



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2018 – 08:52 pm GMT

PDB ID : 3FD8  
Title : Crystal Structure of an oxidoreductase from *Enterococcus faecalis*  
Authors : Damodharan, L.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center for Structural Genomics (NYSGXRC)  
Deposited on : 2008-11-25  
Resolution : 2.45 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

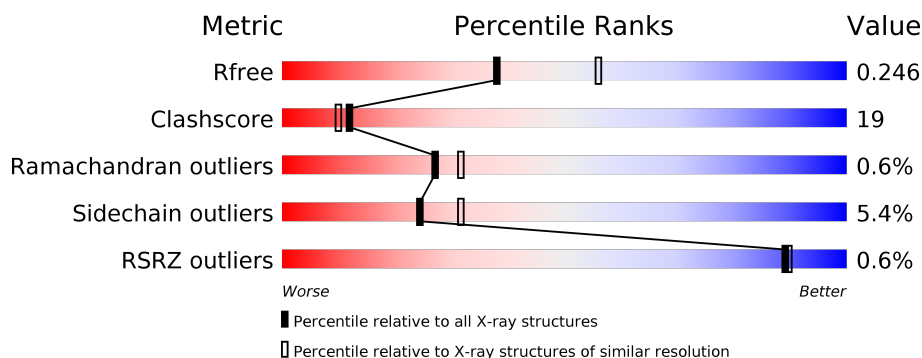
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.45 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))
$R_{free}$	111664	1259 (2.48-2.44)
Clashscore	122126	1323 (2.48-2.44)
Ramachandran outliers	120053	1314 (2.48-2.44)
Sidechain outliers	120020	1314 (2.48-2.44)
RSRZ outliers	108989	1238 (2.48-2.44)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	359	<div> <div>70%</div> <div>26%</div> <div>• •</div> </div>
1	B	359	<div> <div>64%</div> <div>30%</div> <div>• •</div> </div>
1	C	359	<div> <div>%</div> <div>62%</div> <div>32%</div> <div>• •</div> </div>
1	D	359	<div> <div>66%</div> <div>28%</div> <div>• •</div> </div>
1	E	359	<div> <div>%</div> <div>63%</div> <div>30%</div> <div>• •</div> </div>
1	F	359	<div> <div>65%</div> <div>29%</div> <div>• • •</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17472 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 Oxidoreductase, Gfo/Idh/MocA family.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	348	Total	C	N	O	S	Se	0	0	0
			2767	1769	458	530	2	8			
1	B	348	Total	C	N	O	S	Se	0	0	0
			2767	1769	458	530	2	8			
1	C	347	Total	C	N	O	S	Se	0	0	0
			2758	1764	457	527	2	8			
1	D	349	Total	C	N	O	S	Se	0	0	0
			2773	1772	459	532	2	8			
1	E	349	Total	C	N	O	S	Se	0	0	0
			2775	1773	460	532	2	8			
1	F	349	Total	C	N	O	S	Se	0	0	0
			2773	1772	459	532	2	8			

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	expression tag	UNP Q835X4
A	2	SER	-	expression tag	UNP Q835X4
A	3	LEU	-	expression tag	UNP Q835X4
A	352	GLU	-	expression tag	UNP Q835X4
A	353	GLY	-	expression tag	UNP Q835X4
A	354	HIS	-	expression tag	UNP Q835X4
A	355	HIS	-	expression tag	UNP Q835X4
A	356	HIS	-	expression tag	UNP Q835X4
A	357	HIS	-	expression tag	UNP Q835X4
A	358	HIS	-	expression tag	UNP Q835X4
A	359	HIS	-	expression tag	UNP Q835X4
B	1	MSE	-	expression tag	UNP Q835X4
B	2	SER	-	expression tag	UNP Q835X4
B	3	LEU	-	expression tag	UNP Q835X4
B	352	GLU	-	expression tag	UNP Q835X4
B	353	GLY	-	expression tag	UNP Q835X4
B	354	HIS	-	expression tag	UNP Q835X4

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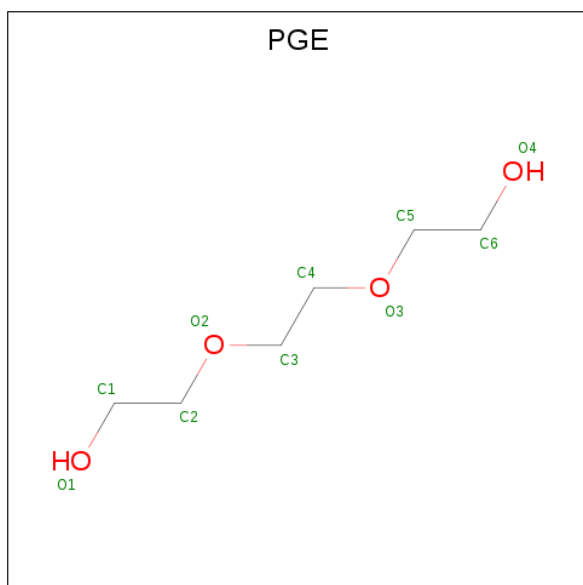
Chain	Residue	Modelled	Actual	Comment	Reference
B	355	HIS	-	expression tag	UNP Q835X4
B	356	HIS	-	expression tag	UNP Q835X4
B	357	HIS	-	expression tag	UNP Q835X4
B	358	HIS	-	expression tag	UNP Q835X4
B	359	HIS	-	expression tag	UNP Q835X4
C	1	MSE	-	expression tag	UNP Q835X4
C	2	SER	-	expression tag	UNP Q835X4
C	3	LEU	-	expression tag	UNP Q835X4
C	352	GLU	-	expression tag	UNP Q835X4
C	353	GLY	-	expression tag	UNP Q835X4
C	354	HIS	-	expression tag	UNP Q835X4
C	355	HIS	-	expression tag	UNP Q835X4
C	356	HIS	-	expression tag	UNP Q835X4
C	357	HIS	-	expression tag	UNP Q835X4
C	358	HIS	-	expression tag	UNP Q835X4
C	359	HIS	-	expression tag	UNP Q835X4
D	1	MSE	-	expression tag	UNP Q835X4
D	2	SER	-	expression tag	UNP Q835X4
D	3	LEU	-	expression tag	UNP Q835X4
D	352	GLU	-	expression tag	UNP Q835X4
D	353	GLY	-	expression tag	UNP Q835X4
D	354	HIS	-	expression tag	UNP Q835X4
D	355	HIS	-	expression tag	UNP Q835X4
D	356	HIS	-	expression tag	UNP Q835X4
D	357	HIS	-	expression tag	UNP Q835X4
D	358	HIS	-	expression tag	UNP Q835X4
D	359	HIS	-	expression tag	UNP Q835X4
E	1	MSE	-	expression tag	UNP Q835X4
E	2	SER	-	expression tag	UNP Q835X4
E	3	LEU	-	expression tag	UNP Q835X4
E	352	GLU	-	expression tag	UNP Q835X4
E	353	GLY	-	expression tag	UNP Q835X4
E	354	HIS	-	expression tag	UNP Q835X4
E	355	HIS	-	expression tag	UNP Q835X4
E	356	HIS	-	expression tag	UNP Q835X4
E	357	HIS	-	expression tag	UNP Q835X4
E	358	HIS	-	expression tag	UNP Q835X4
E	359	HIS	-	expression tag	UNP Q835X4
F	1	MSE	-	expression tag	UNP Q835X4
F	2	SER	-	expression tag	UNP Q835X4
F	3	LEU	-	expression tag	UNP Q835X4
F	352	GLU	-	expression tag	UNP Q835X4

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Chain	Residue	Modelled	Actual	Comment	Reference
F	353	GLY	-	expression tag	UNP Q835X4
F	354	HIS	-	expression tag	UNP Q835X4
F	355	HIS	-	expression tag	UNP Q835X4
F	356	HIS	-	expression tag	UNP Q835X4
F	357	HIS	-	expression tag	UNP Q835X4
F	358	HIS	-	expression tag	UNP Q835X4
F	359	HIS	-	expression tag	UNP Q835X4

- Molecule 2 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula:  $C_6H_{14}O_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			10	6	4		
2	C	1	Total	C	O	0	0
			10	6	4		
2	F	1	Total	C	O	0	0
			10	6	4		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	132	Total	O	0	0
			132	132		
3	B	142	Total	O	0	0
			142	142		
3	C	112	Total	O	0	0
			112	112		

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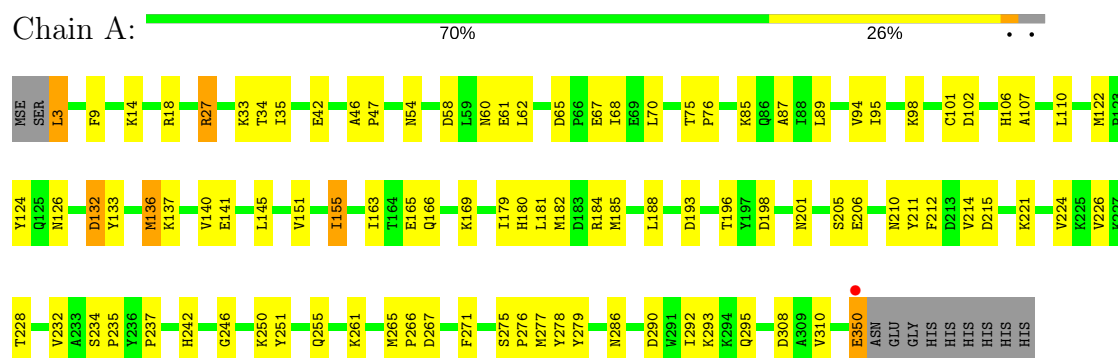
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	142	Total 142	O 142	0	0
3	E	137	Total 137	O 137	0	0
3	F	164	Total 164	O 164	0	0

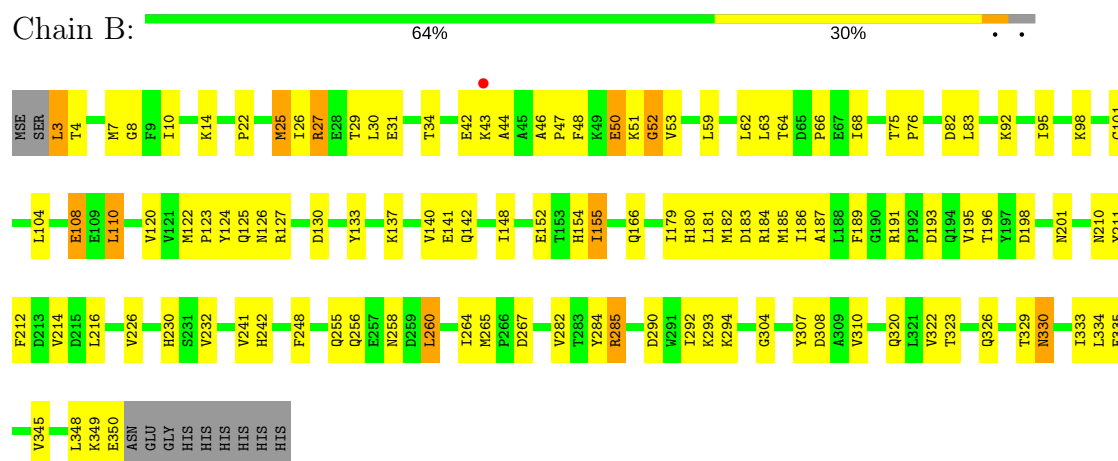
### 3 Residue-property plots

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

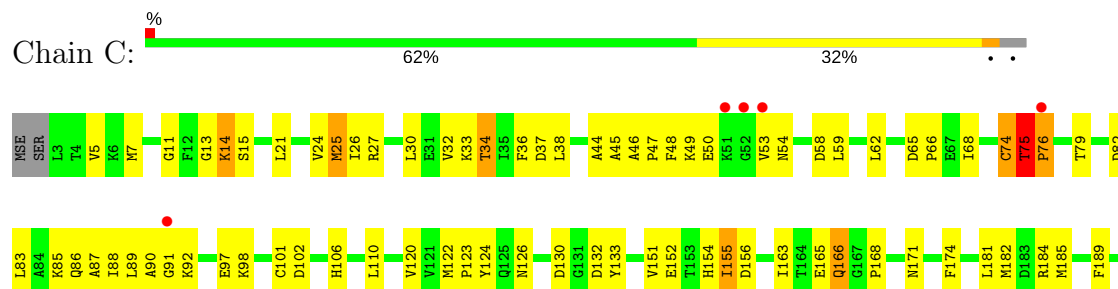
- Molecule 1: Oxidoreductase, Gfo/Idh/MocA family

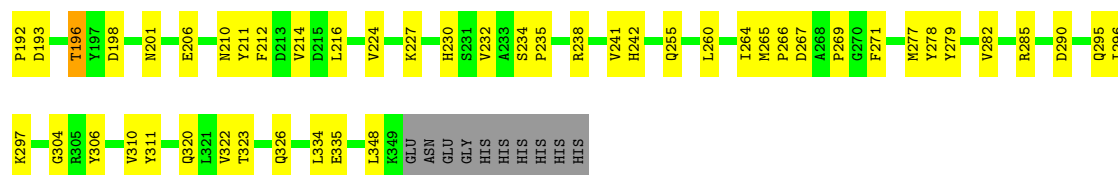


- Molecule 1: Oxidoreductase, Gfo/Idh/MocA family

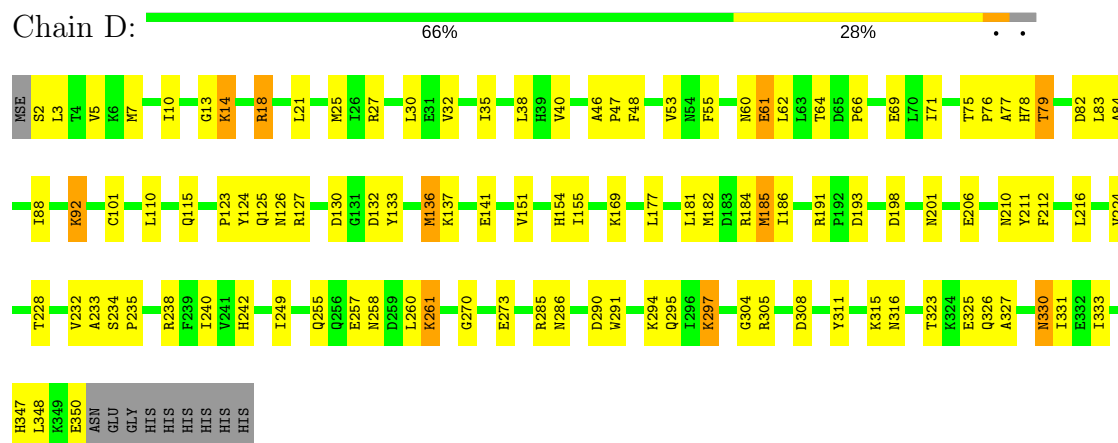


- Molecule 1: Oxidoreductase, Gfo/Idh/MocA family

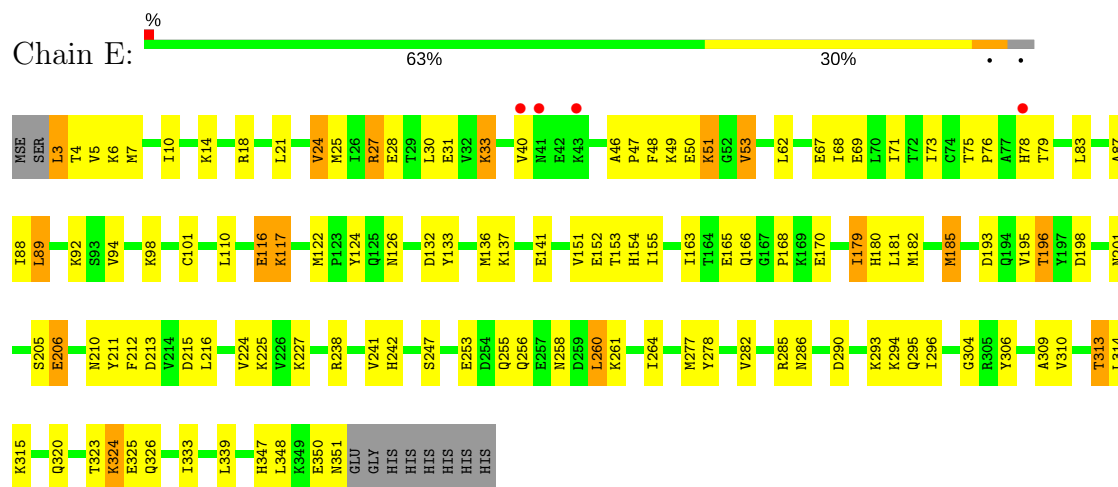




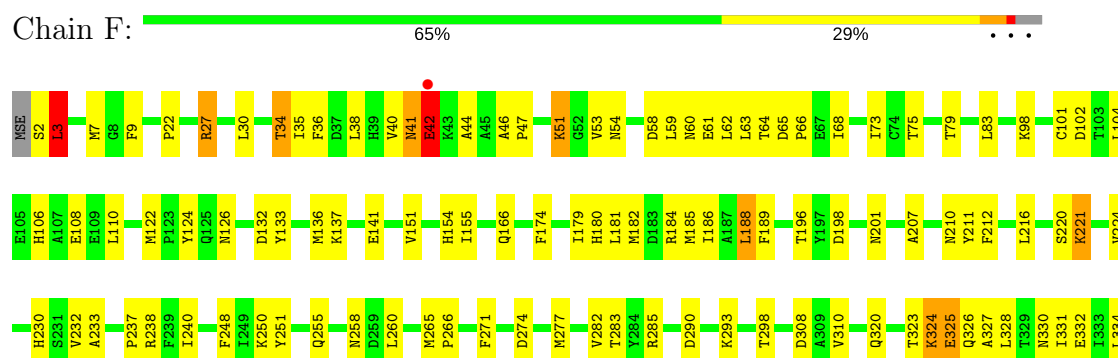
• Molecule 1: Oxidoreductase, Gfo/Idh/MocA family



• Molecule 1: Oxidoreductase, Gfo/Idh/MocA family



• Molecule 1: Oxidoreductase, Gfo/Idh/MocA family





H347	ASN
L348	GLU
K349	GLY
E350	HIS
	HIS
	HIS
	HIS
	HIS
	HIS
	HIS

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	104.57Å 151.32Å 161.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.14 – 2.45 48.80 – 2.45	Depositor EDS
% Data completeness (in resolution range)	91.4 (48.14-2.45) 95.2 (48.80-2.45)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.57 (at 2.45Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.196 , 0.240 0.202 , 0.246	Depositor DCC
$R_{free}$ test set	4544 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.6	Xtriage
Anisotropy	0.183	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 40.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	17472	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.35	0/2826	0.64	0/3815
1	B	0.36	0/2826	0.65	1/3815 (0.0%)
1	C	0.35	0/2817	0.69	1/3803 (0.0%)
1	D	0.36	0/2832	0.66	0/3823
1	E	0.37	0/2834	0.67	0/3826
1	F	0.38	0/2832	0.68	0/3823
All	All	0.36	0/16967	0.66	2/22905 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	75	THR	N-CA-C	7.36	130.86	111.00
1	B	52	GLY	N-CA-C	5.03	125.69	113.10

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	2767	0	2692	82	0
1	B	2767	0	2692	102	0
1	C	2758	0	2686	111	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2773	0	2697	105	0
1	E	2775	0	2698	129	0
1	F	2773	0	2697	100	0
2	B	10	0	14	1	0
2	C	10	0	14	5	0
2	F	10	0	14	2	0
3	A	132	0	0	5	0
3	B	142	0	0	8	0
3	C	112	0	0	9	0
3	D	142	0	0	10	0
3	E	137	0	0	7	0
3	F	164	0	0	5	0
All	All	17472	0	16204	608	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 19.

All (608) 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:E:185:MSE:HG2	1:E:224:VAL:HG11	1.23	1.18
1:D:185:MSE:HG2	1:D:224:VAL:HG11	1.30	1.13
1:E:182:MSE:HE1	1:E:333:ILE:HG21	1.33	1.11
1:C:182:MSE:HE2	1:C:216:LEU:HD21	1.19	1.10
1:F:155:ILE:HD13	1:F:181:LEU:HD21	1.22	1.10
1:D:182:MSE:CE	1:D:216:LEU:HD21	1.83	1.08
1:F:182:MSE:HE2	1:F:216:LEU:HD21	1.38	1.06
1:C:48:PHE:HB3	1:C:53:VAL:HG11	1.42	1.02
1:B:182:MSE:HE2	1:B:216:LEU:HD11	1.42	0.98
1:E:31:GLU:HB3	1:E:33:LYS:HZ1	1.28	0.98
1:D:182:MSE:HE2	1:D:216:LEU:HD21	1.43	0.98
1:E:6:LYS:HD2	1:E:67:GLU:HG3	1.48	0.95
1:E:25:MSE:HA	1:E:25:MSE:HE2	1.49	0.94
1:E:182:MSE:CE	1:E:216:LEU:HD21	1.99	0.93
1:D:7:MSE:CE	1:D:30:LEU:HB3	2.01	0.91
1:B:7:MSE:HE1	1:B:30:LEU:HD23	1.53	0.90
1:F:155:ILE:CD1	1:F:181:LEU:HD21	2.03	0.89
1:C:7:MSE:HE2	1:C:30:LEU:HD12	1.55	0.89
1:A:136:MSE:HE1	1:A:188:LEU:HD22	1.55	0.88
1:D:155:ILE:HD13	1:D:181:LEU:HD21	1.52	0.88
1:C:182:MSE:CE	1:C:216:LEU:HD21	2.04	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:349:LYS:O	1:F:350:GLU:HB2	1.70	0.87
1:B:182:MSE:CE	1:B:216:LEU:HD21	2.05	0.86
1:F:7:MSE:HE3	1:F:30:LEU:HB3	1.58	0.86
1:D:185:MSE:HE3	1:D:185:MSE:HA	1.57	0.85
1:F:7:MSE:CE	1:F:30:LEU:HD12	2.08	0.82
1:A:350:GLU:HG2	1:A:350:GLU:O	1.80	0.81
1:E:75:THR:HG21	1:E:83:LEU:HD12	1.61	0.81
1:B:3:LEU:HD13	1:B:4:THR:H	1.45	0.81
1:D:132:ASP:OD1	1:D:238:ARG:HG2	1.81	0.81
1:B:98:LYS:HE3	1:B:180:HIS:NE2	1.96	0.81
1:E:7:MSE:HE3	1:E:30:LEU:HB3	1.61	0.80
1:D:115:GLN:HG3	3:D:415:HOH:O	1.81	0.80
1:C:14:LYS:H	1:C:14:LYS:HE2	1.45	0.80
1:C:25:MSE:HA	1:C:25:MSE:HE3	1.61	0.80
1:E:255:GLN:HE22	1:E:258:ASN:HD22	1.31	0.79
1:E:7:MSE:HE2	1:E:30:LEU:HD12	1.64	0.79
1:B:182:MSE:HE1	1:B:216:LEU:HD21	1.65	0.79
1:B:7:MSE:CE	1:B:30:LEU:HB3	2.14	0.78
1:E:132:ASP:OD1	1:E:238:ARG:HG2	1.84	0.77
1:E:75:THR:HG23	1:E:79:THR:HG23	1.67	0.77
1:F:34:THR:HG21	3:F:716:HOH:O	1.85	0.77
1:D:7:MSE:HE2	1:D:30:LEU:HD12	1.68	0.76
1:F:182:MSE:CE	1:F:216:LEU:HD21	2.14	0.76
1:F:237:PRO:HG2	1:F:240:ILE:HD11	1.66	0.76
1:F:154:HIS:O	1:F:155:ILE:HD12	1.85	0.76
1:B:182:MSE:HE1	1:B:333:ILE:HG21	1.67	0.76
1:B:25:MSE:HE3	1:B:25:MSE:HA	1.67	0.75
1:C:14:LYS:H	1:C:14:LYS:CE	2.00	0.75
1:F:42:GLU:H	1:F:42:GLU:CD	1.89	0.75
1:A:101:CYS:SG	1:A:110:LEU:HD22	2.25	0.75
1:D:185:MSE:CG	1:D:224:VAL:HG11	2.13	0.75
1:E:25:MSE:HA	1:E:25:MSE:CE	2.17	0.75
1:D:101:CYS:SG	1:D:110:LEU:HD22	2.26	0.75
1:E:48:PHE:O	1:E:53:VAL:HG13	1.87	0.75
1:E:185:MSE:HA	1:E:185:MSE:CE	2.16	0.74
1:C:48:PHE:O	1:C:53:VAL:HG12	1.88	0.74
1:E:7:MSE:CE	1:E:30:LEU:HD12	2.17	0.74
1:F:75:THR:HG21	1:F:83:LEU:HD12	1.69	0.74
1:C:185:MSE:HG3	1:C:224:VAL:HG11	1.69	0.74
1:C:75:THR:HG23	1:C:79:THR:CG2	2.18	0.74
1:D:182:MSE:HE2	1:D:216:LEU:CD2	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:152:GLU:OE2	1:E:154:HIS:HE1	1.71	0.73
1:B:3:LEU:CD1	1:B:4:THR:H	2.01	0.73
1:E:185:MSE:HG2	1:E:224:VAL:CG1	2.12	0.72
1:C:7:MSE:HE3	1:C:30:LEU:HB3	1.71	0.72
1:D:136:MSE:HE3	1:D:137:LYS:N	2.05	0.72
1:D:206:GLU:H	1:D:206:GLU:CD	1.93	0.71
1:C:14:LYS:N	1:C:14:LYS:HE2	2.06	0.71
1:C:265:MSE:HE3	3:C:389:HOH:O	1.91	0.71
1:D:14:LYS:NZ	1:D:14:LYS:H	1.88	0.71
1:C:34:THR:HG23	1:C:68:ILE:HD11	1.72	0.70
1:D:46:ALA:HB3	1:D:47:PRO:HD3	1.72	0.70
1:C:27:ARG:NH2	1:C:304:GLY:HA3	2.06	0.70
1:B:26:ILE:HD13	1:B:267:ASP:HB3	1.74	0.69
1:D:18:ARG:NH1	1:D:261:LYS:HB3	2.07	0.69
1:A:255:GLN:HE21	1:D:294:LYS:HD3	1.57	0.68
1:D:182:MSE:O	1:D:186:ILE:HG12	1.94	0.68
1:C:14:LYS:H	1:C:14:LYS:CD	2.06	0.68
1:D:347:HIS:HB2	3:D:518:HOH:O	1.92	0.68
1:D:155:ILE:CD1	1:D:181:LEU:HD21	2.23	0.68
1:E:6:LYS:HD3	1:E:33:LYS:CD	2.23	0.68
1:C:201:ASN:HA	1:C:210:ASN:OD1	1.93	0.68
1:E:163:ILE:HD12	1:E:210:ASN:HB2	1.76	0.67
1:A:255:GLN:NE2	1:D:294:LYS:HD3	2.10	0.67
1:C:76:PRO:O	1:C:79:THR:HG22	1.94	0.67
1:E:31:GLU:CB	1:E:33:LYS:HZ1	2.06	0.67
1:B:195:VAL:HG21	1:B:333:ILE:HD12	1.77	0.66
1:B:82:ASP:HB3	3:B:410:HOH:O	1.95	0.66
1:D:10:ILE:HG21	1:D:83:LEU:HD13	1.76	0.66
1:D:48:PHE:O	1:D:53:VAL:HG22	1.96	0.66
1:F:182:MSE:O	1:F:186:ILE:HG12	1.96	0.66
1:F:122:MSE:HE1	1:F:310:VAL:HG22	1.79	0.65
1:B:46:ALA:HB3	1:B:47:PRO:HD3	1.77	0.65
1:D:27:ARG:NH2	1:D:304:GLY:HA3	2.11	0.65
1:A:205:SER:HB3	3:A:824:HOH:O	1.97	0.65
1:B:30:LEU:HD21	1:B:307:TYR:HB3	1.79	0.65
1:B:3:LEU:HD13	1:B:4:THR:N	2.12	0.65
1:C:46:ALA:HB3	1:C:47:PRO:HD3	1.78	0.65
1:D:76:PRO:O	1:D:79:THR:HG22	1.96	0.65
1:E:255:GLN:NE2	1:E:258:ASN:HD22	1.95	0.65
2:C:360:PGE:H42	1:E:293:LYS:NZ	2.12	0.65
1:F:2:SER:O	1:F:3:LEU:HB2	1.98	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:7:MSE:HE2	1:F:30:LEU:HD12	1.79	0.65
1:C:58:ASP:O	1:C:59:LEU:HB3	1.98	0.64
1:B:10:ILE:HG21	1:B:83:LEU:HD13	1.80	0.64
1:C:323:THR:OG1	1:C:326:GLN:HG3	1.97	0.64
1:D:7:MSE:HE3	1:D:30:LEU:HB3	1.78	0.63
1:B:155:ILE:HG13	1:B:181:LEU:HD21	1.78	0.63
1:B:27:ARG:HD3	1:B:308:ASP:OD1	1.97	0.63
1:B:294:LYS:HD3	1:C:255:GLN:HE21	1.63	0.63
1:E:50:GLU:O	1:E:51:LYS:HB2	1.97	0.63
1:C:285:ARG:HG3	1:C:285:ARG:HH11	1.64	0.63
1:B:123:PRO:HB2	1:B:125:GLN:HE21	1.62	0.63
1:A:18:ARG:NH1	1:A:261:LYS:NZ	2.46	0.63
1:E:206:GLU:H	1:E:206:GLU:CD	2.02	0.62
1:A:295:GLN:HG3	1:E:277:MSE:HE2	1.80	0.62
1:B:210:ASN:O	1:B:230:HIS:HD2	1.82	0.62
1:C:152:GLU:OE2	1:C:154:HIS:HE1	1.81	0.62
1:A:201:ASN:HA	1:A:210:ASN:OD1	1.99	0.62
1:C:101:CYS:SG	1:C:110:LEU:HD22	2.39	0.62
1:C:75:THR:HG23	1:C:79:THR:HG23	1.79	0.62
1:D:154:HIS:O	1:D:155:ILE:HD12	2.00	0.62
1:D:10:ILE:HD13	1:D:71:ILE:CG2	2.30	0.62
1:F:327:ALA:O	1:F:331:ILE:HD13	2.00	0.61
1:B:255:GLN:HE22	1:B:258:ASN:HD22	1.48	0.61
1:A:75:THR:HB	1:A:76:PRO:HD2	1.82	0.61
1:B:63:LEU:O	1:B:92:LYS:HE2	2.00	0.61
1:C:75:THR:HG21	1:C:83:LEU:CD1	2.30	0.61
1:D:155:ILE:O	1:D:155:ILE:HG22	1.99	0.61
1:F:132:ASP:OD1	1:F:238:ARG:HG2	2.01	0.61
1:D:13:GLY:HA3	1:D:14:LYS:HZ1	1.66	0.61
1:E:3:LEU:HD12	1:E:315:LYS:HZ1	1.65	0.61
1:F:210:ASN:O	1:F:230:HIS:HD2	1.83	0.61
1:A:85:LYS:O	1:A:89:LEU:HG	2.01	0.61
1:E:225:LYS:HD3	1:E:227:LYS:HD2	1.82	0.60
1:C:85:LYS:O	1:C:89:LEU:HD13	2.01	0.60
1:F:133:TYR:CE1	1:F:136:MSE:HE1	2.36	0.60
1:F:151:VAL:HG11	1:F:185:MSE:CE	2.32	0.60
1:C:168:PRO:HD2	1:C:171:ASN:ND2	2.16	0.60
1:A:276:PRO:HA	1:A:279:TYR:CD1	2.37	0.60
1:C:25:MSE:HB2	3:C:470:HOH:O	2.03	0.59
1:E:50:GLU:O	1:E:51:LYS:CB	2.50	0.59
1:F:75:THR:HG21	1:F:83:LEU:CD1	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:174:PHE:CE2	1:C:334:LEU:HD12	2.37	0.59
1:D:27:ARG:HD3	1:D:308:ASP:OD1	2.03	0.59
1:D:2:SER:HA	1:D:315:LYS:HE3	1.83	0.59
1:F:324:LYS:HD2	1:F:328:LEU:HD12	1.85	0.59
1:B:133:TYR:CE1	1:B:184:ARG:HB2	2.37	0.59
1:E:201:ASN:HA	1:E:210:ASN:OD1	2.03	0.59
1:F:104:LEU:O	1:F:108:GLU:HG3	2.01	0.59
1:F:237:PRO:CG	1:F:240:ILE:HD11	2.32	0.59
1:E:185:MSE:HA	1:E:185:MSE:HE3	1.84	0.59
1:C:7:MSE:CE	1:C:30:LEU:HB3	2.32	0.58
1:C:44:ALA:O	1:C:47:PRO:HD2	2.03	0.58
1:D:84:ALA:O	1:D:88:ILE:HG12	2.03	0.58
1:F:185:MSE:HE1	1:F:189:PHE:HE2	1.67	0.58
1:F:75:THR:HG23	1:F:79:THR:OG1	2.03	0.58
1:A:27:ARG:HD3	1:A:308:ASP:OD1	2.03	0.58
1:F:185:MSE:CE	1:F:189:PHE:HE2	2.16	0.58
1:C:36:PHE:CZ	1:C:59:LEU:HB2	2.38	0.58
1:B:201:ASN:HA	1:B:210:ASN:OD1	2.03	0.58
1:C:122:MSE:SE	1:C:320:GLN:HB2	2.53	0.58
1:D:18:ARG:HH12	1:D:261:LYS:NZ	2.01	0.58
1:E:196:THR:HB	1:E:215:ASP:HB2	1.86	0.58
1:F:201:ASN:HA	1:F:210:ASN:OD1	2.04	0.58
1:A:136:MSE:HE3	1:A:137:LYS:CA	2.34	0.58
1:E:286:ASN:ND2	1:E:290:ASP:HB2	2.19	0.58
1:C:25:MSE:HA	1:C:25:MSE:CE	2.33	0.58
1:D:185:MSE:CE	1:D:185:MSE:HA	2.31	0.58
1:D:182:MSE:HE1	1:D:333:ILE:HG21	1.85	0.58
1:D:216:LEU:HD23	1:D:216:LEU:N	2.18	0.57
1:E:182:MSE:CE	1:E:333:ILE:HG21	2.21	0.57
1:D:182:MSE:HE3	1:D:216:LEU:HD21	1.79	0.57
1:D:75:THR:HB	1:D:79:THR:HG21	1.85	0.57
1:E:27:ARG:NH2	3:E:512:HOH:O	2.38	0.57
1:F:182:MSE:HE2	1:F:216:LEU:CD2	2.24	0.57
1:A:136:MSE:HE1	1:A:188:LEU:CD2	2.33	0.57
1:B:152:GLU:OE2	1:B:154:HIS:HE1	1.87	0.57
1:C:26:ILE:O	1:C:26:ILE:HG22	2.05	0.57
1:B:182:MSE:O	1:B:186:ILE:HG12	2.03	0.57
1:E:309:ALA:O	1:E:313:THR:HG22	2.05	0.57
2:C:360:PGE:H42	1:E:293:LYS:HZ2	1.68	0.57
1:C:75:THR:HG21	1:C:83:LEU:HD12	1.87	0.57
1:D:10:ILE:HD13	1:D:71:ILE:HG23	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:46:ALA:HB3	1:E:47:PRO:HD3	1.87	0.57
1:C:65:ASP:O	1:C:92:LYS:NZ	2.38	0.57
1:E:182:MSE:HE2	1:E:216:LEU:HD11	1.87	0.56
1:A:3:LEU:O	1:A:3:LEU:HD22	2.06	0.56
1:E:182:MSE:HE3	1:E:216:LEU:HD21	1.84	0.56
1:E:68:ILE:O	1:E:92:LYS:HE3	2.05	0.56
1:A:137:LYS:O	1:A:141:GLU:HG3	2.04	0.56
1:B:293:LYS:NZ	2:B:360:PGE:H42	2.21	0.56
1:B:179:ILE:HD12	1:B:330:ASN:OD1	2.06	0.56
1:F:155:ILE:HD13	1:F:181:LEU:CD2	2.16	0.56
1:E:3:LEU:HD13	1:E:4:THR:H	1.70	0.56
1:A:102:ASP:OD1	1:A:106:HIS:HD2	1.89	0.56
1:A:75:THR:HB	1:A:76:PRO:CD	2.35	0.56
1:B:256:GLN:O	1:B:260:LEU:HD22	2.05	0.56
1:C:132:ASP:OD1	1:C:238:ARG:HG2	2.05	0.56
1:B:183:ASP:HA	1:B:330:ASN:ND2	2.20	0.56
1:C:34:THR:HG21	3:C:419:HOH:O	2.05	0.56
1:E:6:LYS:HD3	1:E:33:LYS:NZ	2.20	0.56
1:A:179:ILE:HG23	1:A:180:HIS:N	2.20	0.56
1:E:6:LYS:CG	1:E:33:LYS:HZ2	2.19	0.56
1:F:137:LYS:O	1:F:141:GLU:HG3	2.06	0.56
1:B:137:LYS:O	1:B:141:GLU:HG3	2.06	0.56
1:E:168:PRO:HB2	1:E:170:GLU:OE1	2.05	0.56
1:C:155:ILE:HG13	1:C:181:LEU:HD21	1.88	0.55
1:A:137:LYS:HE3	3:A:387:HOH:O	2.06	0.55
1:A:237:PRO:HG3	1:A:251:TYR:CZ	2.41	0.55
1:B:329:THR:O	1:B:333:ILE:HG12	2.06	0.55
1:D:75:THR:CB	1:D:79:THR:HG21	2.37	0.55
1:E:6:LYS:HD3	1:E:33:LYS:HD2	1.88	0.55
1:D:61:GLU:HG3	3:D:534:HOH:O	2.06	0.55
1:A:18:ARG:NH1	1:A:261:LYS:HZ3	2.04	0.55
1:B:350:GLU:HB3	3:B:481:HOH:O	2.06	0.55
1:C:306:TYR:O	1:C:310:VAL:HG23	2.07	0.55
1:C:48:PHE:HB3	1:C:53:VAL:CG1	2.28	0.55
1:D:18:ARG:NH1	1:D:261:LYS:NZ	2.55	0.55
1:F:266:PRO:HA	1:F:271:PHE:CD2	2.41	0.55
1:A:250:LYS:HE3	1:A:278:TYR:O	2.07	0.55
1:C:130:ASP:HB3	1:C:132:ASP:OD2	2.06	0.55
1:D:185:MSE:HG2	1:D:224:VAL:CG1	2.21	0.55
1:D:7:MSE:CE	1:D:30:LEU:HD12	2.36	0.55
1:D:18:ARG:NH1	1:D:261:LYS:HZ3	2.04	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:34:THR:OG1	1:F:62:LEU:HD13	2.05	0.55
1:B:264:ILE:N	1:B:264:ILE:HD12	2.22	0.55
1:D:137:LYS:O	1:D:141:GLU:HG3	2.07	0.55
1:F:179:ILE:HG23	1:F:180:HIS:N	2.22	0.54
1:F:40:VAL:O	1:F:41:ASN:CB	2.55	0.54
1:A:133:TYR:CE1	1:A:136:MSE:HE2	2.42	0.54
1:B:7:MSE:HE3	1:B:30:LEU:HB3	1.89	0.54
1:D:21:LEU:O	1:D:25:MSE:HB2	2.08	0.54
1:B:282:VAL:HG12	1:B:284:TYR:HD2	1.72	0.54
1:B:133:TYR:CZ	1:B:184:ARG:HB2	2.43	0.54
1:F:73:ILE:CG2	1:F:75:THR:HG22	2.38	0.54
1:D:40:VAL:HG23	3:D:377:HOH:O	2.08	0.54
1:F:58:ASP:O	1:F:59:LEU:HB3	2.08	0.53
1:B:31:GLU:HA	3:B:643:HOH:O	2.09	0.53
1:C:36:PHE:CE2	1:C:59:LEU:HD13	2.43	0.53
1:E:40:VAL:HG12	3:E:421:HOH:O	2.08	0.53
1:C:277:MSE:HE3	1:C:278:TYR:CE2	2.44	0.53
1:E:132:ASP:OD2	1:E:132:ASP:N	2.40	0.53
1:B:98:LYS:HE3	1:B:180:HIS:CE1	2.43	0.53
1:E:124:TYR:CZ	1:E:126:ASN:HB3	2.43	0.53
1:E:185:MSE:CA	1:E:185:MSE:HE3	2.39	0.53
1:F:9:PHE:HB2	1:F:35:ILE:HD12	1.90	0.53
1:C:185:MSE:HE1	1:C:189:PHE:HE2	1.73	0.53
1:E:88:ILE:HG22	1:E:117:LYS:HD3	1.91	0.53
1:F:124:TYR:CZ	1:F:126:ASN:HB3	2.43	0.53
1:B:294:LYS:CE	1:C:255:GLN:HE21	2.21	0.53
1:C:7:MSE:CE	1:C:30:LEU:HD12	2.35	0.53
1:B:48:PHE:O	1:B:50:GLU:O	2.26	0.53
1:F:133:TYR:CZ	1:F:184:ARG:HB2	2.44	0.53
1:C:198:ASP:O	1:C:212:PHE:HA	2.09	0.52
1:F:133:TYR:CD1	1:F:184:ARG:HD2	2.43	0.52
1:C:34:THR:CG2	1:C:68:ILE:HD11	2.37	0.52
1:B:124:TYR:CZ	1:B:126:ASN:HB3	2.45	0.52
1:B:50:GLU:C	1:B:52:GLY:H	2.13	0.52
1:B:182:MSE:CE	1:B:216:LEU:HD11	2.27	0.52
1:D:92:LYS:N	1:D:92:LYS:HD2	2.24	0.52
1:E:264:ILE:HD12	1:E:264:ILE:N	2.24	0.52
1:E:6:LYS:CB	1:E:33:LYS:HZ2	2.23	0.52
1:A:18:ARG:HH12	1:A:261:LYS:HZ2	1.57	0.52
1:D:48:PHE:HB3	1:D:53:VAL:HG21	1.90	0.52
1:F:237:PRO:HG3	1:F:251:TYR:CZ	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:283:THR:HG23	1:F:293:LYS:HD2	1.91	0.52
1:E:18:ARG:CZ	1:E:261:LYS:HE2	2.39	0.52
1:A:136:MSE:HE3	1:A:137:LYS:N	2.24	0.52
1:B:182:MSE:CE	1:B:333:ILE:HG21	2.39	0.52
1:E:21:LEU:HA	1:E:24:VAL:HG12	1.91	0.51
1:E:151:VAL:HG22	1:E:241:VAL:HG22	1.92	0.51
1:A:196:THR:OG1	1:A:215:ASP:HB2	2.10	0.51
1:D:18:ARG:HH12	1:D:261:LYS:HZ2	1.56	0.51
1:F:2:SER:O	1:F:3:LEU:CB	2.58	0.51
1:F:60:ASN:O	1:F:64:THR:HB	2.10	0.51
1:E:31:GLU:HB3	1:E:33:LYS:NZ	2.13	0.51
1:A:18:ARG:HH12	1:A:261:LYS:NZ	2.07	0.51
1:C:133:TYR:CD1	1:C:184:ARG:HD2	2.46	0.51
1:D:211:TYR:C	1:D:211:TYR:CD2	2.83	0.51
1:E:18:ARG:NH1	1:E:261:LYS:HE2	2.26	0.51
1:E:3:LEU:HB3	1:E:315:LYS:NZ	2.25	0.51
1:F:58:ASP:CB	1:F:61:GLU:HG3	2.41	0.51
1:A:87:ALA:HB3	1:A:94:VAL:HG11	1.93	0.51
1:B:104:LEU:HG	1:B:108:GLU:OE1	2.10	0.51
1:B:183:ASP:HA	1:B:330:ASN:HD21	1.76	0.51
1:E:196:THR:CG2	3:E:599:HOH:O	2.58	0.51
1:E:198:ASP:O	1:E:212:PHE:HA	2.11	0.51
1:B:285:ARG:HA	1:B:290:ASP:O	2.11	0.51
1:B:323:THR:OG1	1:B:326:GLN:HG3	2.11	0.51
1:C:196:THR:O	1:C:214:VAL:HG13	2.11	0.51
1:E:213:ASP:HA	1:E:227:LYS:HG2	1.93	0.51
1:C:98:LYS:HG3	3:C:466:HOH:O	2.11	0.51
1:C:102:ASP:OD2	1:C:106:HIS:HD2	1.94	0.50
1:C:185:MSE:HG3	1:C:224:VAL:CG1	2.41	0.50
1:C:7:MSE:CE	1:C:24:VAL:HG21	2.41	0.50
1:D:201:ASN:HA	1:D:210:ASN:OD1	2.12	0.50
1:B:50:GLU:O	1:B:51:LYS:HB2	2.10	0.50
1:E:155:ILE:HG13	1:E:181:LEU:HD21	1.91	0.50
1:B:25:MSE:HA	1:B:25:MSE:CE	2.40	0.50
1:E:75:THR:CG2	1:E:79:THR:HG23	2.41	0.50
1:C:295:GLN:HG3	1:F:277:MSE:HE2	1.93	0.50
1:A:214:VAL:HB	1:A:226:VAL:CG2	2.41	0.50
1:C:11:GLY:HA3	1:C:74:CYS:O	2.12	0.50
1:C:192:PRO:O	1:C:348:LEU:HG	2.11	0.50
1:C:7:MSE:HE3	1:C:24:VAL:HG21	1.93	0.50
1:A:70:LEU:HD11	1:A:95:ILE:HG12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:LYS:CD	1:C:255:GLN:HE21	2.24	0.49
1:B:48:PHE:HB3	1:B:53:VAL:HG21	1.94	0.49
1:E:306:TYR:O	1:E:310:VAL:HG23	2.12	0.49
2:C:360:PGE:H12	1:D:233:ALA:O	2.12	0.49
1:D:48:PHE:HB3	1:D:53:VAL:CG2	2.42	0.49
1:E:137:LYS:O	1:E:141:GLU:HG3	2.11	0.49
1:A:133:TYR:CE1	1:A:184:ARG:HB2	2.48	0.49
1:E:7:MSE:CE	1:E:30:LEU:HB3	2.36	0.49
1:F:102:ASP:OD1	1:F:106:HIS:HD2	1.94	0.49
1:F:133:TYR:CE1	1:F:184:ARG:HB2	2.46	0.49
1:A:265:MSE:HB2	1:A:267:ASP:OD2	2.13	0.49
1:B:198:ASP:O	1:B:212:PHE:HA	2.13	0.49
1:E:182:MSE:HE2	1:E:216:LEU:HD21	1.91	0.49
1:A:198:ASP:O	1:A:212:PHE:HA	2.13	0.49
1:C:282:VAL:HG13	1:C:296:ILE:HD13	1.93	0.49
1:A:211:TYR:CD2	1:A:211:TYR:C	2.86	0.49
1:F:38:LEU:HD22	1:F:38:LEU:H	1.78	0.49
1:E:179:ILE:HG23	1:E:180:HIS:N	2.28	0.48
1:E:347:HIS:HE1	1:E:350:GLU:OE2	1.95	0.48
1:E:185:MSE:HE2	1:E:185:MSE:HA	1.94	0.48
1:E:205:SER:HB3	1:F:220:SER:OG	2.13	0.48
1:F:285:ARG:HH11	1:F:285:ARG:HG3	1.77	0.48
1:A:182:MSE:HG2	1:A:226:VAL:HG11	1.95	0.48
1:A:145:LEU:HD22	1:A:246:GLY:C	2.34	0.48
1:A:9:PHE:HB2	1:A:35:ILE:HD13	1.94	0.48
1:F:155:ILE:HG22	1:F:155:ILE:O	2.14	0.48
2:C:360:PGE:H22	1:E:293:LYS:NZ	2.28	0.48
1:F:347:HIS:HB2	3:F:602:HOH:O	2.12	0.48
1:D:32:VAL:CG1	1:D:35:ILE:HD11	2.44	0.48
1:A:275:SER:HB3	1:D:295:GLN:HB2	1.96	0.48
1:B:75:THR:HB	1:B:76:PRO:HD2	1.94	0.48
1:C:266:PRO:HA	1:C:271:PHE:CD2	2.49	0.48
1:E:179:ILE:C	1:E:179:ILE:HD13	2.34	0.48
1:A:136:MSE:HE3	1:A:137:LYS:HB2	1.95	0.48
1:A:166:GLN:HG2	1:A:206:GLU:HG2	1.96	0.48
1:B:34:THR:HB	1:B:62:LEU:HD13	1.96	0.48
1:E:277:MSE:HE3	1:E:278:TYR:CE2	2.48	0.48
1:B:120:VAL:HG12	1:B:122:MSE:HG3	1.96	0.47
1:C:185:MSE:CE	1:C:189:PHE:HE2	2.27	0.47
1:D:327:ALA:O	1:D:331:ILE:HG12	2.14	0.47
1:F:36:PHE:CE1	1:F:59:LEU:HB2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:46:ALA:HB3	1:F:47:PRO:HD3	1.94	0.47
1:C:242:HIS:CE1	1:D:232:VAL:HG13	2.49	0.47
1:D:132:ASP:OD2	1:D:132:ASP:N	2.48	0.47
1:E:165:GLU:HG2	3:E:554:HOH:O	2.14	0.47
1:E:324:LYS:HG3	1:E:325:GLU:OE2	2.14	0.47
1:F:137:LYS:HG3	1:F:188:LEU:HD11	1.96	0.47
1:B:123:PRO:HD2	1:B:322:VAL:HG11	1.94	0.47
1:B:166:GLN:NE2	3:B:510:HOH:O	2.47	0.47
1:B:211:TYR:CD2	1:B:211:TYR:C	2.88	0.47
1:B:48:PHE:O	1:B:53:VAL:HG22	2.13	0.47
1:C:21:LEU:HA	1:C:24:VAL:CG1	2.45	0.47
1:D:182:MSE:CE	1:D:216:LEU:CD2	2.73	0.47
1:A:65:ASP:OD1	1:A:67:GLU:HB2	2.15	0.47
1:B:292:ILE:N	1:B:292:ILE:HD12	2.30	0.47
1:D:5:VAL:HG23	1:D:311:TYR:HD1	1.80	0.47
1:D:38:LEU:HD23	3:D:776:HOH:O	2.14	0.47
1:B:294:LYS:HD3	1:C:255:GLN:NE2	2.29	0.47
1:A:250:LYS:HD3	1:A:251:TYR:N	2.30	0.47
1:C:279:TYR:OH	1:C:297:LYS:HE3	2.14	0.47
1:E:282:VAL:HG13	1:E:296:ILE:CD1	2.44	0.47
1:E:87:ALA:HB3	1:E:94:VAL:HG11	1.97	0.47
1:B:101:CYS:SG	1:B:110:LEU:HD22	2.55	0.47
1:C:163:ILE:HD12	1:C:210:ASN:HB2	1.97	0.47
1:C:88:ILE:O	1:C:90:ALA:O	2.33	0.47
1:C:232:VAL:HG13	1:D:242:HIS:CE1	2.49	0.47
1:D:32:VAL:HG11	1:D:35:ILE:HD11	1.96	0.47
1:D:198:ASP:O	1:D:212:PHE:HA	2.15	0.47
1:D:350:GLU:HB2	3:D:548:HOH:O	2.14	0.47
1:E:79:THR:OG1	1:E:79:THR:O	2.33	0.47
1:E:10:ILE:HG21	1:E:83:LEU:HD13	1.97	0.47
1:C:234:SER:HB3	1:D:249:ILE:CD1	2.45	0.47
1:F:255:GLN:NE2	1:F:258:ASN:HD22	2.11	0.47
1:A:98:LYS:HD3	1:A:179:ILE:HG21	1.96	0.46
1:A:185:MSE:HG3	1:A:224:VAL:HG11	1.96	0.46
1:D:127:ARG:NH1	1:D:130:ASP:OD2	2.48	0.46
1:E:255:GLN:HE22	1:E:258:ASN:ND2	2.07	0.46
1:E:62:LEU:HD21	1:E:71:ILE:HD12	1.97	0.46
1:A:350:GLU:CG	1:A:350:GLU:O	2.58	0.46
1:F:250:LYS:NZ	1:F:274:ASP:OD2	2.48	0.46
1:A:242:HIS:CE1	1:B:232:VAL:HG13	2.50	0.46
1:D:169:LYS:HG2	3:D:576:HOH:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:122:MSE:SE	1:E:320:GLN:HB2	2.65	0.46
1:F:40:VAL:O	1:F:41:ASN:HB3	2.16	0.46
1:F:73:ILE:HG23	1:F:75:THR:HG22	1.97	0.46
1:B:22:PRO:HG3	1:B:265:MSE:HE1	1.97	0.46
1:D:325:GLU:HG2	3:D:388:HOH:O	2.16	0.46
1:B:191:ARG:HB2	3:B:418:HOH:O	2.16	0.46
1:D:323:THR:OG1	1:D:326:GLN:HG3	2.15	0.46
1:B:264:ILE:H	1:B:264:ILE:HD12	1.81	0.46
1:C:211:TYR:C	1:C:211:TYR:CD2	2.88	0.46
1:D:79:THR:HG23	1:D:83:LEU:HD12	1.97	0.46
1:C:26:ILE:HD12	1:C:267:ASP:OD2	2.15	0.46
1:A:212:PHE:CE1	1:A:228:THR:HB	2.50	0.46
1:B:127:ARG:HD2	1:B:130:ASP:OD2	2.16	0.46
1:B:152:GLU:OE2	1:B:154:HIS:CE1	2.69	0.46
1:C:210:ASN:O	1:C:230:HIS:HD2	1.99	0.46
1:C:5:VAL:HG23	1:C:311:TYR:CD1	2.51	0.46
1:D:14:LYS:H	1:D:14:LYS:HZ2	1.63	0.46
1:E:7:MSE:CE	1:E:24:VAL:HG21	2.46	0.46
1:B:214:VAL:HB	1:B:226:VAL:CG2	2.45	0.46
1:B:64:THR:O	1:B:66:PRO:HD3	2.16	0.46
1:D:151:VAL:HB	1:D:224:VAL:HG22	1.98	0.45
1:E:166:GLN:HG3	3:E:684:HOH:O	2.15	0.45
1:E:76:PRO:O	1:E:79:THR:CG2	2.64	0.45
1:C:21:LEU:HA	1:C:24:VAL:HG12	1.97	0.45
1:F:255:GLN:HE22	1:F:258:ASN:HD22	1.64	0.45
1:B:142:GLN:NE2	1:C:264:ILE:HD12	2.31	0.45
1:B:195:VAL:HG22	1:B:216:LEU:HD22	1.97	0.45
1:C:45:ALA:O	1:C:49:LYS:HD3	2.16	0.45
1:D:123:PRO:CG	1:D:125:GLN:HE21	2.29	0.45
1:D:77:ALA:C	1:D:79:THR:H	2.19	0.45
1:E:282:VAL:HG13	1:E:296:ILE:HD13	1.98	0.45
1:C:154:HIS:HD2	1:C:156:ASP:OD2	1.98	0.45
1:C:151:VAL:HG22	1:C:241:VAL:HG13	1.99	0.45
1:A:151:VAL:HG11	1:A:185:MSE:CE	2.46	0.45
1:A:232:VAL:HG13	1:B:242:HIS:CE1	2.52	0.45
1:E:14:LYS:NZ	1:E:18:ARG:NH1	2.65	0.45
1:F:58:ASP:HB3	1:F:61:GLU:HG3	1.98	0.45
1:A:286:ASN:ND2	1:A:290:ASP:HB2	2.31	0.45
1:E:165:GLU:O	1:E:165:GLU:HG3	2.16	0.45
1:F:27:ARG:NH2	3:F:698:HOH:O	2.49	0.45
1:E:3:LEU:HD13	1:E:4:THR:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:285:ARG:HD2	1:D:291:TRP:CZ2	2.51	0.45
1:D:2:SER:HA	1:D:315:LYS:CE	2.47	0.45
1:F:323:THR:OG1	1:F:326:GLN:HG3	2.16	0.45
1:F:211:TYR:CD2	1:F:211:TYR:C	2.90	0.45
1:B:187:ALA:HA	1:B:326:GLN:NE2	2.32	0.45
1:D:212:PHE:CE1	1:D:228:THR:HB	2.52	0.45
1:F:185:MSE:HG3	1:F:224:VAL:HG11	1.98	0.45
1:C:133:TYR:CE1	1:C:184:ARG:HB2	2.52	0.44
1:F:22:PRO:HG3	1:F:265:MSE:HE1	1.98	0.44
1:A:132:ASP:HA	1:A:250:LYS:HZ2	1.83	0.44
1:E:179:ILE:HD13	1:E:179:ILE:O	2.18	0.44
1:E:27:ARG:NH2	1:E:304:GLY:HA3	2.32	0.44
1:E:195:VAL:HG23	1:E:348:LEU:HD21	1.99	0.44
1:F:101:CYS:SG	1:F:110:LEU:HD12	2.56	0.44
1:A:101:CYS:SG	1:A:107:ALA:HA	2.57	0.44
1:D:124:TYR:CZ	1:D:126:ASN:HB3	2.52	0.44
1:F:133:TYR:CD1	1:F:136:MSE:CE	3.00	0.44
1:A:155:ILE:HG13	1:A:181:LEU:HD21	1.99	0.44
1:A:18:ARG:NH1	1:A:261:LYS:HZ2	2.12	0.44
1:B:349:LYS:HG2	1:B:350:GLU:HG3	2.00	0.44
1:F:65:ASP:HA	1:F:66:PRO:HD3	1.73	0.44
1:A:132:ASP:N	1:A:132:ASP:OD1	2.50	0.44
1:C:166:GLN:N	1:C:166:GLN:OE1	2.50	0.44
1:D:155:ILE:CG2	1:D:177:LEU:HD13	2.48	0.44
1:F:151:VAL:HG11	1:F:185:MSE:HE2	1.99	0.44
1:B:29:THR:C	1:B:30:LEU:HD12	2.38	0.44
1:B:333:ILE:HD11	1:B:348:LEU:HD11	2.00	0.44
1:A:286:ASN:HD21	1:A:290:ASP:HB2	1.83	0.44
1:D:255:GLN:NE2	1:D:258:ASN:HD22	2.16	0.44
1:F:132:ASP:OD2	1:F:132:ASP:N	2.51	0.44
1:D:75:THR:OG1	1:D:79:THR:HG21	2.18	0.43
1:E:136:MSE:HE3	1:E:136:MSE:HB3	1.80	0.43
1:E:285:ARG:HA	1:E:290:ASP:O	2.18	0.43
1:E:3:LEU:HB3	1:E:315:LYS:HZ3	1.83	0.43
1:D:155:ILE:HD13	1:D:181:LEU:CD2	2.37	0.43
1:D:270:GLY:HA2	1:D:273:GLU:OE2	2.18	0.43
1:F:324:LYS:HG3	1:F:325:GLU:N	2.33	0.43
1:A:102:ASP:OD1	1:A:102:ASP:N	2.51	0.43
1:D:191:ARG:NE	1:D:350:GLU:OE1	2.49	0.43
1:E:14:LYS:HZ3	1:E:18:ARG:NH1	2.16	0.43
1:E:14:LYS:NZ	1:E:18:ARG:HH12	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:GLN:HE21	1:C:264:ILE:HD12	1.83	0.43
1:F:7:MSE:CE	1:F:30:LEU:HB3	2.38	0.43
1:A:133:TYR:CZ	1:A:184:ARG:HB2	2.53	0.43
1:B:196:THR:HG22	1:B:345:VAL:HG22	2.01	0.43
1:B:8:GLY:HA3	1:B:62:LEU:HD11	2.01	0.43
1:D:155:ILE:HG21	1:D:177:LEU:HD13	2.01	0.43
1:A:169:LYS:HG2	3:A:700:HOH:O	2.18	0.43
1:A:221:LYS:HD3	3:B:644:HOH:O	2.18	0.43
1:A:293:LYS:NZ	2:F:360:PGE:H4	2.33	0.43
1:A:46:ALA:N	1:A:47:PRO:HD2	2.33	0.43
1:B:140:VAL:HG22	1:B:148:ILE:CD1	2.48	0.43
1:B:241:VAL:HB	1:B:248:PHE:HB3	1.99	0.43
1:D:151:VAL:HA	1:D:240:ILE:O	2.19	0.43
1:E:75:THR:HG21	1:E:83:LEU:CD1	2.42	0.43
1:B:25:MSE:HE1	3:B:643:HOH:O	2.19	0.43
1:C:21:LEU:HB3	3:C:470:HOH:O	2.17	0.43
1:C:90:ALA:O	1:C:92:LYS:N	2.47	0.43
1:E:5:VAL:HG21	1:E:314:LEU:HD11	2.01	0.43
1:F:166:GLN:HA	1:F:207:ALA:HA	2.00	0.43
1:A:124:TYR:CZ	1:A:126:ASN:HB3	2.54	0.43
1:C:227:LYS:HG2	3:C:387:HOH:O	2.19	0.43
1:C:75:THR:HG23	1:C:79:THR:HG21	1.98	0.43
1:D:64:THR:O	1:D:66:PRO:HD3	2.19	0.43
1:E:323:THR:OG1	1:E:326:GLN:HG3	2.19	0.43
1:F:237:PRO:HG2	1:F:240:ILE:CD1	2.42	0.43
1:F:34:THR:HA	1:F:54:ASN:O	2.19	0.43
1:A:58:ASP:OD2	1:A:61:GLU:HB3	2.18	0.43
1:B:27:ARG:NH2	1:B:304:GLY:HA3	2.33	0.43
1:C:48:PHE:C	1:C:53:VAL:HG12	2.39	0.43
1:D:14:LYS:H	1:D:14:LYS:HZ1	1.64	0.43
1:D:257:GLU:O	1:D:261:LYS:HG2	2.19	0.43
1:F:198:ASP:O	1:F:212:PHE:HA	2.19	0.43
1:B:30:LEU:CD2	1:B:307:TYR:HB3	2.46	0.42
1:A:62:LEU:HD12	1:A:68:ILE:HD12	2.01	0.42
1:C:123:PRO:HG2	1:C:322:VAL:HG11	2.01	0.42
1:C:82:ASP:O	1:C:86:GLN:HG3	2.19	0.42
1:E:182:MSE:HE1	1:E:216:LEU:HD21	1.94	0.42
1:B:122:MSE:SE	1:B:320:GLN:HB2	2.69	0.42
1:F:285:ARG:HA	1:F:290:ASP:O	2.20	0.42
1:F:174:PHE:CE2	1:F:334:LEU:HD12	2.53	0.42
1:F:75:THR:CG2	1:F:79:THR:OG1	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:59:LEU:O	1:B:63:LEU:HD13	2.20	0.42
3:A:413:HOH:O	1:D:297:LYS:HG3	2.19	0.42
1:E:133:TYR:CD1	1:E:136:MSE:CE	3.03	0.42
3:E:431:HOH:O	1:F:221:LYS:HG3	2.19	0.42
1:E:76:PRO:O	1:E:79:THR:HG22	2.20	0.42
1:C:120:VAL:HG12	1:C:122:MSE:HG3	2.02	0.42
1:D:130:ASP:HB3	1:D:132:ASP:OD2	2.20	0.42
1:F:310:VAL:HG23	3:F:386:HOH:O	2.20	0.42
1:A:293:LYS:NZ	2:F:360:PGE:H62	2.34	0.42
1:A:136:MSE:O	1:A:140:VAL:HG23	2.18	0.42
1:A:295:GLN:HG3	1:E:277:MSE:CE	2.48	0.42
1:A:211:TYR:CD2	1:A:212:PHE:N	2.88	0.42
1:B:10:ILE:CG2	1:B:83:LEU:HD13	2.46	0.42
1:C:87:ALA:O	1:C:90:ALA:O	2.38	0.42
1:E:89:LEU:HD12	1:E:89:LEU:HA	1.90	0.42
1:D:75:THR:HB	1:D:76:PRO:HD2	2.02	0.42
1:A:179:ILE:CG2	1:A:180:HIS:N	2.83	0.42
1:A:266:PRO:HA	1:A:271:PHE:CD2	2.55	0.42
1:A:292:ILE:HD12	1:A:292:ILE:N	2.35	0.42
1:B:248:PHE:HD1	1:B:282:VAL:HG22	1.83	0.42
1:C:25:MSE:HE1	1:C:32:VAL:HB	2.02	0.42
1:D:286:ASN:HD21	1:D:290:ASP:HB2	1.83	0.42
1:D:308:ASP:HA	3:D:400:HOH:O	2.20	0.42
1:E:101:CYS:SG	1:E:110:LEU:HD12	2.59	0.42
1:E:133:TYR:CE1	1:E:136:MSE:HE1	2.54	0.42
1:E:75:THR:OG1	1:E:76:PRO:HD2	2.20	0.42
1:C:124:TYR:CZ	1:C:126:ASN:HB3	2.54	0.41
1:C:13:GLY:HA3	1:C:14:LYS:HE2	2.02	0.41
1:E:185:MSE:CA	1:E:185:MSE:CE	2.92	0.41
1:B:214:VAL:HB	1:B:226:VAL:HG23	2.03	0.41
1:E:294:LYS:HG2	1:E:295:GLN:N	2.35	0.41
1:E:315:LYS:HA	1:E:315:LYS:HD2	1.79	0.41
1:E:10:ILE:HD12	1:E:73:ILE:CD1	2.51	0.41
1:C:269:PRO:HD2	3:C:404:HOH:O	2.18	0.41
1:D:234:SER:HA	1:D:235:PRO:HD2	1.92	0.41
1:E:242:HIS:CE1	1:F:232:VAL:HG13	2.55	0.41
1:A:221:LYS:CD	3:B:644:HOH:O	2.67	0.41
1:B:44:ALA:O	1:B:47:PRO:HD2	2.20	0.41
1:B:294:LYS:HE2	1:C:255:GLN:HE21	1.85	0.41
1:A:234:SER:HA	1:A:235:PRO:HD3	1.82	0.41
1:A:33:LYS:HE2	1:A:67:GLU:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:185:MSE:CE	1:B:189:PHE:HE2	2.34	0.41
1:C:75:THR:CG2	1:C:79:THR:HG23	2.50	0.41
1:F:38:LEU:HD22	1:F:38:LEU:N	2.35	0.41
1:A:163:ILE:HD13	3:A:404:HOH:O	2.19	0.41
1:C:46:ALA:O	1:C:49:LYS:HB2	2.21	0.41
1:D:133:TYR:CZ	1:D:184:ARG:HB2	2.55	0.41
1:F:47:PRO:O	1:F:51:LYS:HE3	2.20	0.41
1:F:34:THR:HG23	1:F:68:ILE:HD11	2.03	0.41
1:B:95:ILE:HD11	1:B:310:VAL:HG21	2.02	0.41
1:C:132:ASP:OD2	1:C:132:ASP:N	2.54	0.41
1:C:14:LYS:HE3	3:C:415:HOH:O	2.21	0.41
1:E:133:TYR:HE1	1:E:185:MSE:HE1	1.84	0.41
1:E:163:ILE:HD12	1:E:210:ASN:CB	2.48	0.41
1:F:185:MSE:CE	1:F:189:PHE:CE2	3.01	0.41
1:A:276:PRO:HA	1:A:279:TYR:CE1	2.56	0.41
1:C:234:SER:HA	1:C:235:PRO:HD3	1.80	0.41
1:C:34:THR:HA	1:C:54:ASN:O	2.21	0.41
1:E:116:GLU:HG3	1:E:117:LYS:N	2.35	0.41
1:B:140:VAL:HG22	1:B:148:ILE:HD13	2.02	0.41
1:C:285:ARG:HA	1:C:290:ASP:O	2.21	0.41
2:C:360:PGE:H42	2:C:360:PGE:H6	1.89	0.41
1:A:255:GLN:HG3	1:D:294:LYS:CD	2.50	0.41
1:D:38:LEU:CD2	3:D:776:HOH:O	2.67	0.41
1:E:247:SER:OG	1:F:233:ALA:HB3	2.21	0.41
1:E:6:LYS:CD	1:E:33:LYS:NZ	2.83	0.41
1:E:6:LYS:HD3	1:E:33:LYS:HZ2	1.86	0.41
1:F:27:ARG:HD3	1:F:308:ASP:OD1	2.20	0.41
1:B:333:ILE:CD1	1:B:348:LEU:HD11	2.51	0.41
1:D:330:ASN:HA	1:D:330:ASN:HD22	1.68	0.41
1:D:55:PHE:N	1:D:55:PHE:CD2	2.89	0.41
1:F:58:ASP:O	1:F:59:LEU:CB	2.69	0.41
1:A:122:MSE:HE1	1:A:310:VAL:HG22	2.02	0.41
1:C:206:GLU:H	1:C:206:GLU:CD	2.24	0.41
1:E:195:VAL:HG22	1:E:216:LEU:CD2	2.51	0.41
1:E:256:GLN:O	1:E:260:LEU:HD22	2.21	0.41
1:E:48:PHE:O	1:E:49:LYS:C	2.59	0.41
1:F:248:PHE:CD1	1:F:282:VAL:HG22	2.56	0.41
1:F:274:ASP:HB3	1:F:298:THR:HB	2.03	0.41
1:B:14:LYS:HE3	1:B:14:LYS:HB2	1.83	0.40
1:C:65:ASP:HA	1:C:66:PRO:HD3	1.89	0.40
1:E:211:TYR:CD2	1:E:211:TYR:C	2.94	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:44:ALA:HB1	3:F:765:HOH:O	2.21	0.40
1:C:25:MSE:SE	3:C:470:HOH:O	2.89	0.40
1:E:133:TYR:CE1	1:E:185:MSE:HE1	2.56	0.40
1:E:62:LEU:HD11	1:E:71:ILE:HD11	2.03	0.40
1:F:59:LEU:HD13	1:F:63:LEU:HD22	2.01	0.40
1:B:282:VAL:HG12	1:B:284:TYR:CD2	2.55	0.40
1:E:3:LEU:CD1	1:E:315:LYS:HZ1	2.34	0.40
1:F:122:MSE:SE	1:F:320:GLN:HB2	2.72	0.40
1:F:332:GLU:OE2	1:F:348:LEU:HD13	2.21	0.40
1:A:34:THR:HA	1:A:54:ASN:O	2.21	0.40
1:C:15:SER:HB3	1:C:97:GLU:OE2	2.21	0.40
1:E:28:GLU:HG2	3:E:495:HOH:O	2.22	0.40
1:F:185:MSE:HE3	1:F:189:PHE:CE2	2.56	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	346/359 (96%)	329 (95%)	16 (5%)	1 (0%)	43	52
1	B	346/359 (96%)	326 (94%)	19 (6%)	1 (0%)	43	52
1	C	345/359 (96%)	327 (95%)	13 (4%)	5 (1%)	12	11
1	D	347/359 (97%)	329 (95%)	17 (5%)	1 (0%)	43	52
1	E	347/359 (97%)	328 (94%)	17 (5%)	2 (1%)	27	32
1	F	347/359 (97%)	326 (94%)	18 (5%)	3 (1%)	19	22
All	All	2078/2154 (96%)	1965 (95%)	100 (5%)	13 (1%)	27	32

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	75	THR
1	F	41	ASN
1	A	155	ILE
1	B	155	ILE
1	E	51	LYS
1	F	42	GLU
1	D	78	HIS
1	F	3	LEU
1	C	37	ASP
1	C	91	GLY
1	C	155	ILE
1	E	78	HIS
1	C	76	PRO

### 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	297/298 (100%)	286 (96%)	11 (4%)	37	49
1	B	297/298 (100%)	282 (95%)	15 (5%)	26	34
1	C	296/298 (99%)	282 (95%)	14 (5%)	29	38
1	D	298/298 (100%)	278 (93%)	20 (7%)	18	22
1	E	298/298 (100%)	276 (93%)	22 (7%)	15	18
1	F	298/298 (100%)	283 (95%)	15 (5%)	27	35
All	All	1784/1788 (100%)	1687 (95%)	97 (5%)	24	32

All (97) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	14	LYS
1	A	27	ARG
1	A	42	GLU
1	A	60	ASN
1	A	132	ASP

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Mol	Chain	Res	Type
1	A	136	MSE
1	A	165	GLU
1	A	193	ASP
1	A	277	MSE
1	A	350	GLU
1	B	3	LEU
1	B	25	MSE
1	B	27	ARG
1	B	42	GLU
1	B	43	LYS
1	B	50	GLU
1	B	68	ILE
1	B	108	GLU
1	B	110	LEU
1	B	193	ASP
1	B	260	LEU
1	B	285	ARG
1	B	330	ASN
1	B	334	LEU
1	B	335	GLU
1	C	14	LYS
1	C	25	MSE
1	C	33	LYS
1	C	34	THR
1	C	38	LEU
1	C	50	GLU
1	C	62	LEU
1	C	74	CYS
1	C	165	GLU
1	C	166	GLN
1	C	193	ASP
1	C	196	THR
1	C	260	LEU
1	C	335	GLU
1	D	3	LEU
1	D	14	LYS
1	D	18	ARG
1	D	60	ASN
1	D	61	GLU
1	D	62	LEU
1	D	69	GLU
1	D	79	THR

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Mol	Chain	Res	Type
1	D	82	ASP
1	D	92	LYS
1	D	136	MSE
1	D	185	MSE
1	D	193	ASP
1	D	260	LEU
1	D	261	LYS
1	D	297	LYS
1	D	305	ARG
1	D	316	ASN
1	D	330	ASN
1	D	348	LEU
1	E	3	LEU
1	E	24	VAL
1	E	27	ARG
1	E	33	LYS
1	E	53	VAL
1	E	69	GLU
1	E	89	LEU
1	E	98	LYS
1	E	116	GLU
1	E	117	LYS
1	E	153	THR
1	E	179	ILE
1	E	185	MSE
1	E	193	ASP
1	E	196	THR
1	E	206	GLU
1	E	253	GLU
1	E	260	LEU
1	E	313	THR
1	E	324	LYS
1	E	339	LEU
1	E	351	ASN
1	F	3	LEU
1	F	27	ARG
1	F	34	THR
1	F	42	GLU
1	F	51	LYS
1	F	53	VAL
1	F	98	LYS
1	F	188	LEU

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Mol	Chain	Res	Type
1	F	196	THR
1	F	221	LYS
1	F	260	LEU
1	F	324	LYS
1	F	325	GLU
1	F	330	ASN
1	F	350	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	106	HIS
1	A	180	HIS
1	A	194	GLN
1	A	255	GLN
1	A	258	ASN
1	A	316	ASN
1	A	330	ASN
1	B	60	ASN
1	B	86	GLN
1	B	125	GLN
1	B	142	GLN
1	B	154	HIS
1	B	166	GLN
1	B	230	HIS
1	B	255	GLN
1	B	288	ASN
1	B	330	ASN
1	C	106	HIS
1	C	154	HIS
1	C	171	ASN
1	C	194	GLN
1	C	217	HIS
1	C	230	HIS
1	C	255	GLN
1	C	258	ASN
1	C	288	ASN
1	C	316	ASN
1	D	115	GLN
1	D	125	GLN
1	D	180	HIS
1	D	194	GLN

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Mol	Chain	Res	Type
1	D	255	GLN
1	D	330	ASN
1	E	115	GLN
1	E	125	GLN
1	E	154	HIS
1	E	180	HIS
1	E	255	GLN
1	E	316	ASN
1	E	347	HIS
1	F	106	HIS
1	F	125	GLN
1	F	194	GLN
1	F	230	HIS
1	F	255	GLN
1	F	288	ASN
1	F	316	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](#)

3 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
2	PGE	B	360	-	9,9,9	0.63	0	8,8,8	1.39	2 (25%)
2	PGE	C	360	-	9,9,9	0.64	0	8,8,8	1.45	2 (25%)
2	PGE	F	360	-	9,9,9	0.74	0	8,8,8	1.43	2 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PGE	B	360	-	-	0/7/7/7	0/0/0/0
2	PGE	C	360	-	-	0/7/7/7	0/0/0/0
2	PGE	F	360	-	-	0/7/7/7	0/0/0/0

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	360	PGE	C3-O2-C2	2.31	123.42	113.30
2	C	360	PGE	C3-O2-C2	2.40	123.84	113.30
2	F	360	PGE	C5-O3-C4	2.41	123.86	113.30
2	B	360	PGE	C5-O3-C4	2.49	124.21	113.30
2	C	360	PGE	C5-O3-C4	2.52	124.36	113.30
2	F	360	PGE	C3-O2-C2	2.60	124.69	113.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	360	PGE	1	0
2	C	360	PGE	5	0
2	F	360	PGE	2	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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	340/359 (94%)	-0.30	1 (0%) 93 95	12, 25, 46, 57	0
1	B	340/359 (94%)	-0.31	1 (0%) 93 95	10, 22, 40, 58	0
1	C	339/359 (94%)	-0.06	5 (1%) 73 71	12, 27, 47, 61	0
1	D	341/359 (94%)	-0.30	0 100 100	11, 22, 40, 57	0
1	E	341/359 (94%)	-0.29	4 (1%) 79 77	9, 22, 40, 64	0
1	F	341/359 (94%)	-0.38	1 (0%) 93 95	11, 19, 36, 65	0
All	All	2042/2154 (94%)	-0.27	12 (0%) 89 90	9, 22, 43, 65	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	52	GLY	4.1
1	E	41	ASN	3.2
1	C	51	LYS	3.2
1	B	43	LYS	3.1
1	E	43	LYS	2.9
1	A	350	GLU	2.8
1	C	53	VAL	2.7
1	E	40	VAL	2.7
1	F	42	GLU	2.6
1	C	91	GLY	2.3
1	E	78	HIS	2.2
1	C	76	PRO	2.1

### 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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PGE	F	360	10/10	0.84	0.22	30,31,37,39	0
2	PGE	C	360	10/10	0.91	0.18	31,34,35,37	0
2	PGE	B	360	10/10	0.91	0.18	31,32,35,36	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.