



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 08:54 am BST

PDB ID : 4H1Z
Title : Crystal structure of putative isomerase from Sinorhizobium meliloti, open loop conformation (target EFI-502104)
Authors : Patskovsky, Y.; Toro, R.; Bhosle, R.; Hillerich, B.; Seidel, R.D.; Washington, E.; Scott Glenn, A.; Chowdhury, S.; Evans, B.; Hammonds, J.; Zencheck, W.D.; Imker, H.J.; Gerlt, J.A.; Almo, S.C.; Enzyme Function Initiative (EFI)
Deposited on : 2012-09-11
Resolution : 2.01 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

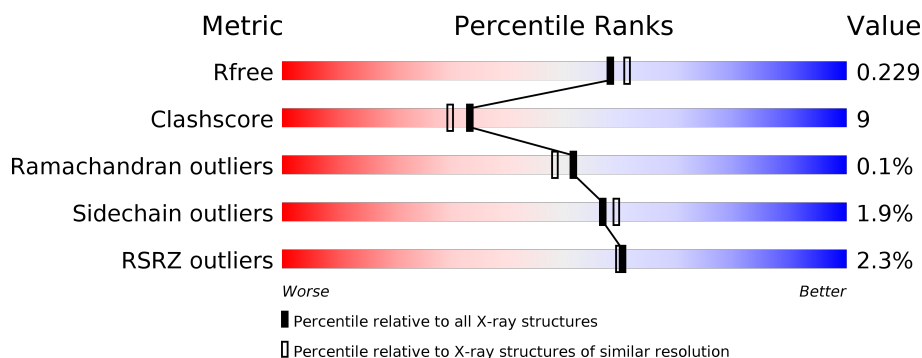
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.01 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}	130704	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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 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	412	<div> <div>3%</div> <div> <div></div> <div>73%</div> <div>18%</div> <div>9%</div> </div> </div>
1	B	412	<div> <div>77%</div> <div>16%</div> <div>6%</div> </div>
1	C	412	<div> <div>3%</div> <div> <div></div> <div>74%</div> <div>16%</div> <div>8%</div> </div> </div>
1	D	412	<div> <div>2%</div> <div> <div></div> <div>77%</div> <div>14%</div> <div>8%</div> </div> </div>
1	E	412	<div> <div>0%</div> <div> <div></div> <div>79%</div> <div>13%</div> <div>8%</div> </div> </div>
1	F	412	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>11%</div> <div>9%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	412	<div> <div>%</div> <div> <div></div> <div>81%</div> <div>11%</div> <div>8%</div> </div> </div>
1	H	412	<div> <div>5%</div> <div> <div></div> <div>69%</div> <div>21%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GOL	B	404	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 24833 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 Enolase Q92Zs5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	376	Total	C	N	O	S	0	0	0
			2880	1824	517	526	13			
1	B	388	Total	C	N	O	S	0	1	0
			2982	1892	535	542	13			
1	C	378	Total	C	N	O	S	0	1	0
			2909	1843	525	528	13			
1	D	379	Total	C	N	O	S	0	1	0
			2913	1845	526	529	13			
1	E	381	Total	C	N	O	S	0	1	0
			2926	1854	528	531	13			
1	F	374	Total	C	N	O	S	0	4	0
			2880	1829	515	523	13			
1	G	380	Total	C	N	O	S	0	1	0
			2916	1849	524	530	13			
1	H	378	Total	C	N	O	S	0	0	0
			2891	1833	519	526	13			

There are 184 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MET	-	EXPRESSION TAG	UNP Q92ZS5
A	-21	HIS	-	EXPRESSION TAG	UNP Q92ZS5
A	-20	HIS	-	EXPRESSION TAG	UNP Q92ZS5
A	-19	HIS	-	EXPRESSION TAG	UNP Q92ZS5
A	-18	HIS	-	EXPRESSION TAG	UNP Q92ZS5
A	-17	HIS	-	EXPRESSION TAG	UNP Q92ZS5
A	-16	HIS	-	EXPRESSION TAG	UNP Q92ZS5
A	-15	SER	-	EXPRESSION TAG	UNP Q92ZS5
A	-14	SER	-	EXPRESSION TAG	UNP Q92ZS5
A	-13	GLY	-	EXPRESSION TAG	UNP Q92ZS5
A	-12	VAL	-	EXPRESSION TAG	UNP Q92ZS5
A	-11	ASP	-	EXPRESSION TAG	UNP Q92ZS5
A	-10	LEU	-	EXPRESSION TAG	UNP Q92ZS5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	GLY	-	EXPRESSION TAG	UNP Q92ZS5
A	-8	THR	-	EXPRESSION TAG	UNP Q92ZS5
A	-7	GLU	-	EXPRESSION TAG	UNP Q92ZS5
A	-6	ASN	-	EXPRESSION TAG	UNP Q92ZS5
A	-5	LEU	-	EXPRESSION TAG	UNP Q92ZS5
A	-4	TYR	-	EXPRESSION TAG	UNP Q92ZS5
A	-3	PHE	-	EXPRESSION TAG	UNP Q92ZS5
A	-2	GLN	-	EXPRESSION TAG	UNP Q92ZS5
A	-1	SER	-	EXPRESSION TAG	UNP Q92ZS5
A	0	MET	-	EXPRESSION TAG	UNP Q92ZS5
B	-22	MET	-	EXPRESSION TAG	UNP Q92ZS5
B	-21	HIS	-	EXPRESSION TAG	UNP Q92ZS5
B	-20	HIS	-	EXPRESSION TAG	UNP Q92ZS5
B	-19	HIS	-	EXPRESSION TAG	UNP Q92ZS5
B	-18	HIS	-	EXPRESSION TAG	UNP Q92ZS5
B	-17	HIS	-	EXPRESSION TAG	UNP Q92ZS5
B	-16	HIS	-	EXPRESSION TAG	UNP Q92ZS5
B	-15	SER	-	EXPRESSION TAG	UNP Q92ZS5
B	-14	SER	-	EXPRESSION TAG	UNP Q92ZS5
B	-13	GLY	-	EXPRESSION TAG	UNP Q92ZS5
B	-12	VAL	-	EXPRESSION TAG	UNP Q92ZS5
B	-11	ASP	-	EXPRESSION TAG	UNP Q92ZS5
B	-10	LEU	-	EXPRESSION TAG	UNP Q92ZS5
B	-9	GLY	-	EXPRESSION TAG	UNP Q92ZS5
B	-8	THR	-	EXPRESSION TAG	UNP Q92ZS5
B	-7	GLU	-	EXPRESSION TAG	UNP Q92ZS5
B	-6	ASN	-	EXPRESSION TAG	UNP Q92ZS5
B	-5	LEU	-	EXPRESSION TAG	UNP Q92ZS5
B	-4	TYR	-	EXPRESSION TAG	UNP Q92ZS5
B	-3	PHE	-	EXPRESSION TAG	UNP Q92ZS5
B	-2	GLN	-	EXPRESSION TAG	UNP Q92ZS5
B	-1	SER	-	EXPRESSION TAG	UNP Q92ZS5
B	0	MET	-	EXPRESSION TAG	UNP Q92ZS5
C	-22	MET	-	EXPRESSION TAG	UNP Q92ZS5
C	-21	HIS	-	EXPRESSION TAG	UNP Q92ZS5
C	-20	HIS	-	EXPRESSION TAG	UNP Q92ZS5
C	-19	HIS	-	EXPRESSION TAG	UNP Q92ZS5
C	-18	HIS	-	EXPRESSION TAG	UNP Q92ZS5
C	-17	HIS	-	EXPRESSION TAG	UNP Q92ZS5
C	-16	HIS	-	EXPRESSION TAG	UNP Q92ZS5
C	-15	SER	-	EXPRESSION TAG	UNP Q92ZS5
C	-14	SER	-	EXPRESSION TAG	UNP Q92ZS5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-13	GLY	-	EXPRESSION TAG	UNP Q92ZS5
C	-12	VAL	-	EXPRESSION TAG	UNP Q92ZS5
C	-11	ASP	-	EXPRESSION TAG	UNP Q92ZS5
C	-10	LEU	-	EXPRESSION TAG	UNP Q92ZS5
C	-9	GLY	-	EXPRESSION TAG	UNP Q92ZS5
C	-8	THR	-	EXPRESSION TAG	UNP Q92ZS5
C	-7	GLU	-	EXPRESSION TAG	UNP Q92ZS5
C	-6	ASN	-	EXPRESSION TAG	UNP Q92ZS5
C	-5	LEU	-	EXPRESSION TAG	UNP Q92ZS5
C	-4	TYR	-	EXPRESSION TAG	UNP Q92ZS5
C	-3	PHE	-	EXPRESSION TAG	UNP Q92ZS5
C	-2	GLN	-	EXPRESSION TAG	UNP Q92ZS5
C	-1	SER	-	EXPRESSION TAG	UNP Q92ZS5
C	0	MET	-	EXPRESSION TAG	UNP Q92ZS5
D	-22	MET	-	EXPRESSION TAG	UNP Q92ZS5
D	-21	HIS	-	EXPRESSION TAG	UNP Q92ZS5
D	-20	HIS	-	EXPRESSION TAG	UNP Q92ZS5
D	-19	HIS	-	EXPRESSION TAG	UNP Q92ZS5
D	-18	HIS	-	EXPRESSION TAG	UNP Q92ZS5
D	-17	HIS	-	EXPRESSION TAG	UNP Q92ZS5
D	-16	HIS	-	EXPRESSION TAG	UNP Q92ZS5
D	-15	SER	-	EXPRESSION TAG	UNP Q92ZS5
D	-14	SER	-	EXPRESSION TAG	UNP Q92ZS5
D	-13	GLY	-	EXPRESSION TAG	UNP Q92ZS5
D	-12	VAL	-	EXPRESSION TAG	UNP Q92ZS5
D	-11	ASP	-	EXPRESSION TAG	UNP Q92ZS5
D	-10	LEU	-	EXPRESSION TAG	UNP Q92ZS5
D	-9	GLY	-	EXPRESSION TAG	UNP Q92ZS5
D	-8	THR	-	EXPRESSION TAG	UNP Q92ZS5
D	-7	GLU	-	EXPRESSION TAG	UNP Q92ZS5
D	-6	ASN	-	EXPRESSION TAG	UNP Q92ZS5
D	-5	LEU	-	EXPRESSION TAG	UNP Q92ZS5
D	-4	TYR	-	EXPRESSION TAG	UNP Q92ZS5
D	-3	PHE	-	EXPRESSION TAG	UNP Q92ZS5
D	-2	GLN	-	EXPRESSION TAG	UNP Q92ZS5
D	-1	SER	-	EXPRESSION TAG	UNP Q92ZS5
D	0	MET	-	EXPRESSION TAG	UNP Q92ZS5
E	-22	MET	-	EXPRESSION TAG	UNP Q92ZS5
E	-21	HIS	-	EXPRESSION TAG	UNP Q92ZS5
E	-20	HIS	-	EXPRESSION TAG	UNP Q92ZS5
E	-19	HIS	-	EXPRESSION TAG	UNP Q92ZS5
E	-18	HIS	-	EXPRESSION TAG	UNP Q92ZS5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-17	HIS	-	EXPRESSION TAG	UNP Q92ZS5
E	-16	HIS	-	EXPRESSION TAG	UNP Q92ZS5
E	-15	SER	-	EXPRESSION TAG	UNP Q92ZS5
E	-14	SER	-	EXPRESSION TAG	UNP Q92ZS5
E	-13	GLY	-	EXPRESSION TAG	UNP Q92ZS5
E	-12	VAL	-	EXPRESSION TAG	UNP Q92ZS5
E	-11	ASP	-	EXPRESSION TAG	UNP Q92ZS5
E	-10	LEU	-	EXPRESSION TAG	UNP Q92ZS5
E	-9	GLY	-	EXPRESSION TAG	UNP Q92ZS5
E	-8	THR	-	EXPRESSION TAG	UNP Q92ZS5
E	-7	GLU	-	EXPRESSION TAG	UNP Q92ZS5
E	-6	ASN	-	EXPRESSION TAG	UNP Q92ZS5
E	-5	LEU	-	EXPRESSION TAG	UNP Q92ZS5
E	-4	TYR	-	EXPRESSION TAG	UNP Q92ZS5
E	-3	PHE	-	EXPRESSION TAG	UNP Q92ZS5
E	-2	GLN	-	EXPRESSION TAG	UNP Q92ZS5
E	-1	SER	-	EXPRESSION TAG	UNP Q92ZS5
E	0	MET	-	EXPRESSION TAG	UNP Q92ZS5
F	-22	MET	-	EXPRESSION TAG	UNP Q92ZS5
F	-21	HIS	-	EXPRESSION TAG	UNP Q92ZS5
F	-20	HIS	-	EXPRESSION TAG	UNP Q92ZS5
F	-19	HIS	-	EXPRESSION TAG	UNP Q92ZS5
F	-18	HIS	-	EXPRESSION TAG	UNP Q92ZS5
F	-17	HIS	-	EXPRESSION TAG	UNP Q92ZS5
F	-16	HIS	-	EXPRESSION TAG	UNP Q92ZS5
F	-15	SER	-	EXPRESSION TAG	UNP Q92ZS5
F	-14	SER	-	EXPRESSION TAG	UNP Q92ZS5
F	-13	GLY	-	EXPRESSION TAG	UNP Q92ZS5
F	-12	VAL	-	EXPRESSION TAG	UNP Q92ZS5
F	-11	ASP	-	EXPRESSION TAG	UNP Q92ZS5
F	-10	LEU	-	EXPRESSION TAG	UNP Q92ZS5
F	-9	GLY	-	EXPRESSION TAG	UNP Q92ZS5
F	-8	THR	-	EXPRESSION TAG	UNP Q92ZS5
F	-7	GLU	-	EXPRESSION TAG	UNP Q92ZS5
F	-6	ASN	-	EXPRESSION TAG	UNP Q92ZS5
F	-5	LEU	-	EXPRESSION TAG	UNP Q92ZS5
F	-4	TYR	-	EXPRESSION TAG	UNP Q92ZS5
F	-3	PHE	-	EXPRESSION TAG	UNP Q92ZS5
F	-2	GLN	-	EXPRESSION TAG	UNP Q92ZS5
F	-1	SER	-	EXPRESSION TAG	UNP Q92ZS5
F	0	MET	-	EXPRESSION TAG	UNP Q92ZS5
G	-22	MET	-	EXPRESSION TAG	UNP Q92ZS5

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-21	HIS	-	EXPRESSION TAG	UNP Q92ZS5
G	-20	HIS	-	EXPRESSION TAG	UNP Q92ZS5
G	-19	HIS	-	EXPRESSION TAG	UNP Q92ZS5
G	-18	HIS	-	EXPRESSION TAG	UNP Q92ZS5
G	-17	HIS	-	EXPRESSION TAG	UNP Q92ZS5
G	-16	HIS	-	EXPRESSION TAG	UNP Q92ZS5
G	-15	SER	-	EXPRESSION TAG	UNP Q92ZS5
G	-14	SER	-	EXPRESSION TAG	UNP Q92ZS5
G	-13	GLY	-	EXPRESSION TAG	UNP Q92ZS5
G	-12	VAL	-	EXPRESSION TAG	UNP Q92ZS5
G	-11	ASP	-	EXPRESSION TAG	UNP Q92ZS5
G	-10	LEU	-	EXPRESSION TAG	UNP Q92ZS5
G	-9	GLY	-	EXPRESSION TAG	UNP Q92ZS5
G	-8	THR	-	EXPRESSION TAG	UNP Q92ZS5
G	-7	GLU	-	EXPRESSION TAG	UNP Q92ZS5
G	-6	ASN	-	EXPRESSION TAG	UNP Q92ZS5
G	-5	LEU	-	EXPRESSION TAG	UNP Q92ZS5
G	-4	TYR	-	EXPRESSION TAG	UNP Q92ZS5
G	-3	PHE	-	EXPRESSION TAG	UNP Q92ZS5
G	-2	GLN	-	EXPRESSION TAG	UNP Q92ZS5
G	-1	SER	-	EXPRESSION TAG	UNP Q92ZS5
G	0	MET	-	EXPRESSION TAG	UNP Q92ZS5
H	-22	MET	-	EXPRESSION TAG	UNP Q92ZS5
H	-21	HIS	-	EXPRESSION TAG	UNP Q92ZS5
H	-20	HIS	-	EXPRESSION TAG	UNP Q92ZS5
H	-19	HIS	-	EXPRESSION TAG	UNP Q92ZS5
H	-18	HIS	-	EXPRESSION TAG	UNP Q92ZS5
H	-17	HIS	-	EXPRESSION TAG	UNP Q92ZS5
H	-16	HIS	-	EXPRESSION TAG	UNP Q92ZS5
H	-15	SER	-	EXPRESSION TAG	UNP Q92ZS5
H	-14	SER	-	EXPRESSION TAG	UNP Q92ZS5
H	-13	GLY	-	EXPRESSION TAG	UNP Q92ZS5
H	-12	VAL	-	EXPRESSION TAG	UNP Q92ZS5
H	-11	ASP	-	EXPRESSION TAG	UNP Q92ZS5
H	-10	LEU	-	EXPRESSION TAG	UNP Q92ZS5
H	-9	GLY	-	EXPRESSION TAG	UNP Q92ZS5
H	-8	THR	-	EXPRESSION TAG	UNP Q92ZS5
H	-7	GLU	-	EXPRESSION TAG	UNP Q92ZS5
H	-6	ASN	-	EXPRESSION TAG	UNP Q92ZS5
H	-5	LEU	-	EXPRESSION TAG	UNP Q92ZS5
H	-4	TYR	-	EXPRESSION TAG	UNP Q92ZS5
H	-3	PHE	-	EXPRESSION TAG	UNP Q92ZS5

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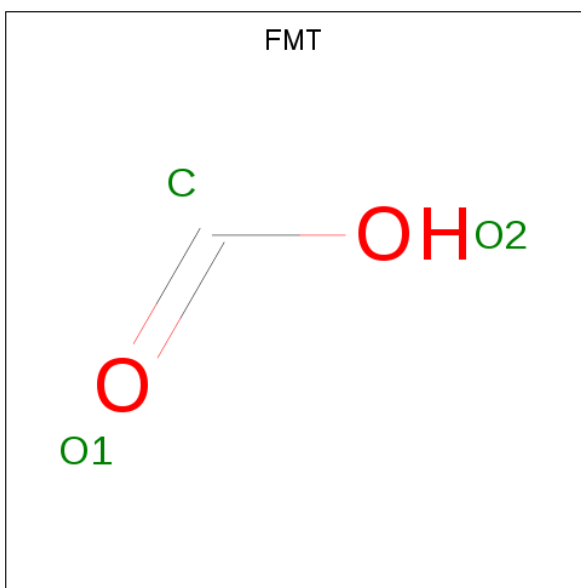
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Chain	Residue	Modelled	Actual	Comment	Reference
H	-2	GLN	-	EXPRESSION TAG	UNP Q92ZS5
H	-1	SER	-	EXPRESSION TAG	UNP Q92ZS5
H	0	MET	-	EXPRESSION TAG	UNP Q92ZS5

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0
2	E	1	Total Mg 1 1	0	0
2	H	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	A	1	Total Mg 1 1	0	0
2	F	1	Total Mg 1 1	0	0

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).

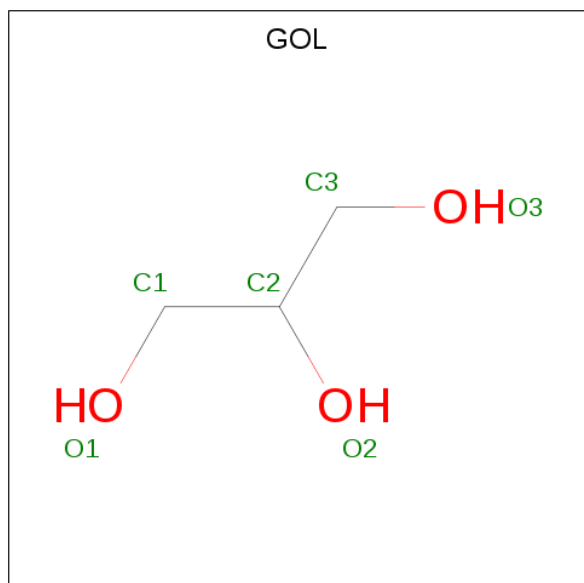


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 3 1 2	0	0
3	B	1	Total C O 3 1 2	0	0
3	C	1	Total C O 3 1 2	0	0
3	E	1	Total C O 3 1 2	0	0
3	F	1	Total C O 3 1 2	0	0
3	G	1	Total C O 3 1 2	0	0
3	H	1	Total C O 3 1 2	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	1	Total Cl 2 2	0	1
4	B	1	Total Cl 2 2	0	1
4	D	1	Total Cl 2 2	0	1
4	C	2	Total Cl 3 3	0	1

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	135	Total	O	0	0
			135	135		
6	B	237	Total	O	0	0
			237	237		
6	C	161	Total	O	0	0
			161	161		
6	D	168	Total	O	0	0
			168	168		
6	E	213	Total	O	0	0
			213	213		
6	F	201	Total	O	0	0
			201	201		
6	G	233	Total	O	0	0
			233	233		
6	H	143	Total	O	0	1
			144	144		

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 ($\text{RSRZ} > 2$). 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.

Chain A:

Sequence logo for Chain A. The y-axis represents information content in bits (0.00 to 0.25). The x-axis shows positions 1 to 300. A bar at the top indicates the percentage of conserved residues: 73% (green), 18% (yellow), and 9% (grey). Red dots above the sequence indicate positions with high conservation (bits > 0.15).

Position	Amino Acid	Information Content (bits)
1	Met	0.00
2	His	0.00
3	His	0.00
4	His	0.00
5	His	0.00
6	His	0.00
7	His	0.00
8	Ser	0.00
9	Ser	0.00
10	Gly	0.00
11	Val	0.00
12	Asp	0.00
13	Leu	0.00
14	Gly	0.00
15	Thr	0.00
16	Glu	0.00
17	Asn	0.00
18	Leu	0.00
19	Tyr	0.00
20	Phe	0.00
21	Gln	0.00
22	Ser	0.00
23	Met	0.00
24	Met	0.00
25	Ser	0.00
26	Asp	0.00
27	Leu	0.00
28	Gly	0.00
29	Arg	0.00
30	Glu	0.00
31	Thr	0.00
32	Pro	0.00
33	Pro	0.00
34	Tyr	0.00
35	Leu	0.00
36	Gly	0.00
37	Lys	0.00
38	Pro	0.00
39	Arg	0.00
40	Pro	0.00
41	Gly	0.00
42	Glu	0.00
43	Pro	0.00
44	Pro	0.00
45	Gly	0.00
46	Asp	0.00
47	Leu	0.00
48	Val	0.00
49	Thr	0.00
50	Leu	0.00
51	Val	0.00
52	Leu	0.00
53	Val	0.00
54	Leu	0.00
55	Val	0.00
56	Leu	0.00
57	Val	0.00
58	Leu	0.00
59	Val	0.00
60	Leu	0.00
61	Val	0.00
62	Leu	0.00
63	Val	0.00
64	Leu	0.00
65	Val	0.00
66	Leu	0.00
67	Val	0.00
68	Leu	0.00
69	Val	0.00
70	Leu	0.00
71	Val	0.00
72	Leu	0.00
73	Val	0.00
74	Leu	0.00
75	Val	0.00
76	Leu	0.00
77	Val	0.00
78	Leu	0.00
79	Val	0.00
80	Leu	0.00
81	Val	0.00
82	Leu	0.00
83	Val	0.00
84	Leu	0.00
85	Val	0.00
86	Leu	0.00
87	Val	0.00
88	Leu	0.00
89	Val	0.00
90	Leu	0.00
91	Val	0.00
92	Leu	0.00
93	Val	0.00
94	Leu	0.00
95	Val	0.00
96	Leu	0.00
97	Val	0.00
98	Leu	0.00
99	Val	0.00
100	Leu	0.00
101	Val	0.00
102	Leu	0.00
103	Val	0.00
104	Leu	0.00
105	Val	0.00
106	Leu	0.00
107	Val	0.00
108	Leu	0.00
109	Val	0.00
110	Leu	0.00
111	Val	0.00
112	Leu	0.00
113	Val	0.00
114	Leu	0.00
115	Val	0.00
116	Leu	0.00
117	Val	0.00
118	Leu	0.00
119	Val	0.00
120	Leu	0.00
121	Val	0.00
122	Leu	0.00
123	Val	0.00
124	Leu	0.00
125	Val	0.00
126	Leu	0.00
127	Val	0.00
128	Leu	0.00
129	Val	0.00
130	Leu	0.00
131	Val	0.00
132	Leu	0.00
133	Val	0.00
134	Leu	0.00
135	Val	0.00
136	Leu	0.00
137	Val	0.00
138	Leu	0.00
139	Val	0.00
140	Leu	0.00
141	Val	0.00
142	Leu	0.00
143	Val	0.00
144	Leu	0.00
145		

Chain B:

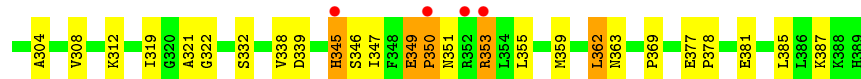
77% 16% 6%

MET HIS HIS HIS HIS HIS HIS HIS GLY VAL ASP GLY THR GLU ASN LEU TRP PHE GLN SER MET MET S2 D3 R4 F11 R17 E18 T19 P20 Y21 L22 G23 K24 P25 G28 E29 E30 P31 L37 V38 R39 K40 D50 E60 R76 D94 P95 E110

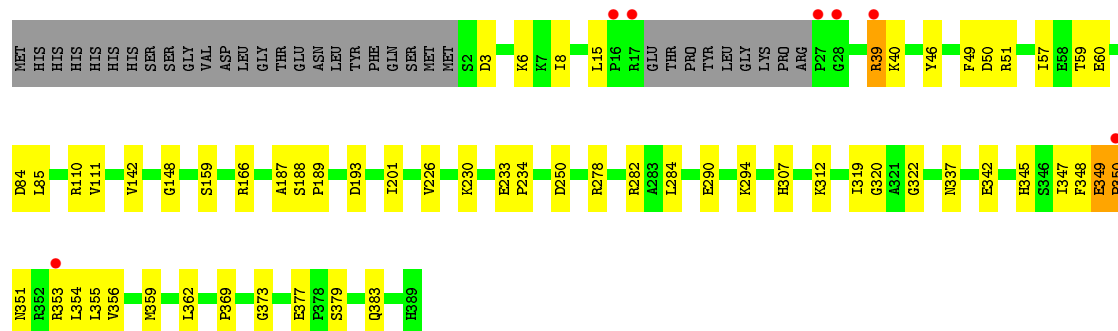
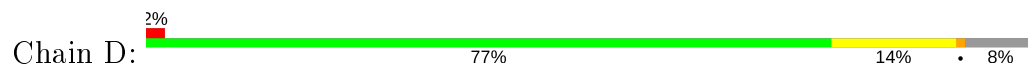
Chain C:

74% 16% 3% 8%

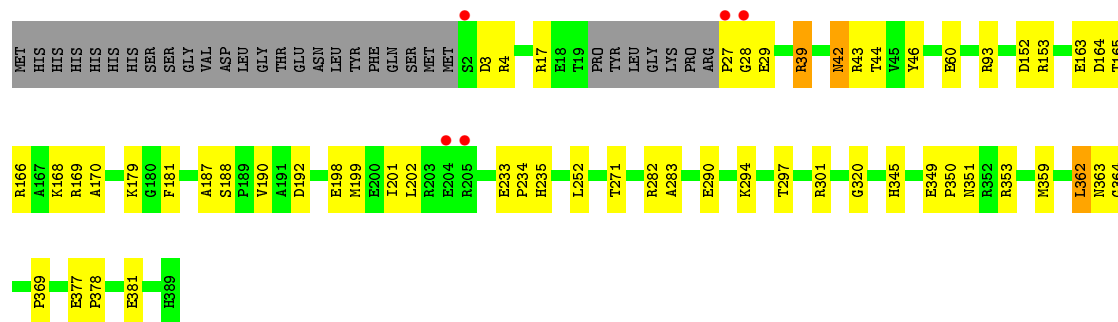
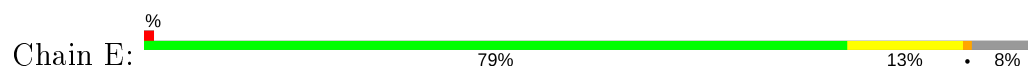
Sequence logo for Chain C, showing amino acid conservation across 200 positions. The y-axis represents information content in bits (0.00 to 0.25). The x-axis shows positions 1 to 200. The bar chart at the top indicates the percentage of each amino acid type: 74% green (mostly Lysine), 16% yellow (mostly Glutamine), 3% orange (mostly Asparagine), and 8% grey (mostly Proline). The sequence logo shows high conservation at positions 1-10, 15-20, 25-30, 35-40, 45-50, 55-60, 65-70, 75-80, 85-90, 95-100, 105-110, 115-120, 125-130, 135-140, 145-150, 155-160, 165-170, 175-180, 185-190, 195-200. The most conserved residues are Lysine (K) and Glutamine (Q).



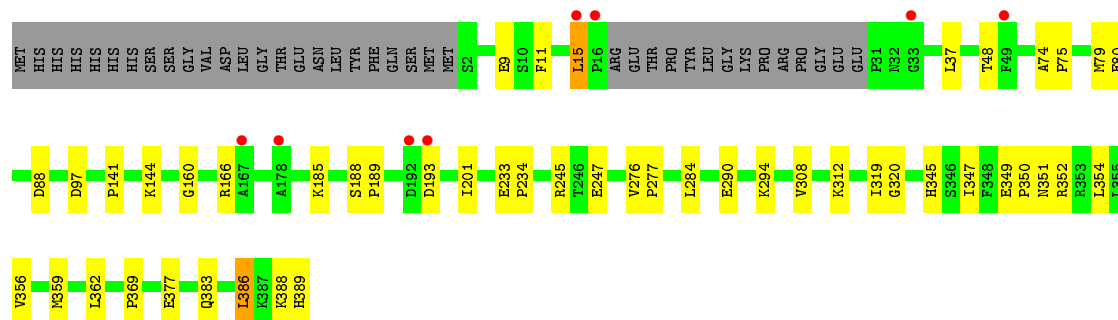
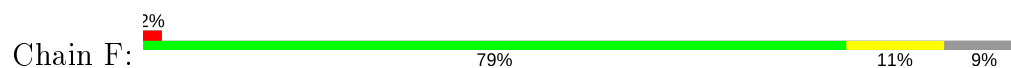
• Molecule 1: Enolase Q92Zs5



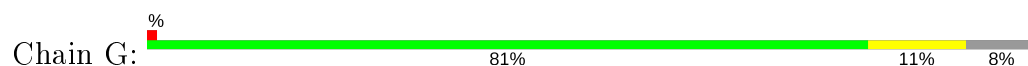
• Molecule 1: Enolase Q92Zs5

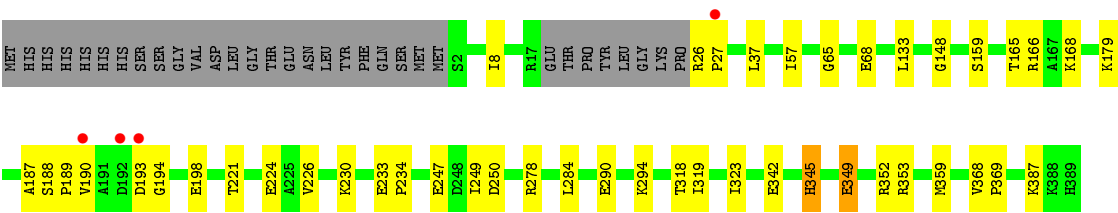


• Molecule 1: Enolase Q92Zs5

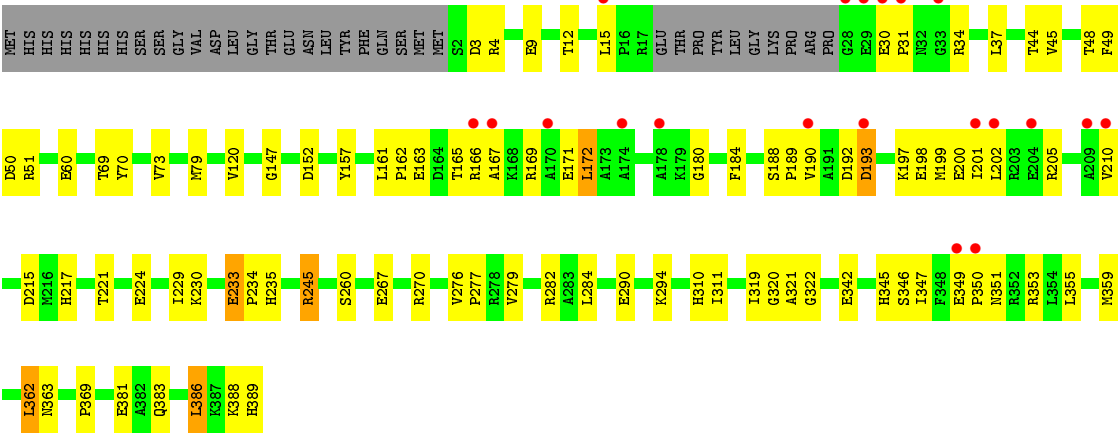


• Molecule 1: Enolase Q92Zs5





● Molecule 1: Enolase Q92Zs5



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	102.72Å 121.70Å 137.69Å 90.00° 99.79° 90.00°	Depositor
Resolution (Å)	45.02 – 2.01 44.98 – 2.01	Depositor EDS
% Data completeness (in resolution range)	98.4 (45.02-2.01) 98.4 (44.98-2.01)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.172 , 0.229 0.173 , 0.229	Depositor DCC
R_{free} test set	6577 reflections (3.02%)	wwPDB-VP
Wilson B-factor (Å ²)	32.7	Xtriage
Anisotropy	0.498	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	24833	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.56% 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, FMT, MG, CL

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	0.39	1/2942 (0.0%)	0.56	1/3990 (0.0%)
1	B	0.45	2/3053 (0.1%)	0.61	2/4144 (0.0%)
1	C	0.44	1/2975 (0.0%)	0.60	2/4032 (0.0%)
1	D	0.44	3/2980 (0.1%)	0.61	3/4039 (0.1%)
1	E	0.43	0/2993	0.61	1/4057 (0.0%)
1	F	0.46	1/2955 (0.0%)	0.63	1/4007 (0.0%)
1	G	0.48	1/2983 (0.0%)	0.66	2/4045 (0.0%)
1	H	0.48	1/2954 (0.0%)	0.62	3/4006 (0.1%)
All	All	0.45	10/23835 (0.0%)	0.61	15/32320 (0.0%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	39[A]	ARG	CA-C	5.97	1.68	1.52
1	D	39[B]	ARG	CA-C	5.97	1.68	1.52
1	H	162	PRO	N-CD	5.32	1.55	1.47
1	D	350	PRO	N-CD	5.31	1.55	1.47
1	B	31	PRO	N-CD	5.30	1.55	1.47
1	A	350	PRO	N-CD	5.28	1.55	1.47
1	C	350	PRO	N-CD	5.25	1.55	1.47
1	F	350	PRO	N-CD	5.14	1.55	1.47
1	B	25	PRO	N-CD	5.09	1.54	1.47
1	G	27	PRO	N-CD	5.06	1.54	1.47

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	26	ARG	C-N-CD	5.80	140.59	128.40
1	B	24	LYS	C-N-CD	5.79	140.56	128.40
1	H	233	GLU	C-N-CD	5.77	140.52	128.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	15	LEU	C-N-CD	5.76	140.50	128.40
1	E	188	SER	C-N-CD	5.63	140.22	128.40
1	F	349	GLU	C-N-CD	5.59	140.14	128.40
1	G	349	GLU	C-N-CD	5.58	140.12	128.40
1	C	188	SER	C-N-CD	5.56	140.08	128.40
1	H	161	LEU	C-N-CD	5.54	140.03	128.40
1	D	349	GLU	C-N-CD	5.53	140.01	128.40
1	C	349	GLU	C-N-CD	5.50	139.94	128.40
1	A	349	GLU	C-N-CD	5.48	139.91	128.40
1	B	30	GLU	C-N-CD	5.37	139.69	128.40
1	D	39[A]	ARG	CA-C-O	5.15	130.92	120.10
1	D	39[B]	ARG	CA-C-O	5.15	130.92	120.10

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	2880	0	2872	60	0
1	B	2982	0	2977	49	0
1	C	2909	0	2908	60	0
1	D	2913	0	2907	53	0
1	E	2926	0	2920	49	0
1	F	2880	0	2881	37	0
1	G	2916	0	2908	34	0
1	H	2891	0	2880	74	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	3	0	1	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	3	0	1	1	0
3	C	3	0	1	0	0
3	E	3	0	1	0	0
3	F	3	0	1	0	0
3	G	3	0	1	0	0
3	H	3	0	1	0	0
4	B	2	0	0	0	0
4	C	3	0	0	0	0
4	D	2	0	0	0	0
4	G	2	0	0	0	0
5	B	6	0	8	5	0
6	A	135	0	0	3	0
6	B	237	0	0	3	0
6	C	161	0	0	6	0
6	D	168	0	0	1	0
6	E	213	0	0	5	0
6	F	201	0	0	4	0
6	G	233	0	0	4	0
6	H	144	0	0	3	0
All	All	24833	0	23268	402	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 9.

All (402) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:LEU:HD11	6:A:605:HOH:O	1.49	1.11
1:H:349:GLU:HB3	1:H:350:PRO:HD3	1.47	0.95
1:D:166:ARG:HG2	1:D:201:ILE:HG21	1.49	0.95
1:H:383:GLN:HA	1:H:386:LEU:HD22	1.50	0.93
1:A:163:GLU:HB2	1:A:169:ARG:CG	1.99	0.92
1:B:31:PRO:HG3	1:B:37:LEU:HD23	1.52	0.91
1:E:166:ARG:HG2	1:E:201:ILE:HD12	1.49	0.91
1:A:163:GLU:HB2	1:A:169:ARG:HG2	1.53	0.91
1:B:344:GLN:HB3	1:B:347:ILE:HD12	1.54	0.89
3:B:403:FMT:H	6:B:638:HOH:O	1.73	0.89
1:C:359:MET:HB2	1:C:369:PRO:HG3	1.55	0.87
1:D:319:ILE:HA	1:D:347:ILE:HD12	1.56	0.87
1:F:15:LEU:HD21	1:F:354:LEU:HD11	1.56	0.85
1:G:345:HIS:CD2	1:G:345:HIS:H	1.90	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:349:GLU:HB2	1:E:350:PRO:HD3	1.57	0.84
1:G:188:SER:OG	1:G:189:PRO:HD3	1.79	0.83
1:C:353:ARG:NH1	1:C:381:GLU:HG2	1.95	0.82
1:E:39:ARG:HG3	1:E:46:TYR:CE1	2.16	0.81
1:E:362:LEU:HD23	1:E:362:LEU:O	1.79	0.81
1:F:15:LEU:CD2	1:F:354:LEU:HD11	2.12	0.77
1:G:250:ASP:HB3	1:H:282:ARG:HH11	1.49	0.77
1:G:221:THR:OG1	1:G:224:GLU:HG3	1.84	0.77
1:E:39:ARG:HG3	1:E:46:TYR:HE1	1.49	0.76
1:H:200:GLU:HB2	1:H:235:HIS:CE1	2.21	0.76
1:D:39[A]:ARG:HG3	1:D:46:TYR:CE1	2.22	0.74
1:H:362:LEU:HD23	1:H:362:LEU:O	1.87	0.74
1:F:290:GLU:H	1:F:294:LYS:HZ2	1.37	0.73
1:A:37:LEU:O	1:A:37:LEU:HD12	1.89	0.73
1:H:349:GLU:CB	1:H:350:PRO:HD3	2.18	0.73
1:A:163:GLU:HB2	1:A:169:ARG:HG3	1.71	0.73
1:E:359:MET:HB2	1:E:369:PRO:HG3	1.72	0.72
1:E:3:ASP:O	1:E:4:ARG:HD3	1.89	0.72
1:A:335:LEU:HB2	1:A:338:VAL:HG23	1.71	0.72
1:G:250:ASP:HB3	1:H:282:ARG:NH1	2.04	0.72
1:B:186:PHE:HE1	1:B:199:MET:CE	2.02	0.71
1:E:198:GLU:O	1:E:201:ILE:HG22	1.90	0.71
1:C:43:ARG:HG2	1:C:43:ARG:HH11	1.55	0.71
1:G:345:HIS:H	1:G:345:HIS:HD2	1.38	0.71
1:C:319:ILE:HA	1:C:347:ILE:HG13	1.72	0.71
1:B:199:MET:HG2	1:B:235:HIS:HB2	1.73	0.71
1:H:31:PRO:HG3	1:H:48:THR:HG21	1.72	0.70
1:E:163:GLU:HB2	1:E:169:ARG:HG2	1.73	0.69
1:A:37:LEU:HD12	1:A:37:LEU:C	2.12	0.69
1:F:15:LEU:HD21	1:F:354:LEU:CD1	2.23	0.68
1:H:322:GLY:HA3	1:H:355:LEU:HD11	1.74	0.68
1:B:21:TYR:O	1:B:22:LEU:HB2	1.91	0.68
1:A:387:LYS:HD3	6:A:544:HOH:O	1.94	0.67
1:C:197:LYS:HE2	1:C:200:GLU:OE1	1.94	0.67
1:F:166:ARG:HG2	1:F:201:ILE:HG21	1.76	0.67
1:H:359:MET:HB2	1:H:369:PRO:HG3	1.77	0.66
1:H:163:GLU:HB2	1:H:169:ARG:HG2	1.77	0.66
1:H:229:ILE:O	1:H:233:GLU:HG3	1.95	0.66
1:G:187:ALA:O	1:G:190:VAL:HG22	1.96	0.66
1:G:345:HIS:CD2	1:G:345:HIS:N	2.64	0.65
1:B:199:MET:CG	1:B:235:HIS:HB2	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:50:ASP:HB3	1:H:319:ILE:HG21	1.78	0.65
1:H:201:ILE:HG23	1:H:202:LEU:N	2.11	0.65
1:H:388:LYS:HG3	1:H:389:HIS:N	2.12	0.64
1:H:349:GLU:HB3	1:H:350:PRO:CD	2.25	0.64
1:D:322:GLY:HA3	1:D:355:LEU:HD11	1.80	0.63
1:A:34:ARG:HD2	1:C:88:ASP:OD2	1.99	0.62
1:F:290:GLU:H	1:F:294:LYS:NZ	1.95	0.62
1:B:199:MET:HE2	1:B:199:MET:HA	1.81	0.62
1:G:37:LEU:C	1:G:37:LEU:HD12	2.19	0.62
1:D:49:PHE:O	1:D:49:PHE:CD1	2.53	0.62
1:A:322:GLY:HA3	1:A:355:LEU:HD11	1.80	0.62
1:A:359:MET:HB2	1:A:369:PRO:HG3	1.81	0.61
1:B:362:LEU:O	1:B:362:LEU:HD23	2.01	0.61
1:H:198:GLU:O	1:H:201:ILE:HG22	2.00	0.61
1:A:347:ILE:HD12	1:A:347:ILE:C	2.21	0.61
1:D:347:ILE:O	1:D:350:PRO:HD2	2.00	0.61
1:A:163:GLU:OE1	1:A:163:GLU:HA	2.01	0.60
1:E:349:GLU:CB	1:E:350:PRO:HD3	2.31	0.60
1:B:31:PRO:HA	1:B:37:LEU:HB3	1.84	0.60
1:D:319:ILE:HG23	1:D:347:ILE:HD12	1.82	0.60
1:C:43:ARG:HG2	1:C:43:ARG:NH1	2.17	0.60
1:D:250:ASP:HB3	1:E:282[A]:ARG:HE	1.67	0.60
1:A:215:ASP:HA	1:A:241:GLU:HB3	1.84	0.60
1:E:187:ALA:O	1:E:190:VAL:HG22	2.01	0.60
1:G:290:GLU:H	1:G:294:LYS:NZ	2.00	0.60
1:F:88:ASP:HB2	6:F:641:HOH:O	2.00	0.59
1:D:159:SER:HB2	1:D:342:GLU:OE2	2.03	0.59
1:G:359:MET:HB2	1:G:369:PRO:HG3	1.83	0.59
1:C:345:HIS:ND1	1:C:349:GLU:HG3	2.18	0.59
1:H:200:GLU:HA	1:H:235:HIS:ND1	2.18	0.59
1:A:201:ILE:HG23	1:A:202:LEU:N	2.18	0.58
1:C:28:GLY:O	1:C:40:LYS:NZ	2.36	0.58
1:A:335:LEU:HB2	1:A:338:VAL:CG2	2.33	0.58
1:A:188:SER:N	1:A:189:PRO:CD	2.67	0.58
1:G:179:LYS:HE3	6:G:625:HOH:O	2.03	0.57
1:H:345:HIS:O	1:H:349:GLU:HB2	2.04	0.57
1:E:201:ILE:HG23	1:E:202:LEU:N	2.19	0.57
1:B:17:ARG:HD2	1:B:50:ASP:OD1	2.04	0.57
6:E:704:HOH:O	1:G:247[B]:GLU:HG3	2.04	0.57
1:G:249:ILE:HG12	6:G:727:HOH:O	2.04	0.57
1:G:37:LEU:O	1:G:37:LEU:HD12	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:MET:HE2	1:A:299:PHE:CD2	2.39	0.57
1:B:300:MET:HB2	5:B:404:GOL:H12	1.87	0.57
1:E:297:THR:O	1:E:301:ARG:HG3	2.04	0.57
1:D:290:GLU:H	1:D:294:LYS:NZ	2.03	0.56
1:H:201:ILE:HG23	1:H:202:LEU:H	1.70	0.56
1:C:176:TRP:HZ2	1:C:345:HIS:CD2	2.23	0.56
1:H:188:SER:OG	1:H:189:PRO:HD3	2.05	0.56
1:C:377:GLU:HB2	1:C:378:PRO:HD2	1.86	0.56
1:H:319:ILE:HA	1:H:347:ILE:HG21	1.88	0.56
1:B:188:SER:OG	1:B:189:PRO:HD3	2.06	0.56
1:F:188:SER:N	1:F:189:PRO:CD	2.68	0.56
1:H:152:ASP:HB2	6:H:625:HOH:O	2.04	0.56
1:B:28:GLY:O	1:B:40:LYS:HE3	2.06	0.56
1:D:166:ARG:HG2	1:D:201:ILE:CG2	2.31	0.56
1:A:164:ASP:OD1	1:A:165:THR:HG23	2.05	0.56
1:E:320:GLY:O	1:E:351:ASN:ND2	2.39	0.56
6:C:565:HOH:O	1:D:282:ARG:HD3	2.06	0.55
1:E:42:ASN:ND2	1:E:44:THR:H	2.04	0.55
1:C:350:PRO:HG2	1:C:351:ASN:HD22	1.71	0.55
1:H:163:GLU:HG2	1:H:172:LEU:HD13	1.87	0.55
1:E:39:ARG:CG	1:E:46:TYR:CE1	2.89	0.55
1:F:383:GLN:HA	1:F:386:LEU:HD22	1.88	0.55
1:E:17:ARG:HB2	6:E:702:HOH:O	2.06	0.55
1:H:290:GLU:H	1:H:294:LYS:NZ	2.04	0.55
1:H:49:PHE:HE2	1:H:51:ARG:CZ	2.19	0.55
1:C:377:GLU:HB2	1:C:378:PRO:CD	2.36	0.54
1:H:49:PHE:CD1	1:H:49:PHE:N	2.75	0.54
1:D:345:HIS:CE1	1:D:349:GLU:HB2	2.42	0.54
1:D:319:ILE:CA	1:D:347:ILE:HD12	2.33	0.54
1:D:6:LYS:HD2	1:D:60:GLU:OE2	2.06	0.54
1:F:312:LYS:HE2	6:F:625:HOH:O	2.08	0.54
1:C:31:PRO:HG3	1:C:48:THR:HG21	1.89	0.54
1:D:278:ARG:HB3	1:D:284:LEU:HD22	1.90	0.54
1:D:356:VAL:CG2	1:D:377:GLU:HG3	2.37	0.54
1:F:308:VAL:HG23	6:F:549:HOH:O	2.07	0.54
1:E:166:ARG:HG2	1:E:201:ILE:CD1	2.32	0.54
1:A:89:PHE:CE1	1:C:38:VAL:HG23	2.43	0.54
1:D:379:SER:O	1:D:383:GLN:HG3	2.09	0.53
1:D:39[A]:ARG:HG3	1:D:46:TYR:HE1	1.70	0.53
1:C:278:ARG:HB3	1:C:284:LEU:CD2	2.39	0.53
1:D:319:ILE:HG12	1:D:347:ILE:HD11	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:ARG:HH21	1:F:247[A]:GLU:CD	2.12	0.53
1:C:278:ARG:HB3	1:C:284:LEU:HD22	1.90	0.53
1:D:8:ILE:HG12	1:D:57:ILE:HG12	1.89	0.53
1:F:166:ARG:HB2	6:F:701:HOH:O	2.06	0.53
1:C:220:HIS:HB2	1:C:243:PRO:O	2.09	0.53
1:D:142:VAL:HG23	1:D:373:GLY:C	2.29	0.53
1:A:335:LEU:CB	1:A:338:VAL:HG23	2.39	0.53
1:E:345:HIS:H	1:E:345:HIS:CD2	2.26	0.53
1:G:349:GLU:O	1:G:352:ARG:HG3	2.09	0.53
1:H:188:SER:N	1:H:189:PRO:CD	2.71	0.53
1:A:171:GLU:O	1:A:174:ALA:HB3	2.10	0.52
1:F:9:GLU:OE2	1:F:388:LYS:HE3	2.09	0.52
1:D:60:GLU:OE2	1:D:60:GLU:HA	2.08	0.52
1:C:198:GLU:O	1:C:201:ILE:HG22	2.10	0.52
1:E:377:GLU:HB2	1:E:378:PRO:HD2	1.90	0.52
1:F:245:ARG:HB3	1:F:247[A]:GLU:OE1	2.09	0.52
1:H:193:ASP:OD1	1:H:193:ASP:N	2.42	0.52
1:B:344:GLN:CB	1:B:347:ILE:HD12	2.34	0.52
1:A:74:ALA:N	1:A:75:PRO:CD	2.72	0.51
1:C:197:LYS:CE	1:C:200:GLU:OE1	2.57	0.51
1:D:290:GLU:H	1:D:294:LYS:HZ2	1.58	0.51
1:D:50:ASP:CG	1:D:319:ILE:HG21	2.30	0.51
1:H:362:LEU:N	1:H:362:LEU:CD2	2.73	0.51
1:C:362:LEU:HG	1:C:362:LEU:O	2.09	0.51
1:G:247[A]:GLU:HG2	1:H:310:HIS:CE1	2.45	0.51
1:C:321:ALA:O	1:C:355:LEU:HD11	2.10	0.51
1:A:43:ARG:NH2	1:C:104:ASP:OD1	2.39	0.51
1:H:205:ARG:O	1:H:205:ARG:HD2	2.10	0.51
1:H:284:LEU:N	1:H:284:LEU:HD23	2.26	0.51
1:B:186:PHE:HE1	1:B:199:MET:HE1	1.73	0.51
1:A:165:THR:OG1	1:A:168:LYS:HG3	2.11	0.51
1:B:180:GLY:HA3	1:B:363:ASN:HD22	1.75	0.51
1:C:176:TRP:HZ2	1:C:345:HIS:CG	2.29	0.51
1:F:188:SER:N	1:F:189:PRO:HD2	2.25	0.51
1:E:42:ASN:HD22	1:E:42:ASN:C	2.14	0.51
1:F:356:VAL:CG2	1:F:377:GLU:HG3	2.40	0.51
1:E:201:ILE:CG2	1:E:202:LEU:N	2.74	0.51
1:A:38:VAL:HG23	1:C:89:PHE:CE1	2.46	0.51
1:B:359:MET:HB2	1:B:369:PRO:HG3	1.93	0.51
1:H:163:GLU:HB2	1:H:169:ARG:CG	2.39	0.51
1:C:282:ARG:CD	6:C:520:HOH:O	2.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:320:GLY:O	1:D:351:ASN:ND2	2.40	0.50
1:F:320:GLY:O	1:F:351:ASN:ND2	2.44	0.50
1:G:8:ILE:HG12	1:G:57:ILE:HG12	1.93	0.50
1:B:358:ASP:OD2	1:B:370:THR:OG1	2.29	0.50
1:F:345:HIS:H	1:F:345:HIS:CD2	2.28	0.50
1:H:167:ALA:O	1:H:171:GLU:HG2	2.11	0.50
1:H:120:VAL:HG11	1:H:270:ARG:HB3	1.93	0.50
1:A:111:VAL:HG22	6:C:521:HOH:O	2.11	0.50
1:H:157:TYR:CZ	1:H:342:GLU:HG3	2.46	0.50
1:G:290:GLU:H	1:G:294:LYS:HZ2	1.58	0.50
1:F:359:MET:HB2	1:F:369:PRO:HG3	1.94	0.50
1:A:37:LEU:CD1	1:A:37:LEU:C	2.80	0.50
1:F:141:PRO:HG2	1:F:144:LYS:HG2	1.94	0.50
1:B:186:PHE:CE1	1:B:199:MET:CE	2.89	0.49
1:B:300:MET:CB	5:B:404:GOL:H12	2.42	0.49
1:A:13:LEU:HD13	1:A:386:LEU:HD23	1.95	0.49
1:H:276:VAL:HB	1:H:277:PRO:HD3	1.93	0.49
1:C:56:ARG:NH1	6:C:544:HOH:O	2.35	0.49
1:B:11:PHE:CD1	1:B:11:PHE:N	2.80	0.49
1:A:201:ILE:CG2	1:A:202:LEU:N	2.75	0.49
1:A:286:ILE:HG12	1:A:312:LYS:HB2	1.95	0.49
1:C:347:ILE:O	1:C:351:ASN:ND2	2.45	0.49
1:D:188:SER:N	1:D:189:PRO:CD	2.75	0.49
1:E:252:LEU:HG	1:E:283:ALA:HB1	1.95	0.48
1:A:233:GLU:N	1:A:234:PRO:CD	2.77	0.48
1:A:278:ARG:HB3	1:A:284:LEU:HD22	1.95	0.48
1:E:353:ARG:NH1	1:E:381:GLU:OE2	2.46	0.48
1:A:362:LEU:HD23	1:A:362:LEU:N	2.27	0.48
1:H:166:ARG:HG2	1:H:201:ILE:HD12	1.95	0.48
1:C:31:PRO:HA	1:C:37:LEU:HB3	1.95	0.48
1:B:349:GLU:HB2	1:B:350:PRO:HD3	1.95	0.48
1:E:42:ASN:HD22	1:E:43:ARG:N	2.11	0.48
1:A:290:GLU:H	1:A:294:LYS:HZ2	1.61	0.48
1:E:290:GLU:H	1:E:294:LYS:NZ	2.12	0.48
1:C:247:GLU:H	1:C:247:GLU:CD	2.18	0.47
1:H:37:LEU:C	1:H:37:LEU:HD12	2.34	0.47
1:C:187:ALA:HB1	1:C:189:PRO:HD2	1.96	0.47
1:D:49:PHE:HE1	1:D:51:ARG:CZ	2.27	0.47
1:E:163:GLU:HB2	1:E:169:ARG:CG	2.41	0.47
1:D:348:PHE:C	1:D:348:PHE:CD1	2.87	0.47
1:D:166:ARG:NE	1:D:193:ASP:OD2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:ASN:O	1:A:34:ARG:N	2.47	0.47
1:B:353:ARG:NE	1:B:381:GLU:OE1	2.47	0.47
1:C:347:ILE:HD13	1:C:347:ILE:N	2.29	0.47
1:E:164:ASP:HB3	1:E:168:LYS:NZ	2.28	0.47
1:A:32:ASN:C	1:A:34:ARG:H	2.18	0.47
1:B:181:PHE:CD2	1:B:364:GLY:HA2	2.50	0.47
1:D:111:VAL:HG13	6:D:598:HOH:O	2.14	0.47
1:A:187:ALA:HB1	1:A:189:PRO:HD2	1.97	0.47
1:E:27:PRO:O	1:E:29:GLU:N	2.47	0.47
1:E:60:GLU:HA	1:E:60:GLU:OE1	2.15	0.47
1:B:2:SER:HB3	1:B:4:ARG:HE	1.80	0.47
1:C:165:THR:HG23	1:C:168:LYS:HD2	1.96	0.47
1:A:97:ASP:HA	1:D:148:GLY:HA3	1.96	0.47
1:H:230:LYS:O	1:H:234:PRO:HD3	2.15	0.47
1:A:320:GLY:O	1:A:351:ASN:ND2	2.47	0.47
1:B:23:GLY:O	1:B:39:ARG:NH2	2.48	0.47
1:C:201:ILE:HG23	1:C:202:LEU:N	2.29	0.46
1:A:290:GLU:H	1:A:294:LYS:NZ	2.13	0.46
1:A:379:SER:O	1:A:383:GLN:HG3	2.15	0.46
1:D:233:GLU:N	1:D:234:PRO:CD	2.78	0.46
1:E:233:GLU:N	1:E:234:PRO:CD	2.78	0.46
1:C:12:THR:HG23	1:C:79:MET:CE	2.45	0.46
1:G:194:GLY:HA2	6:G:577:HOH:O	2.14	0.46
1:A:151:ARG:NH1	1:A:332:SER:O	2.49	0.46
1:B:188:SER:N	1:B:189:PRO:CD	2.78	0.46
1:C:200:GLU:HG3	1:C:235:HIS:CE1	2.51	0.46
1:H:201:ILE:CG2	1:H:202:LEU:N	2.78	0.46
1:H:37:LEU:O	1:H:37:LEU:HD12	2.15	0.46
1:A:50:ASP:HB3	1:A:319:ILE:CG2	2.46	0.46
1:A:229:ILE:O	1:A:233:GLU:HG3	2.16	0.46
1:G:387:LYS:NZ	6:G:676:HOH:O	2.37	0.46
1:A:276:VAL:HB	1:A:277:PRO:HD3	1.98	0.46
1:C:166:ARG:HG2	1:C:201:ILE:HD12	1.98	0.46
1:C:385:LEU:O	1:C:387:LYS:HE2	2.16	0.46
1:C:224:GLU:OE1	1:D:312:LYS:HE3	2.16	0.46
1:E:271:THR:CG2	6:E:573:HOH:O	2.64	0.46
1:C:226:VAL:O	1:C:230:LYS:HG2	2.16	0.46
1:F:284:LEU:N	1:F:284:LEU:HD23	2.31	0.45
1:C:12:THR:HG23	1:C:79:MET:HE1	1.98	0.45
1:E:199:MET:HG3	1:E:235:HIS:HB2	1.98	0.45
1:A:362:LEU:CD2	1:A:362:LEU:N	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:187:ALA:HB1	1:D:189:PRO:HD2	1.98	0.45
1:F:74:ALA:N	1:F:75:PRO:CD	2.79	0.45
1:H:180:GLY:HA3	1:H:363:ASN:HA	1.97	0.45
1:C:233:GLU:N	1:C:234:PRO:CD	2.79	0.45
1:H:147:GLY:HA2	6:H:633:HOH:O	2.15	0.45
1:H:171:GLU:O	1:H:172:LEU:C	2.55	0.45
1:C:166:ARG:HG2	1:C:201:ILE:CD1	2.47	0.45
1:D:351:ASN:HA	1:D:354:LEU:HD12	1.98	0.45
1:F:356:VAL:HG22	1:F:377:GLU:HG3	1.98	0.45
1:B:76:ARG:HB2	1:F:80:GLU:HG2	1.98	0.45
1:E:152:ASP:O	1:E:153:ARG:HD3	2.16	0.45
1:E:93:ARG:NH2	6:E:630:HOH:O	2.38	0.45
1:F:352:ARG:HH11	1:F:352:ARG:HG2	1.82	0.45
1:C:17:ARG:HG3	1:C:17:ARG:O	2.17	0.44
1:D:319:ILE:HG23	1:D:347:ILE:CD1	2.46	0.44
1:D:110:ARG:NH2	1:H:245:ARG:HG3	2.32	0.44
1:F:233:GLU:N	1:F:234:PRO:CD	2.80	0.44
1:B:163:GLU:HB2	1:B:169:ARG:HG2	1.99	0.44
1:B:188:SER:N	1:B:189:PRO:HD2	2.32	0.44
1:E:377:GLU:HB2	1:E:378:PRO:CD	2.48	0.44
1:B:290:GLU:H	1:B:294:LYS:NZ	2.15	0.44
1:C:179:LYS:O	1:C:363:ASN:HA	2.18	0.44
1:D:345:HIS:CE1	1:D:349:GLU:OE1	2.70	0.44
1:D:3:ASP:OD1	1:D:59:THR:HB	2.18	0.44
1:E:165:THR:HG23	1:E:168:LYS:HE3	1.98	0.44
1:E:282[A]:ARG:HA	6:E:711:HOH:O	2.17	0.44
1:B:3:ASP:O	1:B:4:ARG:HD3	2.18	0.44
1:H:320:GLY:O	1:H:351:ASN:ND2	2.50	0.44
1:C:203:ARG:HD3	1:C:203:ARG:HA	1.73	0.44
1:C:322:GLY:HA3	1:C:355:LEU:HD11	2.00	0.44
1:D:226:VAL:O	1:D:230:LYS:HG2	2.18	0.44
1:G:278:ARG:HB3	1:G:284:LEU:HD22	2.00	0.44
1:G:318:THR:OG1	1:G:319:ILE:N	2.50	0.44
1:H:198:GLU:O	1:H:201:ILE:CG2	2.65	0.44
1:H:49:PHE:CD2	1:H:49:PHE:O	2.70	0.44
1:A:181:PHE:CE2	1:A:364:GLY:HA2	2.53	0.43
1:E:42:ASN:ND2	1:E:42:ASN:C	2.72	0.43
1:B:184:PHE:CD1	1:B:184:PHE:N	2.86	0.43
1:A:347:ILE:HD12	1:A:347:ILE:O	2.17	0.43
1:B:279:VAL:HG22	1:B:311:ILE:CD1	2.48	0.43
1:C:176:TRP:CZ2	1:C:345:HIS:HB2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:44:THR:HG22	1:H:45:VAL:N	2.33	0.43
1:H:50:ASP:HB3	1:H:319:ILE:CG2	2.46	0.43
1:G:226:VAL:O	1:G:230:LYS:HG2	2.18	0.43
1:B:186:PHE:CD2	1:B:198:GLU:HG2	2.54	0.43
1:B:21:TYR:CE2	1:B:22:LEU:HG	2.53	0.43
1:D:159:SER:HB3	1:D:342:GLU:HG2	2.01	0.43
1:D:362:LEU:N	1:D:362:LEU:HD23	2.34	0.43
1:D:84:ASP:O	1:H:34:ARG:HD3	2.18	0.43
1:H:193:ASP:O	1:H:197:LYS:HG3	2.19	0.43
1:C:201:ILE:CG2	1:C:202:LEU:N	2.82	0.43
1:A:377:GLU:HB2	1:A:378:PRO:HD2	2.00	0.43
5:B:404:GOL:C3	6:B:689:HOH:O	2.66	0.43
6:A:547:HOH:O	1:C:111:VAL:HG22	2.19	0.43
1:G:166:ARG:HG2	1:G:198:GLU:OE1	2.19	0.42
1:H:279:VAL:HG22	1:H:311:ILE:CD1	2.48	0.42
1:B:300:MET:HB2	5:B:404:GOL:C1	2.49	0.42
1:F:276:VAL:HB	1:F:277:PRO:CD	2.49	0.42
1:G:165:THR:OG1	1:G:168:LYS:HG3	2.19	0.42
1:H:267:GLU:HG2	6:H:510:HOH:O	2.19	0.42
1:H:284:LEU:HD23	1:H:284:LEU:H	1.83	0.42
1:E:179:LYS:O	1:E:363:ASN:HA	2.19	0.42
1:F:166:ARG:NE	1:F:193:ASP:OD2	2.47	0.42
1:F:362:LEU:N	1:F:362:LEU:HD23	2.35	0.42
1:A:55:VAL:CG2	1:A:82:ILE:HD13	2.49	0.42
1:A:3:ASP:CG	1:A:59:THR:HB	2.40	0.42
1:B:376[B]:VAL:HG12	1:B:377:GLU:N	2.34	0.42
1:G:159:SER:HB2	1:G:342:GLU:OE2	2.19	0.42
1:H:199:MET:HB3	1:H:235:HIS:HB2	2.00	0.42
1:B:379:SER:O	1:B:383:GLN:HG3	2.20	0.42
1:E:164:ASP:CB	1:E:168:LYS:NZ	2.82	0.42
1:F:319:ILE:HA	1:F:347:ILE:HD13	2.01	0.42
1:H:190:VAL:CG1	1:H:190:VAL:O	2.67	0.42
1:A:157:TYR:CZ	1:A:342:GLU:HG3	2.55	0.42
1:C:176:TRP:CZ2	1:C:345:HIS:CG	3.07	0.42
1:F:97:ASP:HA	1:G:148:GLY:HA3	2.01	0.42
1:C:268:GLU:N	1:C:268:GLU:OE1	2.42	0.42
1:C:304:ALA:O	1:C:308:VAL:HG23	2.20	0.42
1:F:386:LEU:HA	1:F:386:LEU:HD12	1.92	0.42
1:H:221:THR:OG1	1:H:224:GLU:HG3	2.20	0.42
1:H:30:GLU:H	1:H:30:GLU:CD	2.23	0.42
1:D:50:ASP:CG	1:D:319:ILE:CG2	2.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:165:THR:OG1	1:E:168:LYS:HG3	2.20	0.42
1:F:247[A]:GLU:CD	1:F:247[A]:GLU:H	2.23	0.42
1:F:11:PHE:CB	1:F:386:LEU:HG	2.50	0.42
1:G:188:SER:N	1:G:189:PRO:CD	2.83	0.42
1:H:3:ASP:O	1:H:4:ARG:HD2	2.19	0.42
1:G:65:GLY:HA3	1:G:133:LEU:HG	2.01	0.42
1:G:368:VAL:HA	1:G:369:PRO:HD3	1.91	0.41
1:A:32:ASN:OD1	1:A:32:ASN:C	2.58	0.41
1:A:83:ASP:OD2	1:A:389:HIS:ND1	2.37	0.41
1:B:318:THR:OG1	1:B:319:ILE:N	2.53	0.41
1:A:362:LEU:HD23	1:A:362:LEU:H	1.85	0.41
1:A:94:ASP:HA	1:A:95:PRO:HD3	1.88	0.41
1:D:356:VAL:HG22	1:D:377:GLU:HG3	2.01	0.41
1:E:3:ASP:C	1:E:4:ARG:HD3	2.40	0.41
1:B:133:LEU:HD23	1:B:133:LEU:HA	1.92	0.41
1:C:110:ARG:NH2	6:C:661:HOH:O	2.47	0.41
1:B:199:MET:HE3	1:B:199:MET:HB2	1.79	0.41
1:C:50:ASP:HB3	1:C:319:ILE:HG21	2.02	0.41
1:E:27:PRO:O	1:E:29:GLU:HG3	2.21	0.41
1:H:321:ALA:HA	1:H:351:ASN:HD22	1.85	0.41
1:H:69:THR:OG1	1:H:70:TYR:N	2.53	0.41
1:A:171:GLU:O	1:A:174:ALA:N	2.53	0.41
1:A:94:ASP:O	1:A:97:ASP:HB2	2.21	0.41
1:C:312:LYS:HZ2	1:C:339:ASP:HB2	1.85	0.41
1:F:160:GLY:HA2	1:F:185:LYS:O	2.20	0.41
1:H:290:GLU:H	1:H:294:LYS:HZ2	1.68	0.41
1:B:192:ASP:HB2	6:B:733:HOH:O	2.21	0.41
1:G:166:ARG:NH2	1:G:193:ASP:CB	2.84	0.41
1:H:353:ARG:NH1	1:H:381:GLU:OE1	2.53	0.41
1:B:322:GLY:HA3	1:B:355:LEU:HD11	2.02	0.41
1:C:282:ARG:NE	6:C:520:HOH:O	2.53	0.41
1:D:307:HIS:HA	1:D:337:ASN:ND2	2.36	0.41
1:D:359:MET:HB2	1:D:369:PRO:HG3	2.01	0.41
1:H:184:PHE:HE1	1:H:210:VAL:HG11	1.85	0.41
1:B:185:LYS:HA	1:B:213:ALA:O	2.20	0.41
1:B:297:THR:HA	5:B:404:GOL:H11	2.02	0.41
1:C:222:ALA:O	1:C:226:VAL:HG23	2.20	0.41
1:C:345:HIS:CE1	1:C:349:GLU:HG3	2.55	0.41
1:E:349:GLU:CB	1:E:350:PRO:CD	2.99	0.41
1:G:233:GLU:N	1:G:234:PRO:CD	2.84	0.41
1:H:362:LEU:C	1:H:362:LEU:HD23	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:94:ASP:HA	1:B:95:PRO:HD3	1.96	0.41
1:D:142:VAL:HG23	1:D:373:GLY:O	2.21	0.41
1:E:170:ALA:HB2	1:E:201:ILE:HD13	2.02	0.41
1:H:12:THR:HG23	1:H:79:MET:CE	2.51	0.41
1:H:321:ALA:HA	1:H:351:ASN:ND2	2.36	0.41
1:D:85:LEU:HD22	1:H:73:VAL:HG11	2.03	0.41
1:C:332:SER:HB3	1:C:338:VAL:HG11	2.02	0.40
1:D:362:LEU:H	1:D:362:LEU:HD23	1.86	0.40
1:D:353:ARG:HG3	1:D:354:LEU:HG	2.03	0.40
1:G:68:GLU:HB2	1:G:323:ILE:HB	2.04	0.40
1:H:215:ASP:O	1:H:217:HIS:HD2	2.05	0.40
1:H:9:GLU:OE2	1:H:388:LYS:NZ	2.47	0.40
1:A:187:ALA:C	1:A:189:PRO:HD2	2.42	0.40
1:E:181:PHE:CD2	1:E:364:GLY:HA2	2.57	0.40
1:E:362:LEU:HD23	1:E:362:LEU:C	2.38	0.40
1:B:183:SER:C	1:B:184:PHE:CD1	2.94	0.40
1:F:79:MET:SD	1:F:389:HIS:HB2	2.61	0.40
1:H:349:GLU:CB	1:H:350:PRO:CD	2.92	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	372/412 (90%)	363 (98%)	8 (2%)	1 (0%)	41	36
1	B	387/412 (94%)	378 (98%)	9 (2%)	0	100	100
1	C	375/412 (91%)	367 (98%)	8 (2%)	0	100	100
1	D	376/412 (91%)	366 (97%)	10 (3%)	0	100	100
1	E	378/412 (92%)	369 (98%)	8 (2%)	1 (0%)	41	36
1	F	374/412 (91%)	366 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	377/412 (92%)	367 (97%)	10 (3%)	0	100	100
1	H	374/412 (91%)	362 (97%)	12 (3%)	0	100	100
All	All	3013/3296 (91%)	2938 (98%)	73 (2%)	2 (0%)	51	48

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	33	GLY
1	E	28	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	290/323 (90%)	286 (99%)	4 (1%)	67	70
1	B	301/323 (93%)	292 (97%)	9 (3%)	41	40
1	C	293/323 (91%)	282 (96%)	11 (4%)	33	30
1	D	293/323 (91%)	292 (100%)	1 (0%)	92	94
1	E	294/323 (91%)	290 (99%)	4 (1%)	67	70
1	F	291/323 (90%)	287 (99%)	4 (1%)	67	70
1	G	293/323 (91%)	291 (99%)	2 (1%)	84	87
1	H	290/323 (90%)	280 (97%)	10 (3%)	37	35
All	All	2345/2584 (91%)	2300 (98%)	45 (2%)	57	59

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	ARG
1	A	345	HIS
1	A	347	ILE
1	A	362	LEU
1	B	11	PHE

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Mol	Chain	Res	Type
1	B	60	GLU
1	B	197	LYS
1	B	199	MET
1	B	260	SER
1	B	312	LYS
1	B	339	ASP
1	B	362	LEU
1	B	363	ASN
1	C	15	LEU
1	C	40	LYS
1	C	48	THR
1	C	165	THR
1	C	192	ASP
1	C	254	ARG
1	C	284	LEU
1	C	345	HIS
1	C	346	SER
1	C	353	ARG
1	C	362	LEU
1	D	15	LEU
1	E	39	ARG
1	E	42	ASN
1	E	192	ASP
1	E	362	LEU
1	F	15	LEU
1	F	37	LEU
1	F	48	THR
1	F	386	LEU
1	G	345	HIS
1	G	353	ARG
1	H	60	GLU
1	H	165	THR
1	H	172	LEU
1	H	192	ASP
1	H	193	ASP
1	H	245	ARG
1	H	260	SER
1	H	346	SER
1	H	362	LEU
1	H	386	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	363	ASN
1	B	363	ASN
1	C	235	HIS
1	C	351	ASN
1	D	345	HIS
1	E	42	ASN
1	E	345	HIS
1	F	345	HIS
1	F	351	ASN
1	G	345	HIS
1	H	217	HIS
1	H	351	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 25 ligands modelled in this entry, 17 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	FMT	C	404	2	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	F	402	2	0,2,2	0.00	-	0,1,1	0.00	-
5	GOL	B	404	-	5,5,5	0.18	0	5,5,5	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	FMT	A	402	2	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	E	402	2	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	H	402	2	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	G	403	2	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	B	403	2	0,2,2	0.00	-	0,1,1	0.00	-

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
5	GOL	B	404	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	404	GOL	O1-C1-C2-C3
5	B	404	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	404	GOL	5	0
3	B	403	FMT	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	376/412 (91%)	-0.13	12 (3%) 47 47	26, 44, 78, 119	0
1	B	388/412 (94%)	-0.43	2 (0%) 91 91	22, 34, 67, 100	0
1	C	378/412 (91%)	-0.14	13 (3%) 45 45	20, 38, 80, 131	0
1	D	379/412 (91%)	-0.22	7 (1%) 68 67	24, 40, 69, 114	0
1	E	381/412 (92%)	-0.30	5 (1%) 77 76	20, 34, 66, 113	0
1	F	374/412 (90%)	-0.20	8 (2%) 63 63	20, 34, 67, 103	0
1	G	380/412 (92%)	-0.43	4 (1%) 80 80	19, 31, 60, 111	0
1	H	378/412 (91%)	-0.07	20 (5%) 26 26	25, 39, 84, 128	0
All	All	3034/3296 (92%)	-0.24	71 (2%) 60 59	19, 37, 71, 131	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	27	PRO	5.1
1	F	16	PRO	4.8
1	F	15	LEU	4.6
1	G	27	PRO	4.3
1	G	192	ASP	4.1
1	D	350	PRO	4.1
1	E	27	PRO	3.9
1	A	15	LEU	3.8
1	A	347	ILE	3.7
1	D	28	GLY	3.6
1	H	202	LEU	3.4
1	C	17	ARG	3.4
1	H	201	ILE	3.4
1	C	28	GLY	3.2
1	H	33	GLY	3.2
1	H	167	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	H	15	LEU	3.1
1	F	167	ALA	3.1
1	F	49	PHE	3.0
1	D	353	ARG	3.0
1	H	193	ASP	3.0
1	A	30	GLU	3.0
1	H	170	ALA	2.9
1	F	33	GLY	2.9
1	G	193	ASP	2.9
1	B	18	GLU	2.9
1	G	190	VAL	2.9
1	H	349	GLU	2.9
1	B	19	THR	2.8
1	H	209	ALA	2.8
1	H	31	PRO	2.8
1	H	204	GLU	2.8
1	H	30	GLU	2.8
1	D	16	PRO	2.6
1	C	350	PRO	2.6
1	H	29	GLU	2.6
1	A	350	PRO	2.6
1	A	349	GLU	2.5
1	C	353	ARG	2.5
1	F	193	ASP	2.5
1	C	16	PRO	2.5
1	H	178	ALA	2.4
1	C	31	PRO	2.4
1	H	190	VAL	2.4
1	H	210	VAL	2.4
1	A	29	GLU	2.4
1	H	28	GLY	2.4
1	H	350	PRO	2.4
1	D	39[A]	ARG	2.4
1	H	166	ARG	2.3
1	A	40	LYS	2.3
1	C	192	ASP	2.3
1	E	2	SER	2.3
1	E	204	GLU	2.3
1	E	28	GLY	2.3
1	D	17	ARG	2.2
1	A	192	ASP	2.2
1	C	167	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	33	GLY	2.2
1	C	15	LEU	2.2
1	H	174	ALA	2.2
1	C	193	ASP	2.2
1	F	178	ALA	2.2
1	A	353	ARG	2.1
1	A	39	ARG	2.1
1	E	205	ARG	2.1
1	C	30	GLU	2.1
1	C	352	ARG	2.0
1	A	48	THR	2.0
1	F	192[A]	ASP	2.0
1	C	345	HIS	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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	GOL	B	404	6/6	0.86	0.33	20,20,20,20	0
3	FMT	A	402	3/3	0.91	0.10	59,59,62,63	0
2	MG	A	401	1/1	0.93	0.06	41,41,41,41	0
4	CL	C	403	1/1	0.96	0.08	58,58,58,58	0
3	FMT	B	403	3/3	0.96	0.07	36,36,39,39	0
3	FMT	H	402	3/3	0.96	0.06	34,34,48,65	0
3	FMT	E	402	3/3	0.97	0.07	27,27,37,37	0
4	CL	B	402[A]	1/1	0.98	0.20	27,27,27,27	1
3	FMT	C	404	3/3	0.98	0.06	37,37,44,48	0
2	MG	H	401	1/1	0.98	0.06	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	CL	B	402[B]	1/1	0.98	0.20	26,26,26,26	1
3	FMT	G	403	3/3	0.98	0.06	22,22,38,40	0
2	MG	D	401	1/1	0.99	0.07	29,29,29,29	0
2	MG	C	402	1/1	0.99	0.05	33,33,33,33	0
2	MG	G	402	1/1	0.99	0.07	23,23,23,23	0
3	FMT	F	402	3/3	0.99	0.09	31,31,39,43	0
4	CL	C	401[A]	1/1	0.99	0.20	30,30,30,30	1
4	CL	C	401[B]	1/1	0.99	0.20	29,29,29,29	1
4	CL	G	401[A]	1/1	0.99	0.14	23,23,23,23	1
4	CL	D	402[A]	1/1	0.99	0.13	27,27,27,27	1
4	CL	G	401[B]	1/1	0.99	0.14	23,23,23,23	1
4	CL	D	402[B]	1/1	0.99	0.13	28,28,28,28	1
2	MG	B	401	1/1	0.99	0.04	24,24,24,24	0
2	MG	F	401	1/1	0.99	0.09	32,32,32,32	0
2	MG	E	401	1/1	1.00	0.08	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.