
2	C	532	FBP	O3-C3	-2.17	1.38	1.42
2	A	532	FBP	O5-C2	2.10	1.46	1.43
2	C	532	FBP	O5-C2	2.51	1.47	1.43
2	D	532	FBP	O5-C2	2.74	1.47	1.43
2	B	532	FBP	O5-C2	2.96	1.47	1.43
2	C	532	FBP	O2-C2	3.22	1.46	1.40
4	A	534	PO4	P-O1	3.99	1.59	1.50
4	C	534	PO4	P-O1	4.00	1.59	1.50
4	D	534	PO4	P-O1	4.92	1.61	1.50
4	B	534	PO4	P-O1	5.13	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	532	FBP	P1-O1-C1	2.01	123.83	118.30
2	C	532	FBP	O2P-P1-O1	2.04	112.16	106.73
2	B	532	FBP	O2P-P1-O1	2.04	112.16	106.73
2	B	532	FBP	O2-C2-O5	2.20	113.82	109.45

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

14 monomers are involved in 23 short contacts:

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

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%)	0.12	38 (7%) 16 8	23, 60, 99, 99	0
1	B	519/567 (91%)	0.17	34 (6%) 19 11	29, 65, 99, 99	0
1	C	519/567 (91%)	-0.04	9 (1%) 70 63	26, 65, 97, 99	0
1	D	519/567 (91%)	0.17	35 (6%) 19 11	34, 69, 99, 99	0
All	All	2076/2268 (91%)	0.11	116 (5%) 25 16	23, 65, 99, 99	0

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	142	ILE	6.3
1	C	13	ILE	5.8
1	D	140	LEU	5.8
1	A	13	ILE	5.7
1	A	134	LEU	5.7
1	A	190	ALA	5.6
1	B	13	ILE	5.1
1	D	139	THR	5.0
1	A	157	LEU	5.0
1	C	127	SER	4.9
1	B	165	CYS	4.8
1	D	168	VAL	4.8
1	D	200	GLY	4.8
1	B	148	TYR	4.8
1	D	195	THR	4.7
1	A	14	GLN	4.6
1	D	126	GLY	4.6
1	B	124	ILE	4.5
1	D	14	GLN	4.5
1	B	157	LEU	4.3
1	A	203	LEU	4.2

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Mol	Chain	Res	Type	RSRZ
1	D	125	LYS	4.2
1	B	168	VAL	4.1
1	C	14	GLN	4.1
1	A	132	VAL	4.0
1	A	159	LEU	4.0
1	C	15	THR	3.9
1	D	142	ILE	3.8
1	B	164	ILE	3.8
1	B	192	PHE	3.8
1	D	164	ILE	3.8
1	A	124	ILE	3.7
1	D	13	ILE	3.7
1	A	151	LYS	3.7
1	A	156	ILE	3.7
1	B	185	VAL	3.6
1	B	14	GLN	3.6
1	B	159	LEU	3.6
1	B	122	GLY	3.6
1	D	187	GLN	3.6
1	C	128	GLY	3.6
1	A	195	THR	3.5
1	B	214	ALA	3.5
1	D	165	CYS	3.4
1	A	140	LEU	3.4
1	B	125	LYS	3.4
1	C	126	GLY	3.4
1	D	157	LEU	3.3
1	A	167	VAL	3.3
1	D	202	SER	3.3
1	A	165	CYS	3.3
1	A	193	LEU	3.2
1	B	167	VAL	3.2
1	A	125	LYS	3.1
1	B	141	LYS	3.1
1	B	140	LEU	3.1
1	B	195	THR	3.0
1	A	168	VAL	3.0
1	D	167	VAL	3.0
1	B	193	LEU	2.9
1	A	191	ASP	2.9
1	B	216	VAL	2.9
1	D	124	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	144	LEU	2.8
1	A	127	SER	2.8
1	B	194	VAL	2.8
1	D	138	ALA	2.8
1	D	190	ALA	2.8
1	B	158	TRP	2.8
1	A	152	CYS	2.8
1	A	16	GLN	2.7
1	B	129	THR	2.7
1	D	123	LEU	2.7
1	D	215	ALA	2.7
1	C	91	VAL	2.6
1	A	137	GLY	2.6
1	D	136	LYS	2.6
1	A	183	LEU	2.6
1	B	142	ILE	2.6
1	A	187	GLN	2.6
1	A	158	TRP	2.5
1	B	156	ILE	2.5
1	D	201	GLY	2.5
1	B	169	GLU	2.5
1	D	127	SER	2.5
1	B	15	THR	2.5
1	B	191	ASP	2.5
1	B	123	LEU	2.5
1	D	134	LEU	2.4
1	A	174	ILE	2.4
1	C	130	ALA	2.4
1	A	148	TYR	2.4
1	A	139	THR	2.4
1	D	193	LEU	2.4
1	D	166	LYS	2.3
1	A	182	SER	2.3
1	D	480	GLU	2.3
1	D	192	PHE	2.3
1	B	151	LYS	2.3
1	A	15	THR	2.2
1	B	204	GLY	2.2
1	A	131	GLU	2.2
1	D	203	LEU	2.1
1	D	133	GLU	2.1
1	D	169	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	136	LYS	2.1
1	A	133	GLU	2.1
1	D	162	LYS	2.1
1	A	135	LYS	2.1
1	A	149	MET	2.1
1	B	143	THR	2.1
1	C	132	VAL	2.1
1	B	149	MET	2.1
1	D	512	LEU	2.0
1	A	188	LYS	2.0
1	D	15	THR	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
7	GOL	C	707	6/6	0.77	0.45	8.28	66,66,66,66	0
7	GOL	D	709	6/6	0.93	0.35	7.44	42,42,42,42	0
7	GOL	B	704	6/6	0.79	0.30	6.09	66,66,66,66	0
7	GOL	C	705	6/6	0.77	0.48	5.48	66,66,66,66	0
7	GOL	A	703	6/6	0.90	0.25	3.71	66,66,66,66	0
7	GOL	B	705	6/6	0.76	0.28	3.20	66,66,66,66	0
7	GOL	D	708	6/6	0.78	0.32	2.73	66,66,66,66	0
7	GOL	C	709	6/6	0.90	0.22	2.45	42,42,42,42	0
3	OXL	C	533	6/6	0.92	0.26	2.43	66,66,66,66	0
3	OXL	D	533	6/6	0.95	0.21	2.31	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	GOL	A	704	6/6	0.85	0.34	1.69	66,66,66,66	0
7	GOL	A	705	6/6	0.84	0.26	1.51	66,66,66,66	0
7	GOL	D	706	6/6	0.80	0.26	1.49	66,66,66,66	0
7	GOL	C	708	6/6	0.72	0.31	0.84	66,66,66,66	0
6	K	B	702	1/1	0.93	0.21	0.72	66,66,66,66	0
2	FBP	A	532	20/20	0.97	0.17	0.59	66,66,66,66	0
7	GOL	D	707	6/6	0.92	0.25	0.46	66,66,66,66	0
7	GOL	A	706	6/6	0.85	0.35	0.38	42,42,42,42	0
6	K	A	701	1/1	0.90	0.19	0.31	66,66,66,66	0
2	FBP	B	532	20/20	0.95	0.16	0.25	66,66,66,66	0
7	GOL	C	706	6/6	0.92	0.20	0.13	66,66,66,66	0
3	OXL	B	533	6/6	0.98	0.17	-0.35	66,66,66,66	0
7	GOL	B	706	6/6	0.92	0.16	-0.66	42,42,42,42	0
6	K	C	703	1/1	0.82	0.13	-0.98	66,66,66,66	0
2	FBP	D	532	20/20	0.92	0.14	-1.14	66,66,66,66	0
2	FBP	C	532	20/20	0.94	0.12	-1.51	66,66,66,66	0
3	OXL	A	533	6/6	0.89	0.14	-1.54	66,66,66,66	0
6	K	D	704	1/1	0.98	0.09	-4.87	66,66,66,66	0
4	PO4	B	534	5/5	0.95	0.17	-	66,66,66,66	0
4	PO4	D	534	5/5	0.94	0.17	-	66,66,66,66	0
5	MG	C	603	1/1	0.97	0.33	-	66,66,66,66	0
4	PO4	C	534	5/5	0.93	0.14	-	66,66,66,66	0
5	MG	D	604	1/1	0.95	0.16	-	66,66,66,66	0
5	MG	A	601	1/1	0.94	0.22	-	66,66,66,66	0
7	GOL	C	704	6/6	0.90	0.13	-	66,66,66,66	0
5	MG	B	602	1/1	0.94	0.24	-	66,66,66,66	0
7	GOL	A	702	6/6	0.94	0.15	-	66,66,66,66	0
4	PO4	A	534	5/5	0.94	0.20	-	66,66,66,66	0
7	GOL	B	703	6/6	0.87	0.19	-	66,66,66,66	0
7	GOL	D	705	6/6	0.86	0.25	-	66,66,66,66	0

6.5 Other polymers ⓘ

There are no such residues in this entry.