Full wwPDB X-ray Structure Validation Report (i)

Feb 17, 2024 – 08:45 PM EST

PDB ID	:	3U37
Title	:	An Acetyl Xylan Esterase (Est2A) from the Rumen Bacterium Butyrivibrio proteoclasticus.
Authors	:	Till, M.; Arcus, V.
Deposited on	:	2011-10-05
Resolution	:	2.10 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

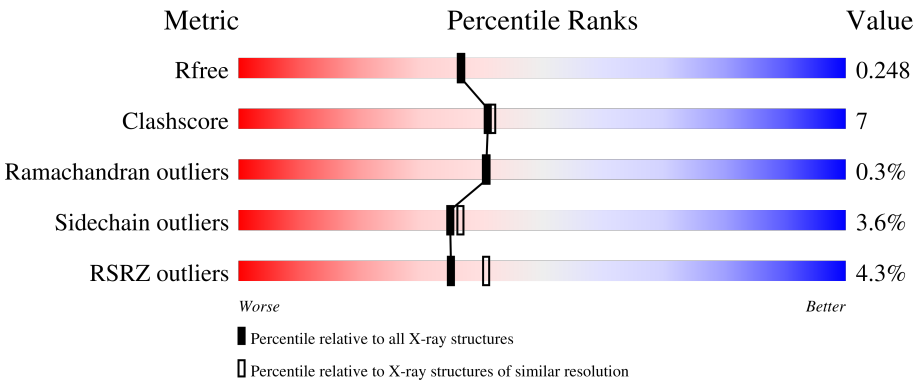
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	408	2%, 78%, 12%, • 9%
1	B	408	3%, 79%, 12%, • 8%
1	C	408	5%, 77%, 13%, • 8%
1	D	408	4%, 78%, 12%, • 8%
1	E	408	3%, 77%, 12%, • 9%

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Mol	Chain	Length	Quality of chain
1	F	408	3% 77% 13% • 9%
1	G	408	5% 76% 14% • 8%
1	H	408	5% 74% 17% • 8%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ACY	B	401	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 24861 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 Acetyl-xylan esterase Est2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	373	2957	1874	501	566	16	0	0	0
1	B	374	2966	1878	502	571	15	0	0	0
1	C	374	2958	1872	500	571	15	0	0	0
1	D	374	2965	1878	502	569	16	0	0	0
1	E	373	2952	1869	500	567	16	0	0	0
1	F	373	2950	1870	500	564	16	0	0	0
1	G	374	2962	1876	502	569	15	0	0	0
1	H	375	2965	1880	502	567	16	0	0	0

There are 256 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-31	MET	-	expression tag	UNP E0RVY7
A	-30	SER	-	expression tag	UNP E0RVY7
A	-29	TYR	-	expression tag	UNP E0RVY7
A	-28	TYR	-	expression tag	UNP E0RVY7
A	-27	HIS	-	expression tag	UNP E0RVY7
A	-26	HIS	-	expression tag	UNP E0RVY7
A	-25	HIS	-	expression tag	UNP E0RVY7
A	-24	HIS	-	expression tag	UNP E0RVY7
A	-23	HIS	-	expression tag	UNP E0RVY7
A	-22	HIS	-	expression tag	UNP E0RVY7
A	-21	LEU	-	expression tag	UNP E0RVY7
A	-20	GLU	-	expression tag	UNP E0RVY7
A	-19	SER	-	expression tag	UNP E0RVY7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	THR	-	expression tag	UNP E0RVY7
A	-17	SER	-	expression tag	UNP E0RVY7
A	-16	LEU	-	expression tag	UNP E0RVY7
A	-15	TYR	-	expression tag	UNP E0RVY7
A	-14	LYS	-	expression tag	UNP E0RVY7
A	-13	LYS	-	expression tag	UNP E0RVY7
A	-12	ALA	-	expression tag	UNP E0RVY7
A	-11	GLY	-	expression tag	UNP E0RVY7
A	-10	PHE	-	expression tag	UNP E0RVY7
A	-9	GLU	-	expression tag	UNP E0RVY7
A	-8	ASN	-	expression tag	UNP E0RVY7
A	-7	LEU	-	expression tag	UNP E0RVY7
A	-6	TYR	-	expression tag	UNP E0RVY7
A	-5	PHE	-	expression tag	UNP E0RVY7
A	-4	GLN	-	expression tag	UNP E0RVY7
A	-3	GLY	-	expression tag	UNP E0RVY7
A	-2	SER	-	expression tag	UNP E0RVY7
A	-1	GLY	-	expression tag	UNP E0RVY7
A	0	ALA	-	expression tag	UNP E0RVY7
B	-31	MET	-	expression tag	UNP E0RVY7
B	-30	SER	-	expression tag	UNP E0RVY7
B	-29	TYR	-	expression tag	UNP E0RVY7
B	-28	TYR	-	expression tag	UNP E0RVY7
B	-27	HIS	-	expression tag	UNP E0RVY7
B	-26	HIS	-	expression tag	UNP E0RVY7
B	-25	HIS	-	expression tag	UNP E0RVY7
B	-24	HIS	-	expression tag	UNP E0RVY7
B	-23	HIS	-	expression tag	UNP E0RVY7
B	-22	HIS	-	expression tag	UNP E0RVY7
B	-21	LEU	-	expression tag	UNP E0RVY7
B	-20	GLU	-	expression tag	UNP E0RVY7
B	-19	SER	-	expression tag	UNP E0RVY7
B	-18	THR	-	expression tag	UNP E0RVY7
B	-17	SER	-	expression tag	UNP E0RVY7
B	-16	LEU	-	expression tag	UNP E0RVY7
B	-15	TYR	-	expression tag	UNP E0RVY7
B	-14	LYS	-	expression tag	UNP E0RVY7
B	-13	LYS	-	expression tag	UNP E0RVY7
B	-12	ALA	-	expression tag	UNP E0RVY7
B	-11	GLY	-	expression tag	UNP E0RVY7
B	-10	PHE	-	expression tag	UNP E0RVY7
B	-9	GLU	-	expression tag	UNP E0RVY7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	ASN	-	expression tag	UNP E0RVY7
B	-7	LEU	-	expression tag	UNP E0RVY7
B	-6	TYR	-	expression tag	UNP E0RVY7
B	-5	PHE	-	expression tag	UNP E0RVY7
B	-4	GLN	-	expression tag	UNP E0RVY7
B	-3	GLY	-	expression tag	UNP E0RVY7
B	-2	SER	-	expression tag	UNP E0RVY7
B	-1	GLY	-	expression tag	UNP E0RVY7
B	0	ALA	-	expression tag	UNP E0RVY7
C	-31	MET	-	expression tag	UNP E0RVY7
C	-30	SER	-	expression tag	UNP E0RVY7
C	-29	TYR	-	expression tag	UNP E0RVY7
C	-28	TYR	-	expression tag	UNP E0RVY7
C	-27	HIS	-	expression tag	UNP E0RVY7
C	-26	HIS	-	expression tag	UNP E0RVY7
C	-25	HIS	-	expression tag	UNP E0RVY7
C	-24	HIS	-	expression tag	UNP E0RVY7
C	-23	HIS	-	expression tag	UNP E0RVY7
C	-22	HIS	-	expression tag	UNP E0RVY7
C	-21	LEU	-	expression tag	UNP E0RVY7
C	-20	GLU	-	expression tag	UNP E0RVY7
C	-19	SER	-	expression tag	UNP E0RVY7
C	-18	THR	-	expression tag	UNP E0RVY7
C	-17	SER	-	expression tag	UNP E0RVY7
C	-16	LEU	-	expression tag	UNP E0RVY7
C	-15	TYR	-	expression tag	UNP E0RVY7
C	-14	LYS	-	expression tag	UNP E0RVY7
C	-13	LYS	-	expression tag	UNP E0RVY7
C	-12	ALA	-	expression tag	UNP E0RVY7
C	-11	GLY	-	expression tag	UNP E0RVY7
C	-10	PHE	-	expression tag	UNP E0RVY7
C	-9	GLU	-	expression tag	UNP E0RVY7
C	-8	ASN	-	expression tag	UNP E0RVY7
C	-7	LEU	-	expression tag	UNP E0RVY7
C	-6	TYR	-	expression tag	UNP E0RVY7
C	-5	PHE	-	expression tag	UNP E0RVY7
C	-4	GLN	-	expression tag	UNP E0RVY7
C	-3	GLY	-	expression tag	UNP E0RVY7
C	-2	SER	-	expression tag	UNP E0RVY7
C	-1	GLY	-	expression tag	UNP E0RVY7
C	0	ALA	-	expression tag	UNP E0RVY7
D	-31	MET	-	expression tag	UNP E0RVY7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-30	SER	-	expression tag	UNP E0RVY7
D	-29	TYR	-	expression tag	UNP E0RVY7
D	-28	TYR	-	expression tag	UNP E0RVY7
D	-27	HIS	-	expression tag	UNP E0RVY7
D	-26	HIS	-	expression tag	UNP E0RVY7
D	-25	HIS	-	expression tag	UNP E0RVY7
D	-24	HIS	-	expression tag	UNP E0RVY7
D	-23	HIS	-	expression tag	UNP E0RVY7
D	-22	HIS	-	expression tag	UNP E0RVY7
D	-21	LEU	-	expression tag	UNP E0RVY7
D	-20	GLU	-	expression tag	UNP E0RVY7
D	-19	SER	-	expression tag	UNP E0RVY7
D	-18	THR	-	expression tag	UNP E0RVY7
D	-17	SER	-	expression tag	UNP E0RVY7
D	-16	LEU	-	expression tag	UNP E0RVY7
D	-15	TYR	-	expression tag	UNP E0RVY7
D	-14	LYS	-	expression tag	UNP E0RVY7
D	-13	LYS	-	expression tag	UNP E0RVY7
D	-12	ALA	-	expression tag	UNP E0RVY7
D	-11	GLY	-	expression tag	UNP E0RVY7
D	-10	PHE	-	expression tag	UNP E0RVY7
D	-9	GLU	-	expression tag	UNP E0RVY7
D	-8	ASN	-	expression tag	UNP E0RVY7
D	-7	LEU	-	expression tag	UNP E0RVY7
D	-6	TYR	-	expression tag	UNP E0RVY7
D	-5	PHE	-	expression tag	UNP E0RVY7
D	-4	GLN	-	expression tag	UNP E0RVY7
D	-3	GLY	-	expression tag	UNP E0RVY7
D	-2	SER	-	expression tag	UNP E0RVY7
D	-1	GLY	-	expression tag	UNP E0RVY7
D	0	ALA	-	expression tag	UNP E0RVY7
E	-31	MET	-	expression tag	UNP E0RVY7
E	-30	SER	-	expression tag	UNP E0RVY7
E	-29	TYR	-	expression tag	UNP E0RVY7
E	-28	TYR	-	expression tag	UNP E0RVY7
E	-27	HIS	-	expression tag	UNP E0RVY7
E	-26	HIS	-	expression tag	UNP E0RVY7
E	-25	HIS	-	expression tag	UNP E0RVY7
E	-24	HIS	-	expression tag	UNP E0RVY7
E	-23	HIS	-	expression tag	UNP E0RVY7
E	-22	HIS	-	expression tag	UNP E0RVY7
E	-21	LEU	-	expression tag	UNP E0RVY7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-20	GLU	-	expression tag	UNP E0RVY7
E	-19	SER	-	expression tag	UNP E0RVY7
E	-18	THR	-	expression tag	UNP E0RVY7
E	-17	SER	-	expression tag	UNP E0RVY7
E	-16	LEU	-	expression tag	UNP E0RVY7
E	-15	TYR	-	expression tag	UNP E0RVY7
E	-14	LYS	-	expression tag	UNP E0RVY7
E	-13	LYS	-	expression tag	UNP E0RVY7
E	-12	ALA	-	expression tag	UNP E0RVY7
E	-11	GLY	-	expression tag	UNP E0RVY7
E	-10	PHE	-	expression tag	UNP E0RVY7
E	-9	GLU	-	expression tag	UNP E0RVY7
E	-8	ASN	-	expression tag	UNP E0RVY7
E	-7	LEU	-	expression tag	UNP E0RVY7
E	-6	TYR	-	expression tag	UNP E0RVY7
E	-5	PHE	-	expression tag	UNP E0RVY7
E	-4	GLN	-	expression tag	UNP E0RVY7
E	-3	GLY	-	expression tag	UNP E0RVY7
E	-2	SER	-	expression tag	UNP E0RVY7
E	-1	GLY	-	expression tag	UNP E0RVY7
E	0	ALA	-	expression tag	UNP E0RVY7
F	-31	MET	-	expression tag	UNP E0RVY7
F	-30	SER	-	expression tag	UNP E0RVY7
F	-29	TYR	-	expression tag	UNP E0RVY7
F	-28	TYR	-	expression tag	UNP E0RVY7
F	-27	HIS	-	expression tag	UNP E0RVY7
F	-26	HIS	-	expression tag	UNP E0RVY7
F	-25	HIS	-	expression tag	UNP E0RVY7
F	-24	HIS	-	expression tag	UNP E0RVY7
F	-23	HIS	-	expression tag	UNP E0RVY7
F	-22	HIS	-	expression tag	UNP E0RVY7
F	-21	LEU	-	expression tag	UNP E0RVY7
F	-20	GLU	-	expression tag	UNP E0RVY7
F	-19	SER	-	expression tag	UNP E0RVY7
F	-18	THR	-	expression tag	UNP E0RVY7
F	-17	SER	-	expression tag	UNP E0RVY7
F	-16	LEU	-	expression tag	UNP E0RVY7
F	-15	TYR	-	expression tag	UNP E0RVY7
F	-14	LYS	-	expression tag	UNP E0RVY7
F	-13	LYS	-	expression tag	UNP E0RVY7
F	-12	ALA	-	expression tag	UNP E0RVY7
F	-11	GLY	-	expression tag	UNP E0RVY7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-10	PHE	-	expression tag	UNP E0RVY7
F	-9	GLU	-	expression tag	UNP E0RVY7
F	-8	ASN	-	expression tag	UNP E0RVY7
F	-7	LEU	-	expression tag	UNP E0RVY7
F	-6	TYR	-	expression tag	UNP E0RVY7
F	-5	PHE	-	expression tag	UNP E0RVY7
F	-4	GLN	-	expression tag	UNP E0RVY7
F	-3	GLY	-	expression tag	UNP E0RVY7
F	-2	SER	-	expression tag	UNP E0RVY7
F	-1	GLY	-	expression tag	UNP E0RVY7
F	0	ALA	-	expression tag	UNP E0RVY7
G	-31	MET	-	expression tag	UNP E0RVY7
G	-30	SER	-	expression tag	UNP E0RVY7
G	-29	TYR	-	expression tag	UNP E0RVY7
G	-28	TYR	-	expression tag	UNP E0RVY7
G	-27	HIS	-	expression tag	UNP E0RVY7
G	-26	HIS	-	expression tag	UNP E0RVY7
G	-25	HIS	-	expression tag	UNP E0RVY7
G	-24	HIS	-	expression tag	UNP E0RVY7
G	-23	HIS	-	expression tag	UNP E0RVY7
G	-22	HIS	-	expression tag	UNP E0RVY7
G	-21	LEU	-	expression tag	UNP E0RVY7
G	-20	GLU	-	expression tag	UNP E0RVY7
G	-19	SER	-	expression tag	UNP E0RVY7
G	-18	THR	-	expression tag	UNP E0RVY7
G	-17	SER	-	expression tag	UNP E0RVY7
G	-16	LEU	-	expression tag	UNP E0RVY7
G	-15	TYR	-	expression tag	UNP E0RVY7
G	-14	LYS	-	expression tag	UNP E0RVY7
G	-13	LYS	-	expression tag	UNP E0RVY7
G	-12	ALA	-	expression tag	UNP E0RVY7
G	-11	GLY	-	expression tag	UNP E0RVY7
G	-10	PHE	-	expression tag	UNP E0RVY7
G	-9	GLU	-	expression tag	UNP E0RVY7
G	-8	ASN	-	expression tag	UNP E0RVY7
G	-7	LEU	-	expression tag	UNP E0RVY7
G	-6	TYR	-	expression tag	UNP E0RVY7
G	-5	PHE	-	expression tag	UNP E0RVY7
G	-4	GLN	-	expression tag	UNP E0RVY7
G	-3	GLY	-	expression tag	UNP E0RVY7
G	-2	SER	-	expression tag	UNP E0RVY7
G	-1	GLY	-	expression tag	UNP E0RVY7

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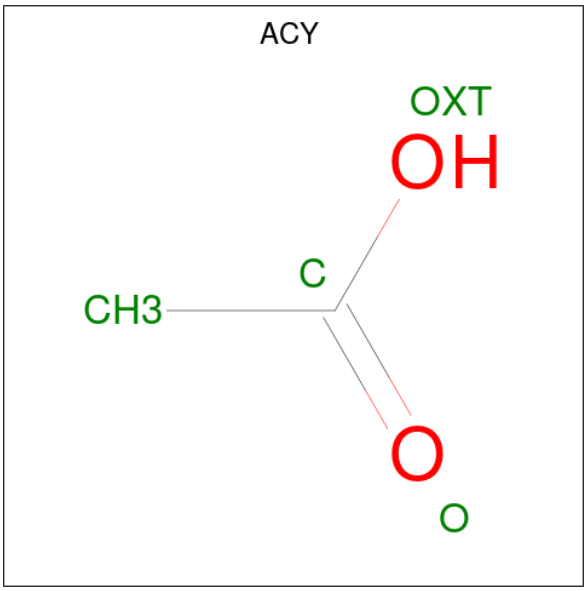
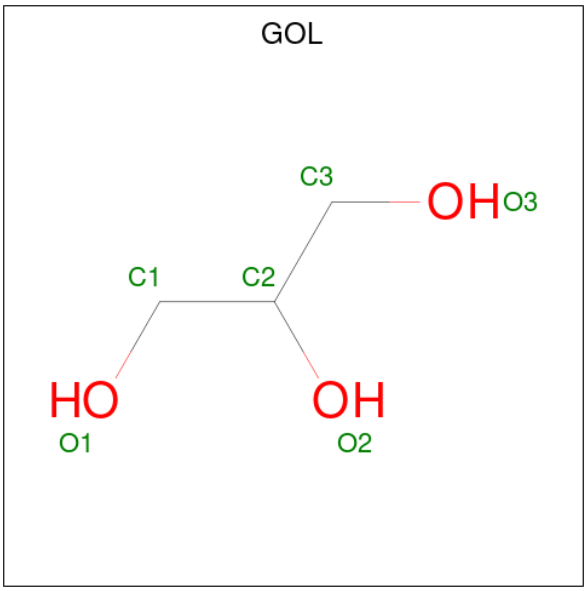
Chain	Residue	Modelled	Actual	Comment	Reference
G	0	ALA	-	expression tag	UNP E0RVY7
H	-31	MET	-	expression tag	UNP E0RVY7
H	-30	SER	-	expression tag	UNP E0RVY7
H	-29	TYR	-	expression tag	UNP E0RVY7
H	-28	TYR	-	expression tag	UNP E0RVY7
H	-27	HIS	-	expression tag	UNP E0RVY7
H	-26	HIS	-	expression tag	UNP E0RVY7
H	-25	HIS	-	expression tag	UNP E0RVY7
H	-24	HIS	-	expression tag	UNP E0RVY7
H	-23	HIS	-	expression tag	UNP E0RVY7
H	-22	HIS	-	expression tag	UNP E0RVY7
H	-21	LEU	-	expression tag	UNP E0RVY7
H	-20	GLU	-	expression tag	UNP E0RVY7
H	-19	SER	-	expression tag	UNP E0RVY7
H	-18	THR	-	expression tag	UNP E0RVY7
H	-17	SER	-	expression tag	UNP E0RVY7
H	-16	LEU	-	expression tag	UNP E0RVY7
H	-15	TYR	-	expression tag	UNP E0RVY7
H	-14	LYS	-	expression tag	UNP E0RVY7
H	-13	LYS	-	expression tag	UNP E0RVY7
H	-12	ALA	-	expression tag	UNP E0RVY7
H	-11	GLY	-	expression tag	UNP E0RVY7
H	-10	PHE	-	expression tag	UNP E0RVY7
H	-9	GLU	-	expression tag	UNP E0RVY7
H	-8	ASN	-	expression tag	UNP E0RVY7
H	-7	LEU	-	expression tag	UNP E0RVY7
H	-6	TYR	-	expression tag	UNP E0RVY7
H	-5	PHE	-	expression tag	UNP E0RVY7
H	-4	GLN	-	expression tag	UNP E0RVY7
H	-3	GLY	-	expression tag	UNP E0RVY7
H	-2	SER	-	expression tag	UNP E0RVY7
H	-1	GLY	-	expression tag	UNP E0RVY7
H	0	ALA	-	expression tag	UNP E0RVY7

- Molecule 2 is ACETIC ACID (three-letter code: ACY) (formula: $C_2H_4O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	4	2	2	0	0
2	B	1	4	2	2	0	0
2	C	1	4	2	2	0	0
2	D	1	4	2	2	0	0
2	E	1	4	2	2	0	0
2	F	1	4	2	2	0	0
2	F	1	4	2	2	0	0
2	G	1	4	2	2	0	0
2	H	1	4	2	2	0	0
2	H	1	4	2	2	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is water.

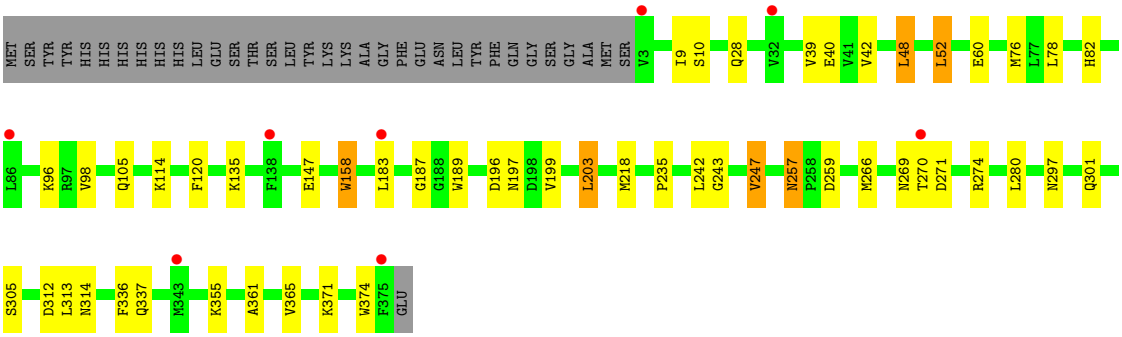
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	159	159	159	0	0
			Total	O		
4	B	154	154	154	0	0
			Total	O		
4	C	132	132	132	0	0
			Total	O		
4	D	138	138	138	0	0
			Total	O		
4	E	161	161	161	0	0
			Total	O		
4	F	154	154	154	0	0
			Total	O		
4	G	121	121	121	0	0
			Total	O		
4	H	121	121	121	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

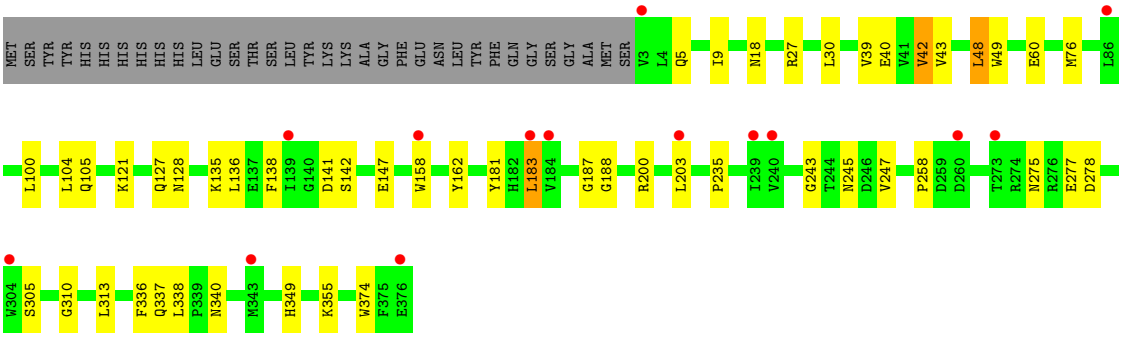
• Molecule 1: Acetyl-xylan esterase Est2A

Chain A:



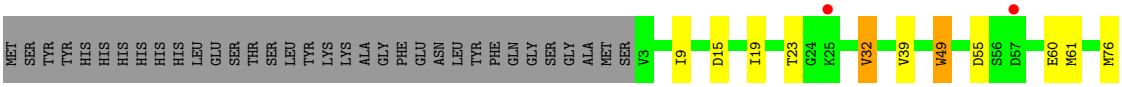
• Molecule 1: Acetyl-xylan esterase Est2A

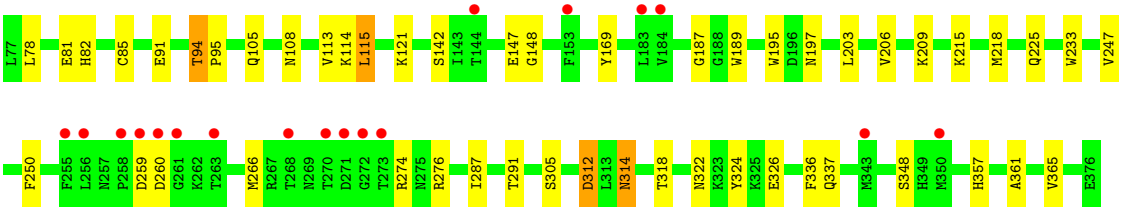
Chain B:



• Molecule 1: Acetyl-xylan esterase Est2A

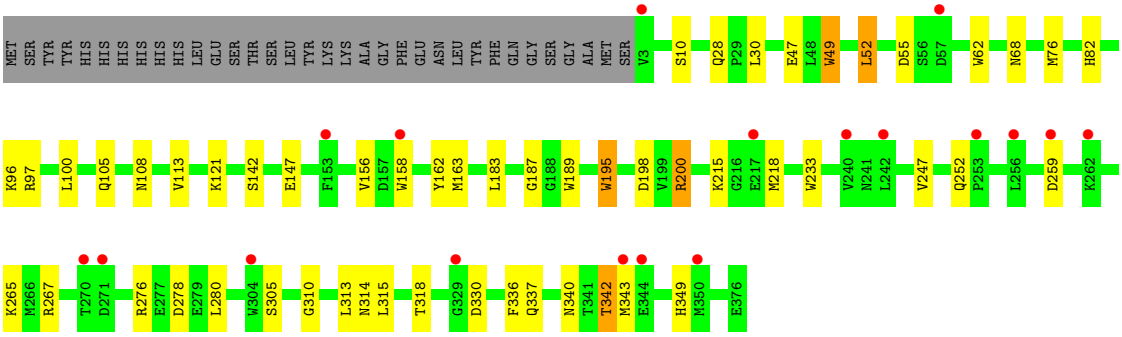
Chain C:





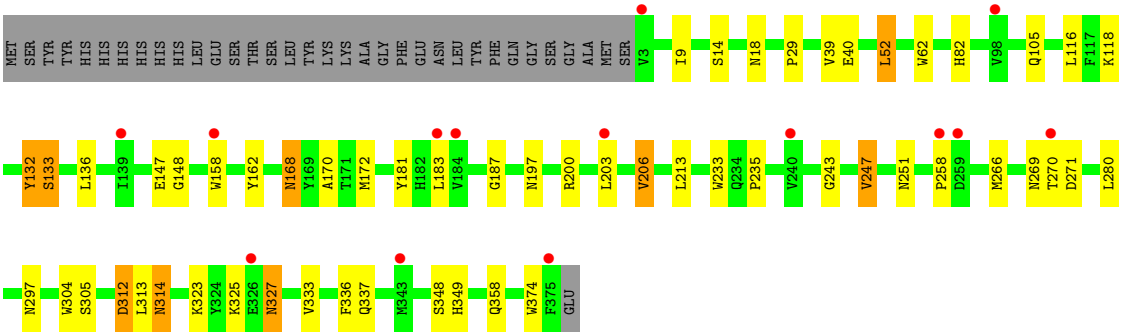
- Molecule 1: Acetyl-xylan esterase Est2A

Chain D:



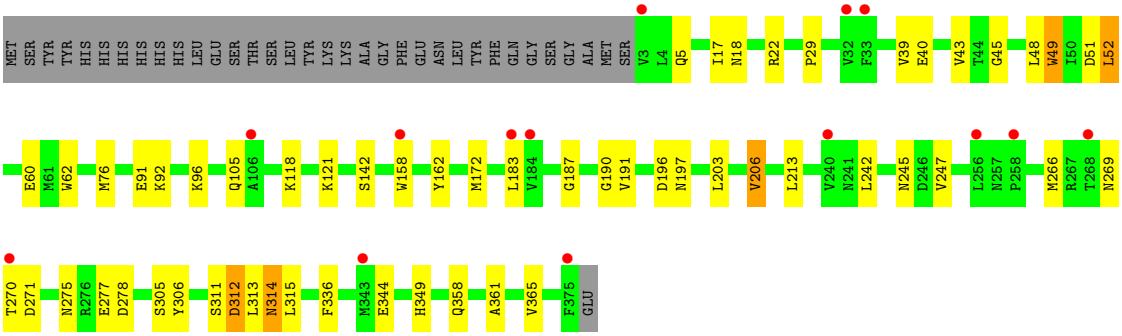
- Molecule 1: Acetyl-xylan esterase Est2A

Chain E:



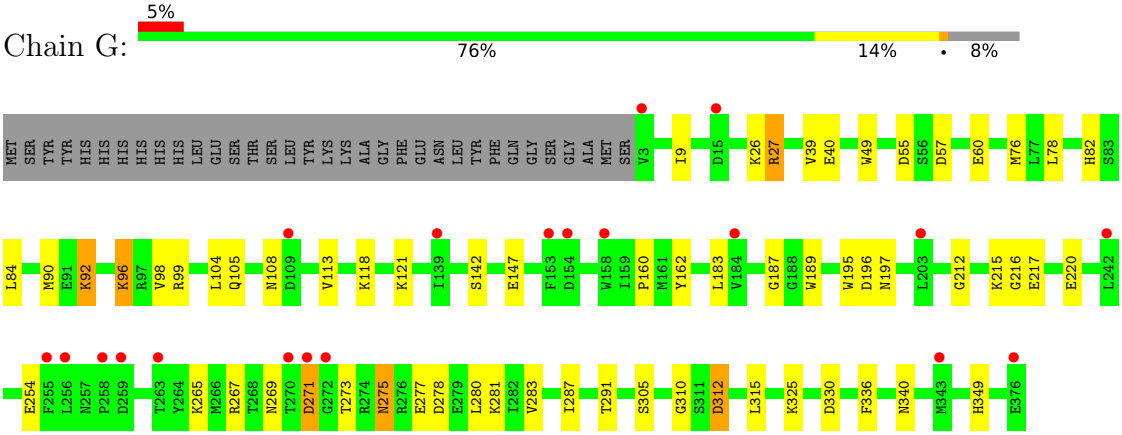
- Molecule 1: Acetyl-xylan esterase Est2A

Chain F:



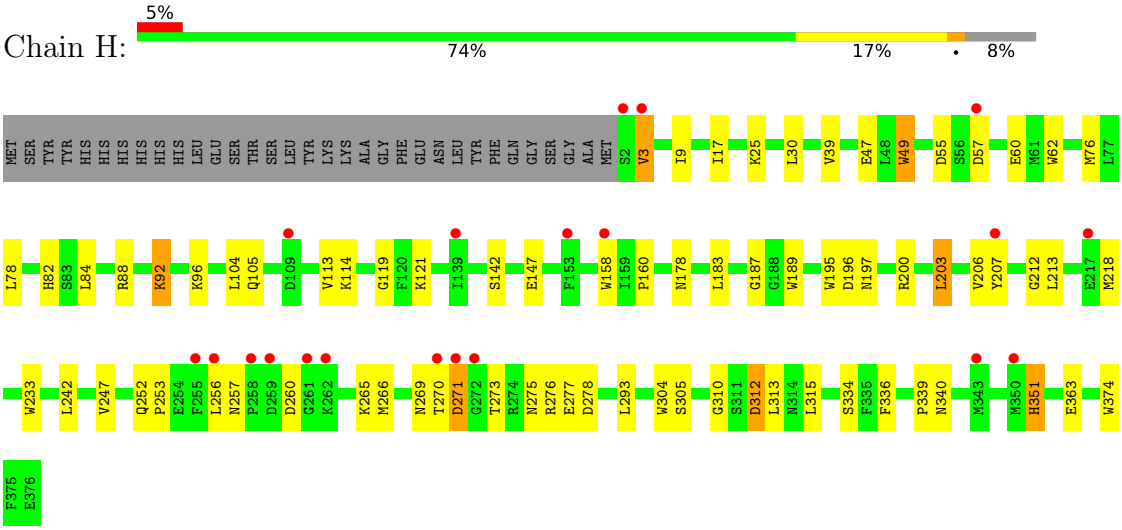
• Molecule 1: Acetyl-xylan esterase Est2A

Chain G:



• Molecule 1: Acetyl-xylan esterase Est2A

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	96.13Å 90.28Å 99.17Å 99.80° 90.21° 92.56°	Depositor
Resolution (Å)	24.86 – 2.10 24.86 – 2.10	Depositor EDS
% Data completeness (in resolution range)	89.3 (24.86-2.10) 89.4 (24.86-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.43 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.206 , 0.242 0.211 , 0.248	Depositor DCC
R_{free} test set	8623 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	26.7	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 40.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.074 for h,-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	24861	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.80% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ACY

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	0.54	3/3026 (0.1%)	0.60	0/4096
1	B	0.53	2/3035 (0.1%)	0.62	0/4108
1	C	0.53	4/3027 (0.1%)	0.57	0/4100
1	D	0.53	5/3034 (0.2%)	0.60	0/4106
1	E	0.53	5/3021 (0.2%)	0.59	0/4091
1	F	0.54	3/3019 (0.1%)	0.58	0/4087
1	G	0.54	2/3031 (0.1%)	0.57	0/4103
1	H	0.53	8/3034 (0.3%)	0.59	0/4106
All	All	0.53	32/24227 (0.1%)	0.59	0/32797

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	62	TRP	CD2-CE2	5.59	1.48	1.41
1	E	158	TRP	CD2-CE2	5.51	1.48	1.41
1	F	158	TRP	CD2-CE2	5.49	1.48	1.41
1	C	189	TRP	CD2-CE2	5.47	1.48	1.41
1	B	158	TRP	CD2-CE2	5.39	1.47	1.41
1	H	195	TRP	CD2-CE2	5.39	1.47	1.41
1	H	49	TRP	CD2-CE2	5.32	1.47	1.41
1	G	195	TRP	CD2-CE2	5.32	1.47	1.41
1	C	195	TRP	CD2-CE2	5.29	1.47	1.41
1	A	158	TRP	CD2-CE2	5.26	1.47	1.41
1	H	158	TRP	CD2-CE2	5.25	1.47	1.41
1	C	233	TRP	CD2-CE2	5.25	1.47	1.41
1	D	195	TRP	CD2-CE2	5.24	1.47	1.41
1	H	374	TRP	CD2-CE2	5.24	1.47	1.41
1	H	233	TRP	CD2-CE2	5.23	1.47	1.41
1	H	189	TRP	CD2-CE2	5.16	1.47	1.41
1	H	62	TRP	CD2-CE2	5.16	1.47	1.41
1	A	374	TRP	CD2-CE2	5.13	1.47	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	49	TRP	CD2-CE2	5.12	1.47	1.41
1	D	158	TRP	CD2-CE2	5.12	1.47	1.41
1	G	189	TRP	CD2-CE2	5.11	1.47	1.41
1	D	189	TRP	CD2-CE2	5.11	1.47	1.41
1	F	49	TRP	CD2-CE2	5.10	1.47	1.41
1	D	233	TRP	CD2-CE2	5.09	1.47	1.41
1	B	374	TRP	CD2-CE2	5.07	1.47	1.41
1	E	233	TRP	CD2-CE2	5.05	1.47	1.41
1	H	304	TRP	CD2-CE2	5.05	1.47	1.41
1	E	304	TRP	CD2-CE2	5.04	1.47	1.41
1	F	62	TRP	CD2-CE2	5.04	1.47	1.41
1	E	374	TRP	CD2-CE2	5.03	1.47	1.41
1	A	189	TRP	CD2-CE2	5.03	1.47	1.41
1	C	49	TRP	CD2-CE2	5.01	1.47	1.41

There are no bond angle outliers.

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	2957	0	2855	41	0
1	B	2966	0	2859	40	0
1	C	2958	0	2837	38	0
1	D	2965	0	2862	34	0
1	E	2952	0	2840	44	0
1	F	2950	0	2845	46	0
1	G	2962	0	2855	42	0
1	H	2965	0	2860	55	0
2	A	4	0	3	0	0
2	B	4	0	3	12	0
2	C	4	0	3	0	0
2	D	4	0	3	0	0
2	E	4	0	3	0	0
2	F	8	0	6	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	4	0	3	0	0
2	H	8	0	6	1	0
3	B	6	0	8	0	0
4	A	159	0	0	2	0
4	B	154	0	0	4	0
4	C	132	0	0	2	0
4	D	138	0	0	1	0
4	E	161	0	0	3	0
4	F	154	0	0	5	0
4	G	121	0	0	3	0
4	H	121	0	0	3	0
All	All	24861	0	22851	329	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 7.

All (329) 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:F:52:LEU:HD23	1:F:52:LEU:O	1.41	1.19
1:G:27:ARG:HG2	1:G:27:ARG:HH11	1.01	1.08
1:F:52:LEU:HD23	1:F:52:LEU:C	1.75	1.05
1:B:245:ASN:HD21	2:B:401:ACY:H3	1.26	1.00
1:E:52:LEU:HD22	1:E:52:LEU:O	1.65	0.97
1:H:207:TYR:CE2	1:H:293:LEU:HD23	2.02	0.94
1:E:52:LEU:C	1:E:52:LEU:CD2	2.37	0.93
1:G:27:ARG:HG2	1:G:27:ARG:NH1	1.78	0.92
1:H:206:VAL:HG22	1:H:206:VAL:O	1.71	0.90
1:B:245:ASN:HD21	2:B:401:ACY:CH3	1.86	0.89
1:A:9:ILE:HD11	1:A:39:VAL:HG11	1.53	0.88
1:D:314:ASN:HD21	1:D:337:GLN:HE21	1.21	0.86
1:A:76:MET:CE	1:C:85:CYS:HB3	2.07	0.84
1:D:105:GLN:HE22	1:D:187:GLY:H	1.25	0.83
1:B:105:GLN:HE22	1:B:187:GLY:H	1.25	0.81
1:E:105:GLN:HE22	1:E:187:GLY:H	1.28	0.81
1:E:325:LYS:HD3	1:E:333:VAL:HB	1.63	0.81
1:F:60:GLU:HG3	1:F:76:MET:HG3	1.62	0.81
1:F:105:GLN:HE22	1:F:187:GLY:H	1.25	0.81
1:H:206:VAL:O	1:H:206:VAL:CG2	2.29	0.80
1:E:325:LYS:HE3	4:E:587:HOH:O	1.80	0.80
1:D:314:ASN:HD21	1:D:337:GLN:NE2	1.79	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:132:TYR:O	1:E:133:SER:CB	2.30	0.79
1:H:207:TYR:CD2	1:H:207:TYR:O	2.35	0.79
1:B:60:GLU:HG3	1:B:76:MET:HG3	1.63	0.78
1:A:76:MET:HE3	1:C:85:CYS:HB3	1.63	0.78
1:E:52:LEU:O	1:E:52:LEU:CD2	2.30	0.78
1:H:206:VAL:HG21	1:H:213:LEU:HG	1.66	0.76
1:A:105:GLN:HE22	1:A:187:GLY:H	1.33	0.76
1:E:9:ILE:HD11	1:E:39:VAL:HG11	1.66	0.75
1:E:52:LEU:C	1:E:52:LEU:HD23	2.06	0.75
1:H:206:VAL:HG23	1:H:212:GLY:HA3	1.65	0.75
1:C:105:GLN:HE22	1:C:187:GLY:H	1.31	0.75
1:A:60:GLU:HG3	1:A:76:MET:HG3	1.69	0.74
1:H:105:GLN:HE22	1:H:187:GLY:H	1.35	0.74
1:H:269:ASN:HD22	1:H:273:THR:HG23	1.52	0.74
1:D:315:LEU:HA	1:D:318:THR:HG22	1.70	0.73
1:G:105:GLN:HE22	1:G:187:GLY:H	1.33	0.73
1:H:9:ILE:HD11	1:H:30:LEU:CB	2.19	0.73
1:E:52:LEU:HD22	1:E:52:LEU:C	2.05	0.73
1:D:52:LEU:HD23	1:D:82:HIS:HB2	1.70	0.72
1:F:206:VAL:HG11	1:F:213:LEU:HG	1.72	0.72
1:A:48:LEU:HD21	1:A:120:PHE:CD2	2.25	0.71
1:F:52:LEU:C	1:F:52:LEU:CD2	2.52	0.71
1:B:188:GLY:H	2:B:401:ACY:H3	1.56	0.70
1:C:60:GLU:HG3	1:C:76:MET:HG3	1.74	0.70
1:E:206:VAL:HG11	1:E:213:LEU:HG	1.71	0.69
1:F:17:ILE:HD11	1:F:39:VAL:CG2	2.22	0.69
1:D:52:LEU:CD2	1:D:82:HIS:HB2	2.23	0.69
1:F:17:ILE:HD11	1:F:39:VAL:HG21	1.75	0.68
1:H:207:TYR:O	1:H:207:TYR:CG	2.44	0.68
1:B:141:ASP:HB2	2:B:401:ACY:H1	1.76	0.68
1:B:9:ILE:HD11	1:B:39:VAL:HG11	1.76	0.68
1:H:60:GLU:HG3	1:H:76:MET:HG3	1.74	0.67
1:E:147:GLU:HG3	4:E:629:HOH:O	1.95	0.67
1:E:269:ASN:C	1:E:271:ASP:H	1.96	0.67
1:H:17:ILE:HD11	1:H:39:VAL:HG21	1.77	0.66
1:D:10:SER:OG	1:D:28:GLN:HB2	1.95	0.66
1:D:198:ASP:OD1	1:D:200:ARG:HG2	1.96	0.66
1:F:312:ASP:HB2	4:F:525:HOH:O	1.94	0.66
1:A:269:ASN:C	1:A:271:ASP:H	1.98	0.65
1:H:207:TYR:CE2	1:H:293:LEU:CD2	2.78	0.65
1:A:52:LEU:CD2	1:A:82:HIS:HB2	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:197:ASN:ND2	1:E:266:MET:H	1.93	0.65
1:H:9:ILE:HD11	1:H:30:LEU:HB2	1.78	0.65
1:E:168:ASN:HD22	1:E:170:ALA:H	1.45	0.65
1:G:27:ARG:HH11	1:G:27:ARG:CG	1.94	0.65
1:A:147:GLU:OE2	1:A:158:TRP:HZ3	1.80	0.64
1:C:9:ILE:HD11	1:C:39:VAL:HG11	1.79	0.64
1:G:9:ILE:HD11	1:G:39:VAL:HG11	1.78	0.64
1:B:245:ASN:ND2	2:B:401:ACY:H3	2.08	0.63
1:G:108:ASN:HD21	1:G:215:LYS:NZ	1.96	0.63
1:B:42:VAL:HG22	1:B:127:GLN:HB2	1.80	0.63
1:E:312:ASP:HB2	4:E:530:HOH:O	1.98	0.63
1:H:275:ASN:HD22	1:H:278:ASP:H	1.45	0.63
1:A:76:MET:HE1	1:C:85:CYS:HB3	1.81	0.62
1:G:312:ASP:HB2	4:G:546:HOH:O	1.97	0.62
1:F:52:LEU:O	1:F:52:LEU:CD2	2.33	0.62
1:B:275:ASN:HD22	1:B:278:ASP:H	1.46	0.61
1:G:92:LYS:HE3	1:G:92:LYS:H	1.64	0.61
1:C:318:THR:HB	1:D:318:THR:HG21	1.80	0.61
1:G:275:ASN:HD21	1:G:277:GLU:HB3	1.65	0.61
1:B:60:GLU:CG	1:B:76:MET:HG3	2.29	0.61
1:C:314:ASN:OD1	1:C:337:GLN:NE2	2.34	0.61
1:A:114:LYS:HD3	1:A:218:MET:SD	2.40	0.61
1:H:206:VAL:HG23	1:H:212:GLY:CA	2.31	0.61
1:E:132:TYR:O	1:E:133:SER:HB3	2.00	0.61
1:C:169:TYR:H	1:C:357:HIS:CD2	2.19	0.61
1:G:60:GLU:HG3	1:G:76:MET:HG3	1.83	0.61
1:F:197:ASN:ND2	1:F:266:MET:H	1.99	0.60
1:D:68:ASN:ND2	1:D:97:ARG:H	1.99	0.60
1:D:47:GLU:HG3	4:D:515:HOH:O	2.01	0.60
1:F:242:LEU:HB3	4:F:629:HOH:O	2.01	0.60
1:A:60:GLU:CG	1:A:76:MET:HG3	2.31	0.60
1:H:9:ILE:CD1	1:H:30:LEU:HB3	2.33	0.59
1:B:188:GLY:H	2:B:401:ACY:CH3	2.16	0.59
1:E:168:ASN:ND2	1:E:170:ALA:H	1.99	0.59
1:H:9:ILE:HD11	1:H:30:LEU:HB3	1.85	0.59
1:G:92:LYS:H	1:G:92:LYS:CE	2.16	0.58
1:A:48:LEU:HD21	1:A:120:PHE:HD2	1.67	0.58
1:F:172:MET:HE3	1:F:358:GLN:HG3	1.84	0.58
1:C:287:ILE:O	1:C:291:THR:HG23	2.03	0.58
1:C:114:LYS:HD3	1:C:218:MET:SD	2.44	0.58
1:A:135:LYS:HE2	4:A:595:HOH:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:9:ILE:CD1	1:H:30:LEU:CB	2.82	0.58
1:H:92:LYS:H	1:H:92:LYS:NZ	2.01	0.58
1:A:247:VAL:HG12	1:A:313:LEU:HD13	1.86	0.57
1:B:275:ASN:HD21	1:B:277:GLU:HB3	1.69	0.57
1:C:60:GLU:CG	1:C:76:MET:HG3	2.35	0.57
1:F:247:VAL:CG2	1:F:313:LEU:HB2	2.34	0.57
1:F:275:ASN:HD22	1:F:278:ASP:H	1.52	0.57
1:A:78:LEU:O	1:A:82:HIS:HE1	1.87	0.57
1:A:203:LEU:HD13	1:A:242:LEU:HD21	1.87	0.57
1:F:45:GLY:HA2	1:F:92:LYS:HD2	1.87	0.56
1:F:60:GLU:HG3	1:F:76:MET:CG	2.34	0.56
1:G:118:LYS:HD3	4:G:580:HOH:O	2.05	0.56
1:C:78:LEU:O	1:C:82:HIS:HE1	1.87	0.56
1:B:142:SER:H	2:B:401:ACY:CH3	2.19	0.56
1:G:104:LEU:HD13	1:G:160:PRO:HB3	1.88	0.55
1:C:94:THR:HG21	1:F:5:GLN:NE2	2.22	0.55
1:H:60:GLU:CG	1:H:76:MET:HG3	2.36	0.55
1:H:312:ASP:HB2	4:H:592:HOH:O	2.07	0.55
1:A:247:VAL:CG1	1:A:313:LEU:HB2	2.36	0.55
1:E:243:GLY:O	1:E:247:VAL:HG23	2.07	0.55
1:C:55:ASP:O	1:C:113:VAL:HA	2.07	0.55
1:D:267:ARG:HG2	1:D:278:ASP:OD2	2.07	0.55
1:H:178:ASN:HB2	4:H:618:HOH:O	2.07	0.54
1:B:142:SER:H	2:B:401:ACY:H2	1.72	0.54
1:E:132:TYR:O	1:E:133:SER:HB2	2.07	0.54
1:G:275:ASN:HD22	1:G:278:ASP:H	1.53	0.54
1:C:197:ASN:ND2	1:C:266:MET:H	2.05	0.54
1:E:247:VAL:CG2	1:E:313:LEU:HB2	2.38	0.54
1:E:247:VAL:HG22	1:E:313:LEU:HB2	1.90	0.54
1:E:197:ASN:HD21	1:E:266:MET:H	1.56	0.54
1:B:337:GLN:NE2	4:B:588:HOH:O	2.35	0.53
1:A:197:ASN:ND2	1:A:266:MET:H	2.07	0.53
1:C:32:VAL:HG13	1:C:115:LEU:HB3	1.90	0.53
1:C:91:GLU:HG3	1:C:94:THR:HG23	1.90	0.53
1:G:287:ILE:O	1:G:291:THR:HG23	2.08	0.53
1:H:104:LEU:HD13	1:H:160:PRO:HB3	1.90	0.53
1:A:243:GLY:O	1:A:247:VAL:HG13	2.08	0.53
1:B:247:VAL:CG2	1:B:313:LEU:HB2	2.39	0.53
1:H:200:ARG:HD3	1:H:257:ASN:HD21	1.74	0.52
1:G:196:ASP:O	1:G:197:ASN:HB2	2.09	0.52
1:D:105:GLN:HE22	1:D:187:GLY:N	2.02	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:114:LYS:HD3	1:H:218:MET:SD	2.49	0.52
1:F:197:ASN:HD21	1:F:266:MET:H	1.58	0.52
1:A:305:SER:HA	1:A:336:PHE:O	2.10	0.52
1:G:142:SER:HB2	1:G:147:GLU:HB2	1.91	0.52
1:D:342:THR:HG22	1:D:343:MET:H	1.75	0.51
1:H:55:ASP:O	1:H:113:VAL:HA	2.09	0.51
1:A:78:LEU:O	1:A:82:HIS:CE1	2.63	0.51
1:C:318:THR:HB	1:D:318:THR:CG2	2.41	0.51
1:F:172:MET:HE1	1:F:358:GLN:HA	1.92	0.51
1:E:162:TYR:CD2	1:E:349:HIS:HE1	2.28	0.51
1:G:325:LYS:HE3	1:H:315:LEU:HD13	1.93	0.51
1:B:162:TYR:CD2	1:B:349:HIS:HE1	2.28	0.51
1:B:305:SER:HA	1:B:336:PHE:O	2.10	0.51
1:B:310:GLY:H	1:B:340:ASN:ND2	2.09	0.51
1:A:52:LEU:HD23	1:A:82:HIS:HB2	1.93	0.50
1:F:29:PRO:HB3	1:F:118:LYS:HG2	1.93	0.50
1:H:197:ASN:ND2	1:H:266:MET:H	2.09	0.50
1:A:105:GLN:HE22	1:A:187:GLY:N	2.07	0.50
1:H:269:ASN:O	1:H:271:ASP:N	2.45	0.50
1:D:49:TRP:HB2	1:D:121:LYS:HB2	1.93	0.50
1:E:172:MET:CE	1:E:358:GLN:HG3	2.41	0.50
1:B:243:GLY:O	1:B:247:VAL:HG23	2.11	0.50
1:D:252:GLN:O	1:D:265:LYS:HE2	2.12	0.50
1:G:49:TRP:HB2	1:G:121:LYS:HB2	1.92	0.50
1:B:60:GLU:HG3	1:B:76:MET:CG	2.38	0.50
1:B:142:SER:CB	2:B:401:ACY:H2	2.42	0.50
1:G:216:GLY:O	1:G:220:GLU:HG3	2.11	0.50
1:A:301:GLN:NE2	4:A:513:HOH:O	2.45	0.50
1:F:51:ASP:HB2	4:F:544:HOH:O	2.12	0.50
1:F:196:ASP:O	1:F:197:ASN:HB2	2.12	0.49
1:H:200:ARG:HD3	1:H:257:ASN:ND2	2.27	0.49
1:E:325:LYS:HE2	1:F:315:LEU:HD13	1.93	0.49
1:F:142:SER:HB3	1:F:187:GLY:HA2	1.95	0.49
1:C:322:ASN:HD21	1:D:318:THR:HG23	1.78	0.49
1:H:339:PRO:HG3	1:H:363:GLU:HG3	1.94	0.49
1:B:141:ASP:HB2	2:B:401:ACY:CH3	2.42	0.49
1:E:29:PRO:HB3	1:E:118:LYS:HG2	1.95	0.49
1:C:142:SER:HB3	1:C:187:GLY:HA2	1.93	0.49
1:G:60:GLU:CG	1:G:76:MET:HG3	2.42	0.49
1:B:27:ARG:HD2	4:B:578:HOH:O	2.12	0.48
1:C:305:SER:HA	1:C:336:PHE:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:314:ASN:ND2	1:D:337:GLN:HE21	2.00	0.48
1:D:62:TRP:CE2	1:D:76:MET:HB3	2.49	0.48
1:C:19:ILE:HG21	1:C:23:THR:HG21	1.95	0.48
1:E:172:MET:HE1	1:E:358:GLN:HG3	1.96	0.48
1:G:162:TYR:CD2	1:G:349:HIS:HE1	2.31	0.48
1:G:310:GLY:H	1:G:340:ASN:ND2	2.12	0.48
1:H:9:ILE:CD1	1:H:30:LEU:HB2	2.42	0.48
1:B:247:VAL:HG22	1:B:313:LEU:HB2	1.95	0.48
1:D:305:SER:HA	1:D:336:PHE:O	2.14	0.48
1:A:314:ASN:OD1	1:A:337:GLN:NE2	2.47	0.48
1:E:269:ASN:C	1:E:271:ASP:N	2.67	0.48
1:G:27:ARG:NH2	4:G:605:HOH:O	2.47	0.48
1:D:55:ASP:O	1:D:113:VAL:HA	2.13	0.47
1:H:351:HIS:NE2	2:H:401:ACY:H2	2.29	0.47
1:F:49:TRP:HB2	1:F:121:LYS:HB2	1.96	0.47
1:G:305:SER:HA	1:G:336:PHE:O	2.14	0.47
1:F:43:VAL:HG21	1:F:48:LEU:HD22	1.97	0.47
1:H:247:VAL:CG2	1:H:313:LEU:HB2	2.44	0.47
1:E:314:ASN:OD1	1:E:337:GLN:NE2	2.47	0.47
1:H:60:GLU:HG3	1:H:76:MET:CG	2.41	0.47
1:F:18:ASN:HB2	1:F:40:GLU:HB3	1.97	0.47
1:G:60:GLU:HG3	1:G:76:MET:CG	2.45	0.47
1:H:121:LYS:NZ	4:H:601:HOH:O	2.35	0.47
1:H:142:SER:HB2	1:H:147:GLU:HB3	1.96	0.47
1:A:247:VAL:HG11	1:A:313:LEU:HB2	1.95	0.46
1:D:108:ASN:HD21	1:D:215:LYS:NZ	2.13	0.46
1:D:247:VAL:HG22	1:D:313:LEU:HD13	1.97	0.46
1:F:22:ARG:O	2:F:402:ACY:OXT	2.34	0.46
1:A:147:GLU:OE2	1:A:158:TRP:CZ3	2.63	0.46
1:A:235:PRO:HD2	1:A:297:ASN:HD22	1.80	0.46
1:C:250:PHE:CD2	1:C:274:ARG:HG2	2.51	0.46
1:A:361:ALA:O	1:A:365:VAL:HG23	2.15	0.46
1:B:142:SER:HB3	2:B:401:ACY:H2	1.98	0.46
1:H:305:SER:HA	1:H:336:PHE:O	2.16	0.46
1:A:257:ASN:ND2	1:A:259:ASP:H	2.14	0.46
1:D:147:GLU:HG3	1:D:163:MET:HG3	1.97	0.46
1:F:247:VAL:HG22	1:F:313:LEU:HD13	1.96	0.46
1:G:40:GLU:HA	1:G:98:VAL:O	2.15	0.46
1:H:247:VAL:HG23	1:H:313:LEU:HB2	1.98	0.46
1:C:108:ASN:ND2	1:C:215:LYS:HE2	2.31	0.45
1:F:269:ASN:C	1:F:271:ASP:H	2.20	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:310:GLY:H	1:H:340:ASN:ND2	2.13	0.45
1:A:60:GLU:HG3	1:A:76:MET:CG	2.42	0.45
1:B:138:PHE:HB2	1:B:183:LEU:HD12	1.98	0.45
1:F:60:GLU:CG	1:F:76:MET:HG3	2.38	0.45
1:D:68:ASN:HD21	1:D:97:ARG:H	1.63	0.45
1:G:90:MET:SD	1:G:96:LYS:HD2	2.56	0.45
1:B:135:LYS:HB2	1:B:235:PRO:HA	1.98	0.45
1:B:200:ARG:NH1	1:B:258:PRO:HD2	2.31	0.45
1:C:312:ASP:HB2	4:C:568:HOH:O	2.15	0.45
1:F:245:ASN:HD21	2:F:401:ACY:C	2.30	0.45
1:F:311:SER:O	1:F:314:ASN:HB2	2.17	0.45
1:C:78:LEU:O	1:C:82:HIS:CE1	2.68	0.45
1:G:212:GLY:O	1:G:215:LYS:HE3	2.17	0.45
1:A:257:ASN:HD22	1:A:259:ASP:H	1.63	0.45
1:G:55:ASP:O	1:G:113:VAL:HA	2.16	0.45
1:A:52:LEU:HD21	1:A:82:HIS:HB2	1.97	0.45
1:F:190:GLY:HA2	4:F:629:HOH:O	2.16	0.45
1:C:91:GLU:CG	1:C:94:THR:HG23	2.47	0.45
1:H:49:TRP:HB2	1:H:121:LYS:HB2	1.99	0.45
1:F:275:ASN:HD21	1:F:277:GLU:HB3	1.82	0.44
1:G:325:LYS:HE3	1:H:315:LEU:CD1	2.46	0.44
1:B:43:VAL:HG21	1:B:48:LEU:HG	1.99	0.44
1:C:209:LYS:HD3	1:C:225:GLN:HA	1.99	0.44
1:G:269:ASN:HD22	1:G:273:THR:HG23	1.82	0.44
1:H:252:GLN:O	1:H:265:LYS:HE3	2.17	0.44
1:B:141:ASP:CB	2:B:401:ACY:H1	2.46	0.44
1:H:275:ASN:HD21	1:H:277:GLU:HB3	1.83	0.44
1:E:168:ASN:HD22	1:E:170:ALA:N	2.12	0.44
1:B:5:GLN:NE2	4:B:628:HOH:O	2.31	0.44
1:B:142:SER:HB3	1:B:187:GLY:HA2	1.98	0.44
1:C:61:MET:HG2	1:C:115:LEU:HG	2.00	0.44
1:F:162:TYR:CD2	1:F:349:HIS:HE1	2.36	0.44
1:H:47:GLU:HB3	1:H:88:ARG:HA	1.99	0.44
1:D:105:GLN:HG2	1:D:163:MET:SD	2.58	0.44
1:E:305:SER:HA	1:E:336:PHE:O	2.17	0.44
1:A:9:ILE:CD1	1:A:39:VAL:HG11	2.37	0.44
1:E:235:PRO:HD2	1:E:297:ASN:HD22	1.83	0.43
1:E:266:MET:HA	1:E:266:MET:CE	2.49	0.43
1:C:169:TYR:H	1:C:357:HIS:HD2	1.65	0.43
1:E:52:LEU:HD21	1:E:82:HIS:HB2	1.99	0.43
1:E:52:LEU:HB2	1:E:116:LEU:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:247:VAL:HG22	1:E:313:LEU:HD13	2.00	0.43
1:G:92:LYS:HD3	1:G:92:LYS:N	2.33	0.43
1:G:78:LEU:O	1:G:82:HIS:NE2	2.47	0.43
1:D:52:LEU:HD21	1:D:82:HIS:HB2	2.00	0.43
1:F:45:GLY:O	1:F:96:LYS:NZ	2.47	0.43
1:F:361:ALA:O	1:F:365:VAL:HG23	2.18	0.43
1:G:92:LYS:N	1:G:92:LYS:CD	2.82	0.43
1:H:207:TYR:HE2	1:H:293:LEU:HD23	1.75	0.43
1:C:108:ASN:HD21	1:C:215:LYS:HE2	1.83	0.43
1:G:271:ASP:HB2	1:G:273:THR:H	1.83	0.43
1:E:323:LYS:O	1:E:327:ASN:HB2	2.19	0.43
1:B:49:TRP:HB2	1:B:121:LYS:HB2	2.01	0.43
1:C:361:ALA:O	1:C:365:VAL:HG23	2.18	0.43
1:E:52:LEU:CD2	1:E:82:HIS:HB2	2.49	0.42
1:D:315:LEU:CA	1:D:318:THR:HG22	2.46	0.42
1:E:18:ASN:HB2	1:E:40:GLU:HB3	2.02	0.42
1:F:172:MET:CE	1:F:358:GLN:HG3	2.48	0.42
1:A:196:ASP:O	1:A:197:ASN:HB2	2.20	0.42
1:C:49:TRP:HB2	1:C:121:LYS:HB2	2.00	0.42
1:D:195:TRP:O	1:D:252:GLN:HG3	2.20	0.42
1:E:105:GLN:HE22	1:E:187:GLY:N	2.07	0.42
1:G:142:SER:HB3	1:G:187:GLY:HA2	2.02	0.42
1:H:78:LEU:O	1:H:82:HIS:NE2	2.47	0.42
1:H:207:TYR:CZ	1:H:293:LEU:CD2	3.03	0.42
1:H:9:ILE:HG23	1:H:119:GLY:HA2	2.01	0.42
1:G:280:LEU:HA	1:G:283:VAL:HB	2.02	0.42
1:B:18:ASN:HB2	1:B:40:GLU:HB3	2.02	0.42
1:A:274:ARG:NH2	1:A:312:ASP:HB3	2.35	0.41
1:F:305:SER:HA	1:F:336:PHE:O	2.20	0.41
1:A:40:GLU:HA	1:A:98:VAL:O	2.20	0.41
1:F:51:ASP:CG	1:F:118:LYS:HE3	2.40	0.41
1:B:136:LEU:O	1:B:181:TYR:HA	2.20	0.41
1:D:142:SER:HB3	1:D:187:GLY:HA2	2.03	0.41
1:E:148:GLY:HA2	1:E:348:SER:OG	2.20	0.41
1:F:306:TYR:CE2	1:F:311:SER:HA	2.56	0.41
1:C:94:THR:HA	1:C:95:PRO:HD3	1.87	0.41
1:D:162:TYR:CD2	1:D:349:HIS:HE1	2.39	0.41
1:C:291:THR:HG22	1:C:324:TYR:CE2	2.56	0.41
1:G:92:LYS:H	1:G:92:LYS:CD	2.34	0.41
1:F:17:ILE:HD11	1:F:39:VAL:HG23	2.01	0.41
1:B:247:VAL:HG22	1:B:313:LEU:HD13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:142:SER:HB2	1:C:147:GLU:HB3	2.03	0.41
1:D:310:GLY:H	1:D:340:ASN:ND2	2.18	0.41
1:H:92:LYS:H	1:H:92:LYS:HZ2	1.68	0.41
1:A:96:LYS:HE3	4:C:571:HOH:O	2.21	0.41
1:D:315:LEU:HA	1:D:318:THR:CG2	2.45	0.41
1:F:191:VAL:N	4:F:629:HOH:O	2.54	0.41
1:G:315:LEU:HD23	1:G:315:LEU:HA	1.94	0.41
1:G:325:LYS:HG3	1:G:330:ASP:O	2.21	0.41
1:H:203:LEU:HD13	1:H:242:LEU:HD21	2.03	0.41
1:A:269:ASN:C	1:A:271:ASP:N	2.70	0.40
1:B:147:GLU:HG3	4:B:630:HOH:O	2.20	0.40
1:C:148:GLY:HA2	1:C:348:SER:OG	2.22	0.40
1:E:136:LEU:O	1:E:181:TYR:HA	2.21	0.40
1:H:252:GLN:HG3	1:H:253:PRO:HD2	2.03	0.40
1:A:10:SER:H	1:A:28:GLN:NE2	2.18	0.40
1:F:105:GLN:HE22	1:F:187:GLY:N	2.04	0.40
1:E:200:ARG:HH12	1:E:258:PRO:HD2	1.86	0.40
1:H:196:ASP:O	1:H:197:ASN:HB2	2.20	0.40
1:B:128:ASN:HB2	1:H:3:VAL:HG21	2.04	0.40
1:G:254:GLU:HG2	1:G:265:LYS:HB2	2.03	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	371/408 (91%)	362 (98%)	8 (2%)	1 (0%)	41 41
1	B	372/408 (91%)	362 (97%)	10 (3%)	0	100 100
1	C	372/408 (91%)	363 (98%)	8 (2%)	1 (0%)	41 41
1	D	372/408 (91%)	357 (96%)	13 (4%)	2 (0%)	29 26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	371/408 (91%)	361 (97%)	7 (2%)	3 (1%)	19	15
1	F	371/408 (91%)	362 (98%)	8 (2%)	1 (0%)	41	41
1	G	372/408 (91%)	359 (96%)	13 (4%)	0	100	100
1	H	373/408 (91%)	358 (96%)	13 (4%)	2 (0%)	29	26
All	All	2974/3264 (91%)	2884 (97%)	80 (3%)	10 (0%)	41	41

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	259	ASP
1	D	259	ASP
1	D	330	ASP
1	E	133	SER
1	H	271	ASP
1	E	132	TYR
1	E	270	THR
1	F	270	THR
1	H	270	THR
1	A	270	THR

5.3.2 Protein sidechains (i)

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	320/352 (91%)	309 (97%)	11 (3%)	37	39
1	B	321/352 (91%)	312 (97%)	9 (3%)	43	47
1	C	319/352 (91%)	306 (96%)	13 (4%)	30	31
1	D	321/352 (91%)	310 (97%)	11 (3%)	37	39
1	E	319/352 (91%)	307 (96%)	12 (4%)	33	34
1	F	318/352 (90%)	310 (98%)	8 (2%)	47	52
1	G	320/352 (91%)	306 (96%)	14 (4%)	28	28
1	H	319/352 (91%)	305 (96%)	14 (4%)	28	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2557/2816 (91%)	2465 (96%)	92 (4%)	35 36

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	VAL
1	A	48	LEU
1	A	52	LEU
1	A	183	LEU
1	A	199	VAL
1	A	203	LEU
1	A	247	VAL
1	A	257	ASN
1	A	280	LEU
1	A	355	LYS
1	A	371	LYS
1	B	30	LEU
1	B	42	VAL
1	B	48	LEU
1	B	100	LEU
1	B	104	LEU
1	B	183	LEU
1	B	203	LEU
1	B	338	LEU
1	B	355	LYS
1	C	15	ASP
1	C	32	VAL
1	C	81	GLU
1	C	94	THR
1	C	115	LEU
1	C	203	LEU
1	C	206	VAL
1	C	247	VAL
1	C	260	ASP
1	C	276	ARG
1	C	312	ASP
1	C	314	ASN
1	C	326	GLU
1	D	30	LEU
1	D	52	LEU
1	D	96	LYS
1	D	100	LEU

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Mol	Chain	Res	Type
1	D	156	VAL
1	D	183	LEU
1	D	200	ARG
1	D	218	MET
1	D	276	ARG
1	D	280	LEU
1	D	342	THR
1	E	14	SER
1	E	52	LEU
1	E	168	ASN
1	E	183	LEU
1	E	203	LEU
1	E	206	VAL
1	E	247	VAL
1	E	251	ASN
1	E	280	LEU
1	E	312	ASP
1	E	314	ASN
1	E	327	ASN
1	F	52	LEU
1	F	91	GLU
1	F	183	LEU
1	F	203	LEU
1	F	206	VAL
1	F	312	ASP
1	F	314	ASN
1	F	344	GLU
1	G	26	LYS
1	G	27	ARG
1	G	57	ASP
1	G	84	LEU
1	G	92	LYS
1	G	96	LYS
1	G	99	ARG
1	G	183	LEU
1	G	217	GLU
1	G	267	ARG
1	G	271	ASP
1	G	275	ASN
1	G	281	LYS
1	G	312	ASP
1	H	3	VAL

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Mol	Chain	Res	Type
1	H	25	LYS
1	H	57	ASP
1	H	84	LEU
1	H	92	LYS
1	H	96	LYS
1	H	183	LEU
1	H	203	LEU
1	H	256	LEU
1	H	260	ASP
1	H	276	ARG
1	H	312	ASP
1	H	334	SER
1	H	351	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (88) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	ASN
1	A	18	ASN
1	A	28	GLN
1	A	82	HIS
1	A	105	GLN
1	A	108	ASN
1	A	128	ASN
1	A	197	ASN
1	A	252	GLN
1	A	257	ASN
1	A	297	ASN
1	A	301	GLN
1	A	314	ASN
1	A	337	GLN
1	A	358	GLN
1	A	359	ASN
1	B	18	ASN
1	B	28	GLN
1	B	105	GLN
1	B	108	ASN
1	B	128	ASN
1	B	245	ASN
1	B	252	GLN
1	B	275	ASN
1	B	340	ASN

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Mol	Chain	Res	Type
1	B	358	GLN
1	B	359	ASN
1	C	18	ASN
1	C	28	GLN
1	C	82	HIS
1	C	105	GLN
1	C	108	ASN
1	C	127	GLN
1	C	128	ASN
1	C	197	ASN
1	C	252	GLN
1	C	297	ASN
1	C	314	ASN
1	C	337	GLN
1	C	357	HIS
1	C	359	ASN
1	D	68	ASN
1	D	105	GLN
1	D	108	ASN
1	D	127	GLN
1	D	186	GLN
1	D	202	ASN
1	D	252	GLN
1	D	337	GLN
1	D	340	ASN
1	D	345	ASN
1	D	359	ASN
1	E	11	ASN
1	E	105	GLN
1	E	168	ASN
1	E	197	ASN
1	E	297	ASN
1	E	314	ASN
1	E	337	GLN
1	E	359	ASN
1	F	5	GLN
1	F	105	GLN
1	F	128	ASN
1	F	197	ASN
1	F	275	ASN
1	F	314	ASN
1	F	359	ASN

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Mol	Chain	Res	Type
1	G	18	ASN
1	G	105	GLN
1	G	108	ASN
1	G	127	GLN
1	G	269	ASN
1	G	275	ASN
1	G	340	ASN
1	G	349	HIS
1	G	359	ASN
1	H	28	GLN
1	H	105	GLN
1	H	108	ASN
1	H	128	ASN
1	H	178	ASN
1	H	197	ASN
1	H	202	ASN
1	H	257	ASN
1	H	269	ASN
1	H	275	ASN
1	H	340	ASN
1	H	359	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

11 ligands are modelled in this entry.

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	GOL	B	402	-	5,5,5	0.45	0	5,5,5	0.39	0
2	ACY	B	401	-	3,3,3	0.63	0	3,3,3	1.15	0
2	ACY	F	402	-	3,3,3	0.77	0	3,3,3	0.84	0
2	ACY	F	401	-	3,3,3	0.70	0	3,3,3	0.82	0
2	ACY	G	401	-	3,3,3	0.82	0	3,3,3	0.74	0
2	ACY	D	401	-	3,3,3	0.75	0	3,3,3	0.75	0
2	ACY	E	401	-	3,3,3	0.74	0	3,3,3	0.91	0
2	ACY	H	401	-	3,3,3	0.83	0	3,3,3	0.53	0
2	ACY	A	401	-	3,3,3	0.77	0	3,3,3	0.77	0
2	ACY	H	402	-	3,3,3	0.82	0	3,3,3	0.49	0
2	ACY	C	401	-	3,3,3	0.71	0	3,3,3	0.80	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
3	GOL	B	402	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	402	GOL	C1-C2-C3-O3
3	B	402	GOL	O2-C2-C3-O3
3	B	402	GOL	O1-C1-C2-C3
3	B	402	GOL	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	ACY	12	0
2	F	402	ACY	1	0
2	F	401	ACY	1	0
2	H	401	ACY	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 (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	373/408 (91%)	0.11	8 (2%)	63	68	18, 26, 39, 54	0
1	B	374/408 (91%)	0.14	14 (3%)	41	48	18, 27, 41, 53	0
1	C	374/408 (91%)	0.33	20 (5%)	26	32	20, 32, 53, 68	0
1	D	374/408 (91%)	0.27	18 (4%)	30	36	20, 31, 50, 64	0
1	E	373/408 (91%)	0.21	14 (3%)	40	46	20, 29, 42, 54	0
1	F	373/408 (91%)	0.18	14 (3%)	40	46	19, 28, 42, 54	0
1	G	374/408 (91%)	0.31	20 (5%)	26	32	21, 34, 53, 66	0
1	H	375/408 (91%)	0.31	20 (5%)	26	32	20, 33, 51, 68	0
All	All	2990/3264 (91%)	0.23	128 (4%)	35	41	18, 29, 48, 68	0

All (128) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	2	SER	6.4
1	H	343	MET	5.7
1	H	270	THR	5.3
1	G	270	THR	5.1
1	D	270	THR	4.9
1	C	272	GLY	4.6
1	E	270	THR	4.5
1	C	260	ASP	4.4
1	C	270	THR	4.2
1	H	256	LEU	4.1
1	G	258	PRO	4.0
1	H	258	PRO	3.9
1	A	270	THR	3.9
1	C	258	PRO	3.9
1	E	3	VAL	3.8
1	G	259	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	343	MET	3.7
1	B	3	VAL	3.6
1	A	343	MET	3.6
1	G	343	MET	3.6
1	H	272	GLY	3.5
1	E	343	MET	3.4
1	F	3	VAL	3.4
1	G	153	PHE	3.4
1	F	184	VAL	3.4
1	C	343	MET	3.3
1	B	158	TRP	3.3
1	F	158	TRP	3.3
1	F	343	MET	3.3
1	D	259	ASP	3.3
1	H	271	ASP	3.2
1	H	261	GLY	3.2
1	H	153	PHE	3.1
1	G	272	GLY	3.0
1	C	255	PHE	3.0
1	D	262	LYS	3.0
1	C	350	MET	3.0
1	A	183	LEU	3.0
1	G	256	LEU	3.0
1	C	259	ASP	2.9
1	B	139	ILE	2.9
1	D	158	TRP	2.9
1	H	255	PHE	2.9
1	H	207	TYR	2.9
1	E	203	LEU	2.9
1	H	262	LYS	2.9
1	F	183	LEU	2.8
1	H	3	VAL	2.8
1	A	32	VAL	2.8
1	G	158	TRP	2.8
1	C	256	LEU	2.7
1	E	183	LEU	2.7
1	F	256	LEU	2.7
1	C	25	LYS	2.7
1	F	33	PHE	2.6
1	H	57	ASP	2.6
1	B	376	GLU	2.6
1	C	263	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	F	32	VAL	2.6
1	C	271	ASP	2.6
1	E	98	VAL	2.5
1	C	261	GLY	2.5
1	C	153	PHE	2.5
1	E	184	VAL	2.5
1	F	240	VAL	2.5
1	G	263	THR	2.5
1	G	255	PHE	2.5
1	D	344	GLU	2.5
1	F	106	ALA	2.5
1	C	273	THR	2.5
1	B	240	VAL	2.5
1	F	270	THR	2.5
1	H	259	ASP	2.5
1	C	144	THR	2.5
1	G	184	VAL	2.5
1	H	109	ASP	2.5
1	F	375	PHE	2.5
1	D	242	LEU	2.4
1	G	3	VAL	2.4
1	B	343	MET	2.4
1	F	268	THR	2.4
1	F	258	PRO	2.4
1	G	271	ASP	2.4
1	G	109	ASP	2.4
1	C	184	VAL	2.3
1	D	253	PRO	2.3
1	E	158	TRP	2.3
1	A	86	LEU	2.3
1	H	350	MET	2.3
1	C	268	THR	2.3
1	B	239	ILE	2.3
1	D	350	MET	2.2
1	G	376	GLU	2.2
1	D	271	ASP	2.2
1	B	183	LEU	2.2
1	D	256	LEU	2.2
1	A	138	PHE	2.2
1	D	3	VAL	2.2
1	H	158	TRP	2.2
1	H	139	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	240	VAL	2.2
1	E	326	GLU	2.2
1	D	329	GLY	2.2
1	E	258	PRO	2.1
1	H	217	GLU	2.1
1	A	3	VAL	2.1
1	C	57	ASP	2.1
1	D	153	PHE	2.1
1	B	203	LEU	2.1
1	A	375	PHE	2.1
1	E	259	ASP	2.1
1	G	154	ASP	2.1
1	B	86	LEU	2.1
1	D	217	GLU	2.1
1	E	139	ILE	2.1
1	G	139	ILE	2.1
1	G	203	LEU	2.1
1	B	184	VAL	2.1
1	B	260	ASP	2.1
1	G	15	ASP	2.1
1	B	304	TRP	2.1
1	D	57	ASP	2.0
1	G	242	LEU	2.0
1	E	375	PHE	2.0
1	D	304	TRP	2.0
1	C	183	LEU	2.0
1	B	273	THR	2.0
1	E	240	VAL	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 monosaccharides 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
3	GOL	B	402	6/6	0.71	0.39	38,39,40,41	0
2	ACY	B	401	4/4	0.82	0.21	19,23,23,25	0
2	ACY	G	401	4/4	0.88	0.18	25,27,27,28	0
2	ACY	D	401	4/4	0.92	0.18	27,29,29,30	0
2	ACY	C	401	4/4	0.93	0.16	21,22,22,24	0
2	ACY	F	402	4/4	0.94	0.19	32,33,33,34	0
2	ACY	A	401	4/4	0.94	0.11	17,18,18,19	0
2	ACY	H	402	4/4	0.94	0.11	28,29,29,29	0
2	ACY	E	401	4/4	0.94	0.12	24,24,25,26	0
2	ACY	F	401	4/4	0.95	0.13	24,26,26,29	0
2	ACY	H	401	4/4	0.96	0.10	23,24,24,24	0

6.5 Other polymers (i)

There are no such residues in this entry.