



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 05:21 am GMT

PDB ID : 3KOX  
Title : Crystal Structure of ornithine 4,5 aminomutase in complex with 2,4-diaminobutyrate (Anaerobic)  
Authors : Wolthers, K.R.; Levy, C.W.; Scrutton, N.S.; Leys, D.  
Deposited on : 2009-11-14  
Resolution : 2.40 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

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

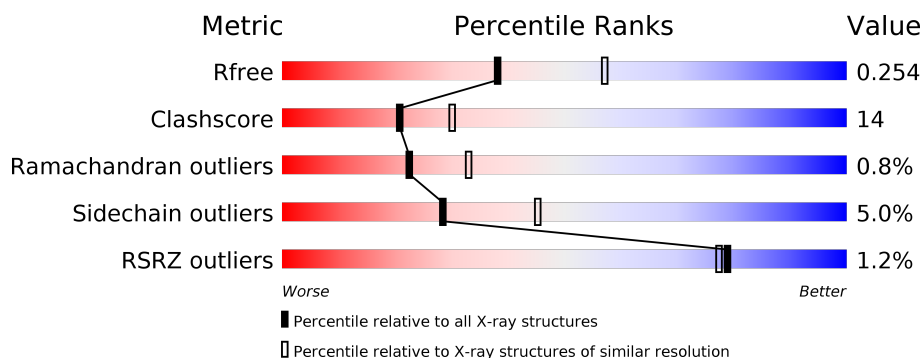
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)

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	763	<div> <div>3%</div> <div> <div></div> <div>73%</div> <div>21%</div> <div>• 5%</div> </div> </div>
1	B	763	<div> <div></div> <div> <div>73%</div> <div>20%</div> <div>• 5%</div> </div> </div>
1	C	763	<div> <div></div> <div> <div>72%</div> <div>21%</div> <div>• 5%</div> </div> </div>
1	D	763	<div> <div>%</div> <div> <div></div> <div>74%</div> <div>19%</div> <div>• 5%</div> </div> </div>
2	E	121	<div> <div>%</div> <div> <div></div> <div>69%</div> <div>18%</div> <div>• 10%</div> </div> </div>
2	F	121	<div> <div>%</div> <div> <div></div> <div>69%</div> <div>21%</div> <div>• 10%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	G	121	
2	H	121	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	B12	A	1801	X	-	-	-
3	B12	B	1801	X	-	-	-
3	B12	C	1801	X	-	-	-
4	5AD	A	1500	X	-	-	X
4	5AD	D	1500	X	-	-	-
5	Z98	A	767	-	-	X	X
5	Z98	B	767	-	-	X	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 27379 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 D-ornithine aminomutase E component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	728	Total	C	N	O	S	0	0	0
			5651	3561	981	1075	34			
1	B	728	Total	C	N	O	S	0	0	0
			5672	3579	984	1075	34			
1	C	728	Total	C	N	O	S	0	0	0
			5654	3570	981	1069	34			
1	D	728	Total	C	N	O	S	0	0	0
			5664	3575	984	1071	34			

There are 104 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ILE	SEE REMARK 999	UNP Q8VPJ5
A	?	-	ASP	SEE REMARK 999	UNP Q8VPJ5
A	?	-	GLY	SEE REMARK 999	UNP Q8VPJ5
A	744	SER	-	EXPRESSION TAG	UNP Q8VPJ5
A	745	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
A	746	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
A	747	PRO	-	EXPRESSION TAG	UNP Q8VPJ5
A	748	ASN	-	EXPRESSION TAG	UNP Q8VPJ5
A	749	SER	-	EXPRESSION TAG	UNP Q8VPJ5
A	750	SER	-	EXPRESSION TAG	UNP Q8VPJ5
A	751	SER	-	EXPRESSION TAG	UNP Q8VPJ5
A	752	VAL	-	EXPRESSION TAG	UNP Q8VPJ5
A	753	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
A	754	LYS	-	EXPRESSION TAG	UNP Q8VPJ5
A	755	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
A	756	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
A	757	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
A	758	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
A	759	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
A	760	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
A	761	HIS	-	EXPRESSION TAG	UNP Q8VPJ5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	762	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
A	763	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
A	764	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
A	765	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
A	766	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	?	-	ILE	SEE REMARK 999	UNP Q8VPJ5
B	?	-	ASP	SEE REMARK 999	UNP Q8VPJ5
B	?	-	GLY	SEE REMARK 999	UNP Q8VPJ5
B	744	SER	-	EXPRESSION TAG	UNP Q8VPJ5
B	745	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
B	746	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
B	747	PRO	-	EXPRESSION TAG	UNP Q8VPJ5
B	748	ASN	-	EXPRESSION TAG	UNP Q8VPJ5
B	749	SER	-	EXPRESSION TAG	UNP Q8VPJ5
B	750	SER	-	EXPRESSION TAG	UNP Q8VPJ5
B	751	SER	-	EXPRESSION TAG	UNP Q8VPJ5
B	752	VAL	-	EXPRESSION TAG	UNP Q8VPJ5
B	753	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
B	754	LYS	-	EXPRESSION TAG	UNP Q8VPJ5
B	755	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
B	756	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
B	757	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
B	758	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
B	759	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
B	760	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
B	761	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	762	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	763	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	764	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	765	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	766	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	?	-	ILE	SEE REMARK 999	UNP Q8VPJ5
C	?	-	ASP	SEE REMARK 999	UNP Q8VPJ5
C	?	-	GLY	SEE REMARK 999	UNP Q8VPJ5
C	744	SER	-	EXPRESSION TAG	UNP Q8VPJ5
C	745	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
C	746	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
C	747	PRO	-	EXPRESSION TAG	UNP Q8VPJ5
C	748	ASN	-	EXPRESSION TAG	UNP Q8VPJ5
C	749	SER	-	EXPRESSION TAG	UNP Q8VPJ5
C	750	SER	-	EXPRESSION TAG	UNP Q8VPJ5
C	751	SER	-	EXPRESSION TAG	UNP Q8VPJ5

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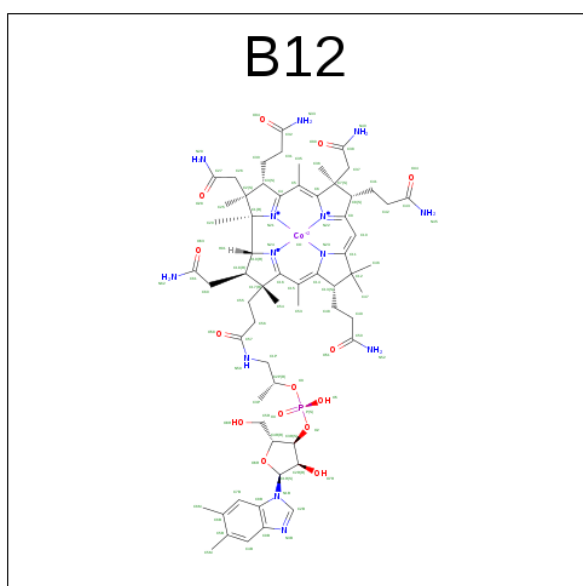
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Chain	Residue	Modelled	Actual	Comment	Reference
C	752	VAL	-	EXPRESSION TAG	UNP Q8VPJ5
C	753	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
C	754	LYS	-	EXPRESSION TAG	UNP Q8VPJ5
C	755	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
C	756	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
C	757	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
C	758	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
C	759	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
C	760	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
C	761	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	762	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	763	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	764	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	765	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	766	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	?	-	ILE	SEE REMARK 999	UNP Q8VPJ5
D	?	-	ASP	SEE REMARK 999	UNP Q8VPJ5
D	?	-	GLY	SEE REMARK 999	UNP Q8VPJ5
D	744	SER	-	EXPRESSION TAG	UNP Q8VPJ5
D	745	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
D	746	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
D	747	PRO	-	EXPRESSION TAG	UNP Q8VPJ5
D	748	ASN	-	EXPRESSION TAG	UNP Q8VPJ5
D	749	SER	-	EXPRESSION TAG	UNP Q8VPJ5
D	750	SER	-	EXPRESSION TAG	UNP Q8VPJ5
D	751	SER	-	EXPRESSION TAG	UNP Q8VPJ5
D	752	VAL	-	EXPRESSION TAG	UNP Q8VPJ5
D	753	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
D	754	LYS	-	EXPRESSION TAG	UNP Q8VPJ5
D	755	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
D	756	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
D	757	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
D	758	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
D	759	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
D	760	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
D	761	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	762	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	763	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	764	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	765	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	766	HIS	-	EXPRESSION TAG	UNP Q8VPJ5

- Molecule 2 is a protein called D-ornithine aminomutase S component.

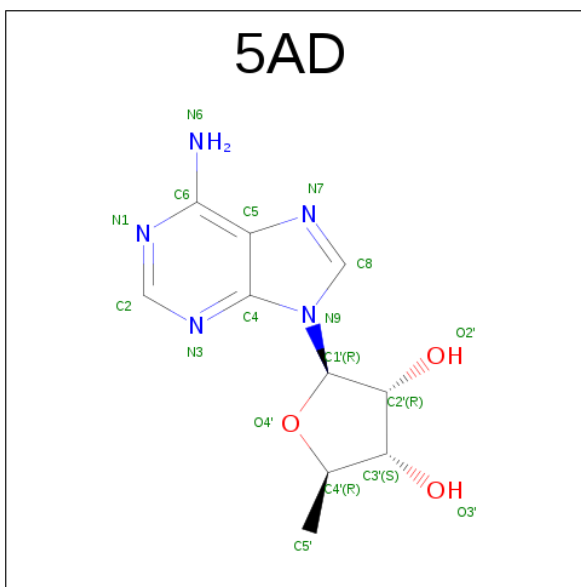
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	109	Total	C	N	O	S	0	0	0
			855	538	152	161	4			
2	F	109	Total	C	N	O	S	0	0	0
			858	539	152	163	4			
2	G	109	Total	C	N	O	S	0	0	0
			855	538	152	161	4			
2	H	109	Total	C	N	O	S	0	0	0
			855	538	152	161	4			

- Molecule 3 is COBALAMIN (three-letter code: B12) (formula:  $C_{62}H_{89}CoN_{13}O_{14}P$ ).



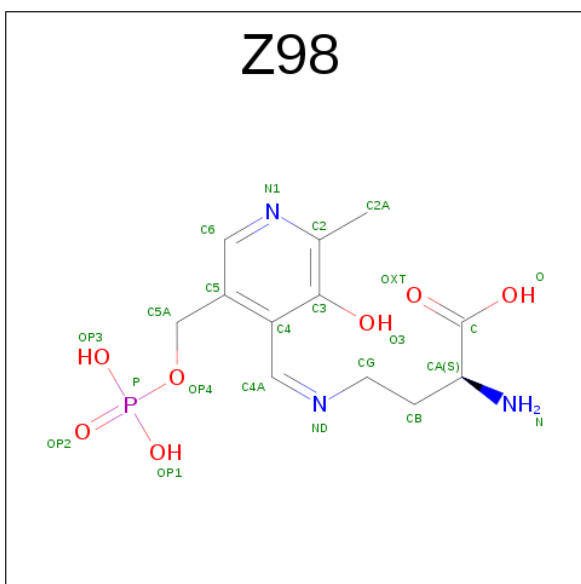
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
3	B	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
3	C	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
3	D	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0

- Molecule 4 is 5'-DEOXYADENOSINE (three-letter code: 5AD) (formula:  $C_{10}H_{13}N_5O_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			18	10	5	3		
4	B	1	Total	C	N	O	0	0
			18	10	5	3		
4	C	1	Total	C	N	O	0	0
			18	10	5	3		
4	D	1	Total	C	N	O	0	0
			18	10	5	3		

- Molecule 5 is (2S)-2-AMINO-4-{[(1Z)-{3-HYDROXY-2-METHYL-5-[(PHOSPHONOOXY)METHYL]PYRIDIN-4-YL}METHYLIDENE]AMINO}BUTANOIC ACID (three-letter code: Z98) (formula: C<sub>12</sub>H<sub>18</sub>N<sub>3</sub>O<sub>7</sub>P).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total 23	C 12	N 3	O 7	P 1	0	0
5	B	1	Total 23	C 12	N 3	O 7	P 1	0	0
5	C	1	Total 23	C 12	N 3	O 7	P 1	0	0
5	D	1	Total 23	C 12	N 3	O 7	P 1	0	0

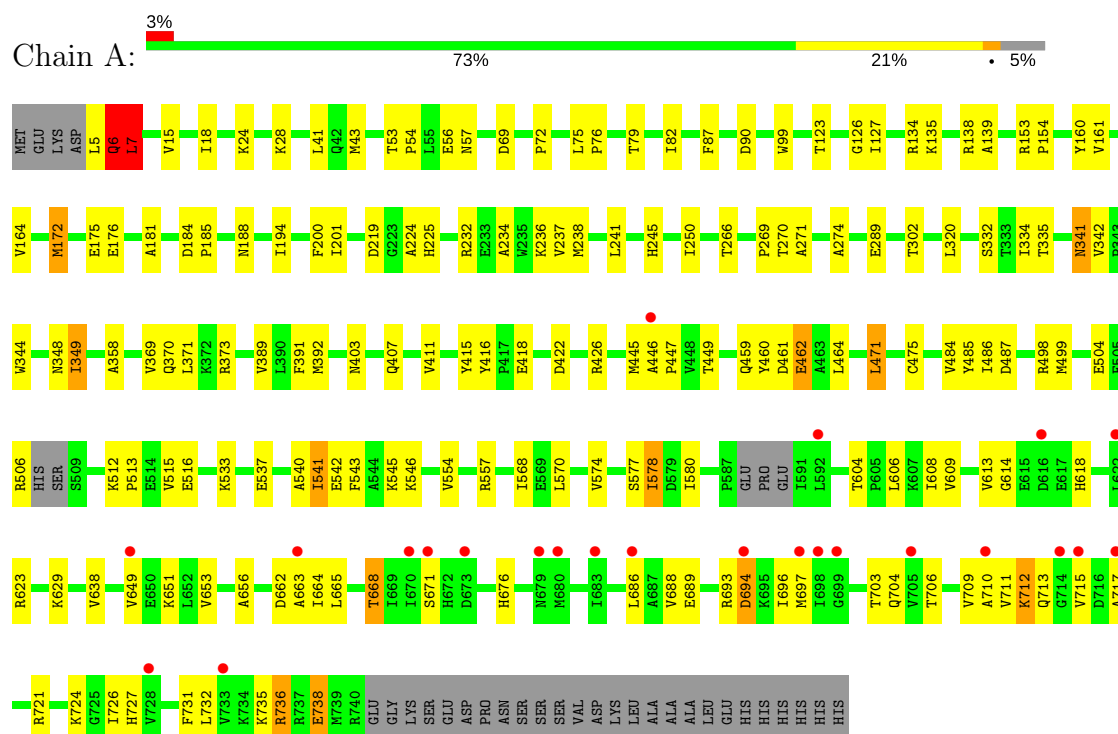
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	144	Total 144	O 144	0	0
6	E	15	Total 15	O 15	0	0
6	B	199	Total 199	O 199	0	0
6	F	33	Total 33	O 33	0	0
6	C	145	Total 145	O 145	0	0
6	G	17	Total 17	O 17	0	0
6	D	217	Total 217	O 217	0	0
6	H	17	Total 17	O 17	0	0

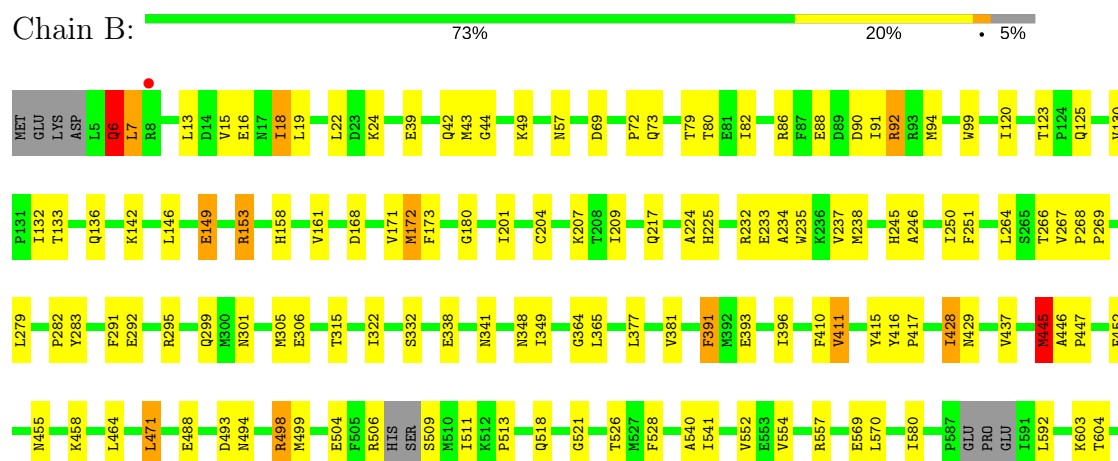
### 3 Residue-property plots

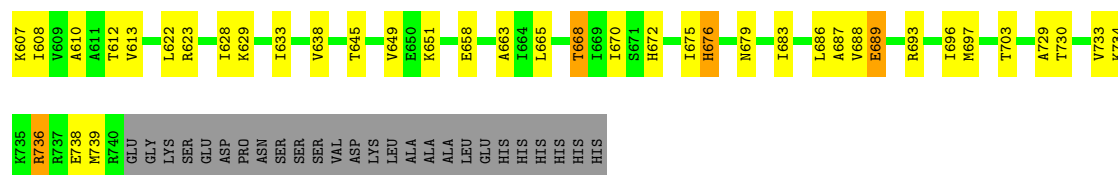
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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



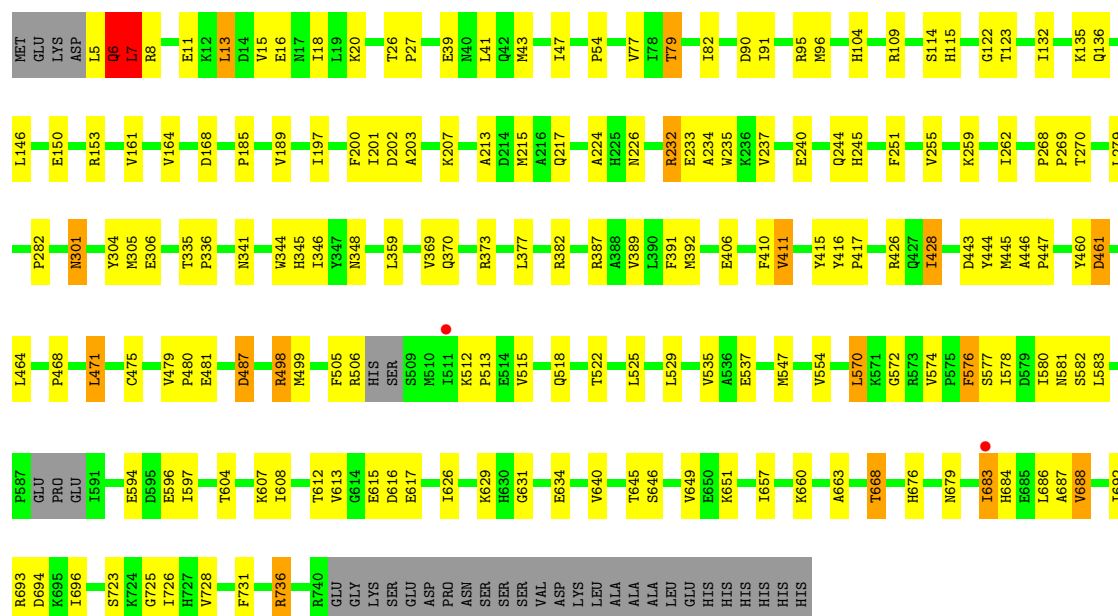
#### • Molecule 1: D-ornithine aminomutase E component





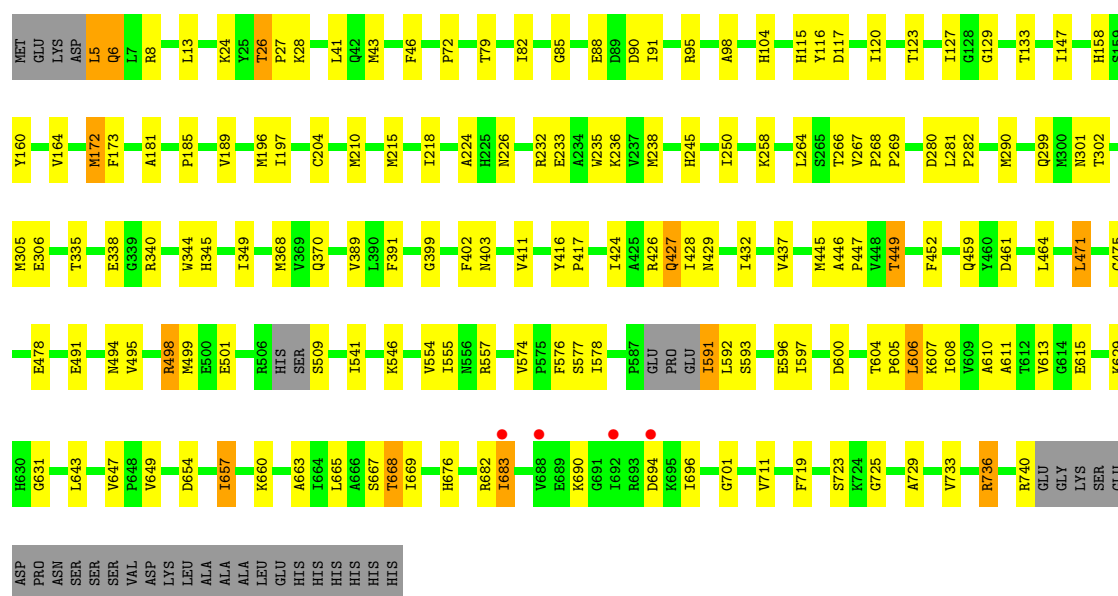
• Molecule 1: D-ornithine aminomutase E component

Chain C: 72% 21% 5%

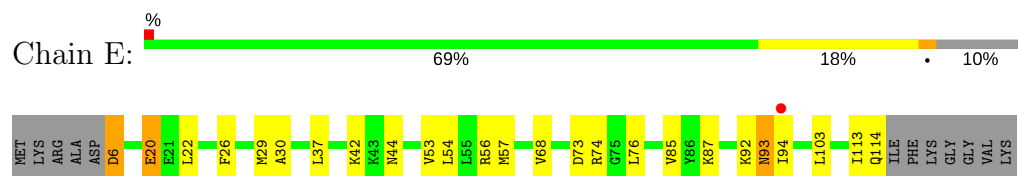


• Molecule 1: D-ornithine aminomutase E component

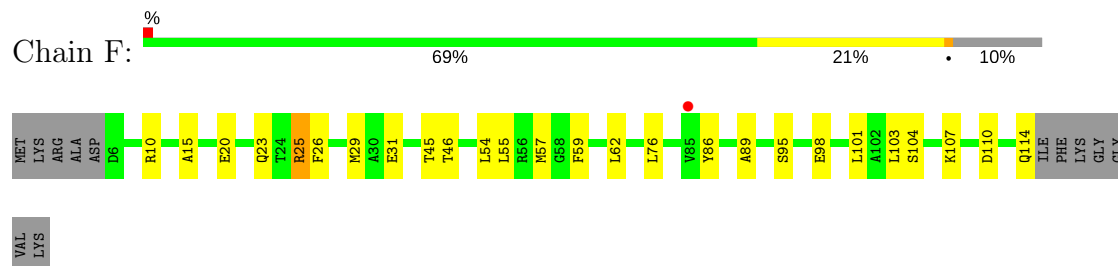
Chain D: 74% 19% 5%



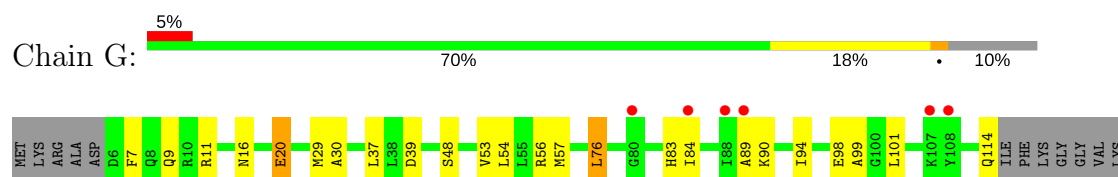
• Molecule 2: D-ornithine aminomutase S component



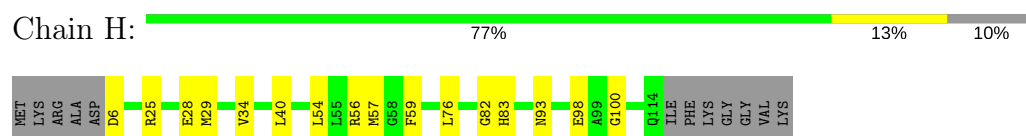
- Molecule 2: D-ornithine aminomutase S component



- Molecule 2: D-ornithine aminomutase S component



- Molecule 2: D-ornithine aminomutase S component



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.96Å 231.69Å 123.89Å 90.00° 103.16° 90.00°	Depositor
Resolution (Å)	64.23 – 2.40 64.23 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (64.23-2.40) 99.9 (64.23-2.40)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.46 (at 2.40Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.190 , 0.257 0.191 , 0.254	Depositor DCC
$R_{free}$ test set	7055 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	30.5	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 44.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.036 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	27379	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.36% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: B12, 5AD, Z98

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	0.73	1/5756 (0.0%)	0.79	1/7794 (0.0%)
1	B	0.81	1/5777 (0.0%)	0.85	7/7818 (0.1%)
1	C	0.72	0/5759	0.79	4/7796 (0.1%)
1	D	0.82	0/5769	0.81	2/7808 (0.0%)
2	E	0.74	0/867	0.72	1/1163 (0.1%)
2	F	0.86	0/870	0.85	1/1167 (0.1%)
2	G	0.69	1/867 (0.1%)	0.75	0/1163
2	H	0.79	0/867	0.73	0/1163
All	All	0.77	3/26532 (0.0%)	0.80	16/35872 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	D	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	56	GLU	CG-CD	5.84	1.60	1.51
2	G	20	GLU	CG-CD	5.45	1.60	1.51
1	B	149	GLU	CG-CD	5.39	1.60	1.51

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	498	ARG	NE-CZ-NH2	-9.04	115.78	120.30
1	D	498	ARG	NE-CZ-NH2	-8.10	116.25	120.30
1	D	498	ARG	NE-CZ-NH1	7.61	124.10	120.30
1	B	92	ARG	NE-CZ-NH1	7.05	123.83	120.30
1	B	498	ARG	NE-CZ-NH1	6.91	123.75	120.30
1	C	382	ARG	NE-CZ-NH1	6.24	123.42	120.30
1	C	498	ARG	NE-CZ-NH1	6.12	123.36	120.30
1	C	498	ARG	NE-CZ-NH2	-6.07	117.27	120.30
2	F	25	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	C	736	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	A	219	ASP	CB-CG-OD1	5.42	123.18	118.30
2	E	6	ASP	N-CA-C	5.40	125.59	111.00
1	B	153	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	B	445	MET	CG-SD-CE	-5.23	91.83	100.20
1	B	493	ASP	CB-CG-OD1	5.09	122.89	118.30
1	B	493	ASP	CB-CG-OD2	-5.04	113.77	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	6	GLN	Peptide
1	D	6	GLN	Peptide

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5651	0	5584	158	0
1	B	5672	0	5644	174	0
1	C	5654	0	5621	172	0
1	D	5664	0	5636	148	0
2	E	855	0	863	17	0
2	F	858	0	865	17	0
2	G	855	0	863	19	0
2	H	855	0	863	15	0
3	A	91	0	87	15	0
3	B	91	0	87	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	91	0	87	16	0
3	D	91	0	87	14	0
4	A	18	0	11	2	0
4	B	18	0	12	2	0
4	C	18	0	12	3	0
4	D	18	0	12	4	0
5	A	23	0	14	10	0
5	B	23	0	14	9	0
5	C	23	0	14	8	0
5	D	23	0	14	8	0
6	A	144	0	0	9	0
6	B	199	0	0	14	0
6	C	145	0	0	15	0
6	D	217	0	0	20	0
6	E	15	0	0	1	0
6	F	33	0	0	2	0
6	G	17	0	0	2	0
6	H	17	0	0	1	0
All	All	27379	0	26390	730	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 14.

All (730) 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)
5:B:767:Z98:H4A	1:D:629:LYS:NZ	1.46	1.28
1:B:649:VAL:HG22	1:B:683:ILE:HD11	1.20	1.17
1:B:396:ILE:HD12	2:F:29:MET:HE3	1.15	1.15
1:A:629:LYS:NZ	5:C:767:Z98:H4A	1.64	1.12
1:C:41:LEU:HD23	1:C:43:MET:HE2	1.28	1.12
2:F:54:LEU:HD23	2:F:57:MET:CE	1.78	1.12
3:C:1801:B12:H362	3:C:1801:B12:H351	1.30	1.11
2:F:54:LEU:HD23	2:F:57:MET:HE2	1.14	1.11
3:B:1801:B12:H351	3:B:1801:B12:H362	1.29	1.11
1:B:649:VAL:CG2	1:B:683:ILE:HD11	1.79	1.10
1:B:629:LYS:NZ	5:D:767:Z98:C4A	2.14	1.10
3:D:1801:B12:H351	3:D:1801:B12:H362	1.27	1.09
1:B:649:VAL:HG13	1:B:683:ILE:CD1	1.82	1.09
1:B:172:MET:HE3	1:B:172:MET:C	1.73	1.07
5:A:767:Z98:H4A	1:C:629:LYS:CE	1.83	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1801:B12:H351	3:A:1801:B12:H362	1.31	1.06
1:B:649:VAL:CG1	1:B:683:ILE:CD1	2.34	1.05
1:C:41:LEU:HD23	1:C:43:MET:CE	1.87	1.04
5:B:767:Z98:H4A	1:D:629:LYS:CE	1.86	1.04
1:B:445:MET:HE1	1:B:447:PRO:HB3	1.41	1.02
1:B:649:VAL:CG1	1:B:683:ILE:HD12	1.88	1.00
1:A:629:LYS:HZ3	5:C:767:Z98:C4A	1.73	1.00
5:B:767:Z98:C4A	1:D:629:LYS:NZ	2.26	0.99
1:B:649:VAL:HG22	1:B:683:ILE:CD1	1.93	0.98
1:B:649:VAL:CG2	1:B:683:ILE:CD1	2.42	0.97
1:B:153:ARG:HD2	6:B:783:HOH:O	1.63	0.97
3:B:1801:B12:H552	3:B:1801:B12:H531	1.45	0.97
1:A:629:LYS:NZ	5:C:767:Z98:C4A	2.28	0.97
1:B:629:LYS:CE	5:D:767:Z98:H4A	1.95	0.97
5:B:767:Z98:H4A	1:D:629:LYS:HZ3	1.27	0.96
5:A:767:Z98:C4A	1:C:629:LYS:NZ	2.29	0.96
5:A:767:Z98:H4A	1:C:629:LYS:NZ	1.83	0.94
1:C:406:GLU:OE2	1:C:428:ILE:HG22	1.68	0.94
1:A:649:VAL:HG12	1:A:686:LEU:HD12	1.48	0.93
1:B:649:VAL:HG11	1:B:683:ILE:HD12	1.50	0.93
1:B:396:ILE:CD1	2:F:29:MET:HE3	1.98	0.93
5:B:767:Z98:C4A	1:D:629:LYS:HZ3	1.82	0.93
2:H:54:LEU:HD23	2:H:57:MET:HE2	1.50	0.93
1:B:172:MET:C	1:B:172:MET:CE	2.38	0.92
1:D:445:MET:HE1	1:D:447:PRO:HB3	1.51	0.92
1:B:629:LYS:HZ3	5:D:767:Z98:C4A	1.83	0.91
1:B:396:ILE:HD12	2:F:29:MET:CE	2.01	0.91
1:D:172:MET:C	1:D:172:MET:HE3	1.91	0.91
1:A:445:MET:HE1	1:A:447:PRO:HB3	1.54	0.89
1:A:668:THR:HG21	1:A:676:HIS:HA	1.53	0.88
1:B:629:LYS:NZ	5:D:767:Z98:H4A	1.88	0.88
1:B:172:MET:O	1:B:172:MET:HE3	1.73	0.87
1:C:445:MET:HE1	1:C:447:PRO:HB3	1.55	0.87
1:C:240:GLU:OE2	1:C:244:GLN:NE2	2.07	0.87
1:A:537:GLU:HG3	1:A:554:VAL:HG21	1.57	0.85
2:H:54:LEU:HD23	2:H:57:MET:CE	2.06	0.85
1:A:606:LEU:HD21	1:A:732:LEU:HD13	1.57	0.85
1:A:629:LYS:HZ3	5:C:767:Z98:H4A	1.34	0.83
3:D:1801:B12:H351	3:D:1801:B12:C36	2.07	0.83
1:D:301:ASN:O	1:D:305:MET:CE	2.27	0.83
1:B:629:LYS:HZ1	5:D:767:Z98:C4A	1.88	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:41:LEU:HD23	1:D:43:MET:HE2	1.61	0.83
3:B:1801:B12:C35	3:B:1801:B12:H362	2.06	0.82
1:B:541:ILE:HD11	1:B:554:VAL:HG23	1.61	0.82
2:G:54:LEU:HD23	2:G:57:MET:CE	2.10	0.82
1:B:43:MET:HE3	1:B:72:PRO:HB3	1.60	0.81
1:D:172:MET:C	1:D:172:MET:CE	2.48	0.81
1:D:41:LEU:HD23	1:D:43:MET:CE	2.10	0.81
1:D:668:THR:HG23	1:D:676:HIS:HB2	1.63	0.81
1:C:679:ASN:O	1:C:683:ILE:HG13	1.80	0.80
1:B:123:THR:O	1:B:498:ARG:NH2	2.12	0.80
3:D:1801:B12:C35	3:D:1801:B12:H362	2.11	0.80
1:B:668:THR:CG2	1:B:668:THR:O	2.29	0.79
3:B:1801:B12:H351	3:B:1801:B12:C36	2.11	0.79
1:B:86:ARG:NE	1:B:125:GLN:HE22	1.80	0.79
1:D:607:LYS:O	1:D:608:ILE:HD12	1.81	0.79
3:D:1801:B12:H552	3:D:1801:B12:H531	1.65	0.79
1:B:649:VAL:CG1	1:B:683:ILE:HD11	2.12	0.79
1:C:445:MET:HE2	1:C:446:ALA:C	2.03	0.79
3:A:1801:B12:H351	3:A:1801:B12:C36	2.10	0.79
1:B:445:MET:HE1	1:B:447:PRO:CB	2.12	0.78
5:A:767:Z98:H4A	1:C:629:LYS:HE2	1.65	0.78
1:D:172:MET:HE3	1:D:172:MET:O	1.81	0.78
1:D:233:GLU:OE1	1:D:236:LYS:NZ	2.16	0.78
1:B:649:VAL:HG13	1:B:683:ILE:HD11	1.65	0.78
1:C:406:GLU:CD	1:C:428:ILE:HG22	2.04	0.78
1:C:445:MET:HE1	1:C:447:PRO:CB	2.13	0.78
1:A:41:LEU:HD21	1:A:43:MET:HE2	1.66	0.77
5:B:767:Z98:H4A	1:D:629:LYS:HZ1	1.46	0.77
1:B:608:ILE:HG13	1:B:663:ALA:HB3	1.66	0.77
1:D:445:MET:HE2	1:D:447:PRO:N	2.00	0.77
1:D:445:MET:HE2	1:D:447:PRO:CA	2.15	0.77
2:G:54:LEU:HD23	2:G:57:MET:HE1	1.65	0.77
1:B:172:MET:HE2	1:B:173:PHE:N	1.99	0.77
1:C:301:ASN:HD21	1:C:304:TYR:H	1.31	0.77
1:B:668:THR:CG2	1:B:676:HIS:HB2	2.15	0.76
3:A:1801:B12:H362	3:A:1801:B12:C35	2.16	0.75
1:C:445:MET:HE1	1:C:447:PRO:CA	2.17	0.75
1:A:629:LYS:CE	5:C:767:Z98:H4A	2.15	0.75
1:C:537:GLU:HG3	1:C:554:VAL:HG21	1.69	0.74
1:B:649:VAL:HG13	1:B:683:ILE:CG1	2.17	0.74
1:A:403:ASN:O	1:A:407:GLN:HG3	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:41:LEU:CD2	1:C:43:MET:HE2	2.14	0.74
1:B:649:VAL:CB	1:B:683:ILE:HD11	2.18	0.74
1:D:238:MET:SD	6:D:831:HOH:O	2.46	0.73
1:D:668:THR:CG2	1:D:676:HIS:HB2	2.18	0.73
1:A:302:THR:CG2	1:A:334:ILE:HD12	2.19	0.73
5:A:767:Z98:H5A	6:A:919:HOH:O	1.89	0.72
1:D:592:LEU:HD22	6:D:960:HOH:O	1.89	0.72
5:A:767:Z98:C4A	1:C:629:LYS:HZ3	2.03	0.72
1:D:158:HIS:CE1	1:D:218:ILE:HD12	2.25	0.72
2:F:54:LEU:CD2	2:F:57:MET:CE	2.64	0.71
1:C:47:ILE:HG21	6:C:900:HOH:O	1.89	0.71
1:B:738:GLU:HG3	1:B:738:GLU:O	1.91	0.71
1:D:445:MET:CE	1:D:447:PRO:HB3	2.21	0.71
1:B:172:MET:CE	1:B:173:PHE:N	2.54	0.71
1:C:26:THR:HG22	1:C:27:PRO:HD2	1.74	0.70
1:A:464:LEU:HD22	1:A:471:LEU:CD1	2.21	0.70
1:C:445:MET:CE	1:C:447:PRO:CA	2.70	0.70
1:A:461:ASP:CG	1:A:464:LEU:HD13	2.11	0.70
1:C:649:VAL:HG12	1:C:686:LEU:HD12	1.73	0.70
5:A:767:Z98:C4A	1:C:629:LYS:HZ1	2.03	0.69
1:C:479:VAL:O	1:C:479:VAL:HG12	1.92	0.69
1:C:251:PHE:O	1:C:255:VAL:HG23	1.92	0.69
3:C:1801:B12:H362	3:C:1801:B12:C35	2.16	0.69
1:C:41:LEU:CD2	1:C:43:MET:CE	2.67	0.69
1:C:445:MET:HE2	1:C:447:PRO:N	2.08	0.69
1:D:711:VAL:O	1:D:711:VAL:HG12	1.93	0.68
2:F:10:ARG:HD2	6:F:823:HOH:O	1.92	0.68
3:C:1801:B12:H351	3:C:1801:B12:C36	2.11	0.68
1:B:668:THR:HG21	1:B:676:HIS:HB2	1.75	0.68
1:D:541:ILE:HD11	1:D:554:VAL:HG23	1.76	0.68
1:A:5:LEU:O	1:A:6:GLN:HB2	1.93	0.68
1:A:577:SER:O	1:A:578:ILE:HD12	1.94	0.68
1:B:668:THR:HG23	1:B:676:HIS:CB	2.24	0.67
1:B:668:THR:HG23	1:B:668:THR:O	1.94	0.67
1:D:235:TRP:C	6:D:831:HOH:O	2.33	0.67
2:F:62:LEU:HD23	6:F:429:HOH:O	1.94	0.67
1:B:649:VAL:HG13	1:B:683:ILE:HG13	1.77	0.67
1:D:740:ARG:C	6:D:845:HOH:O	2.33	0.66
1:A:5:LEU:O	1:A:5:LEU:HD23	1.96	0.66
1:C:406:GLU:OE2	1:C:428:ILE:CG2	2.43	0.66
1:B:233:GLU:HG2	1:B:235:TRP:CH2	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:ALA:O	1:A:237:VAL:HG12	1.96	0.66
1:A:75:LEU:CB	6:A:911:HOH:O	2.44	0.66
5:B:767:Z98:H4A	1:D:629:LYS:HE2	1.75	0.66
1:B:629:LYS:HZ3	5:D:767:Z98:C4	2.09	0.66
1:A:703:THR:HG22	1:A:704:GLN:HE21	1.59	0.66
1:C:305:MET:CE	6:C:829:HOH:O	2.43	0.66
1:C:608:ILE:HD11	1:C:663:ALA:HB3	1.78	0.66
1:A:41:LEU:HD23	1:A:43:MET:HE3	1.78	0.65
1:A:41:LEU:CD2	1:A:43:MET:CE	2.74	0.65
1:C:597:ILE:CD1	1:C:726:ILE:CD1	2.74	0.65
3:A:1801:B12:N29	3:A:1801:B12:H251	2.09	0.65
1:D:172:MET:CE	1:D:173:PHE:HD1	2.08	0.65
1:B:73:GLN:NE2	1:B:153:ARG:HH22	1.94	0.65
1:C:207:LYS:NZ	1:C:217:GLN:HE22	1.95	0.65
1:B:92:ARG:HD2	6:D:841:HOH:O	1.97	0.64
1:B:86:ARG:HE	1:B:125:GLN:NE2	1.95	0.64
1:C:723:SER:O	3:C:1801:B12:O8R	2.16	0.64
1:D:120:ILE:HG13	1:D:133:THR:HG22	1.77	0.64
1:A:15:VAL:HG13	1:A:499:MET:HE1	1.78	0.64
1:A:41:LEU:HD21	1:A:43:MET:CE	2.26	0.64
1:B:149:GLU:HG2	6:B:795:HOH:O	1.98	0.64
1:D:464:LEU:HD23	1:D:471:LEU:HD13	1.78	0.64
1:B:86:ARG:HE	1:B:125:GLN:HE22	1.46	0.64
1:D:429:ASN:HB3	6:D:873:HOH:O	1.98	0.64
1:C:475:CYS:HB2	2:G:56:ARG:O	1.98	0.64
1:B:445:MET:HE1	1:B:471:LEU:HD23	1.79	0.64
1:A:568:ILE:HG22	1:A:570:LEU:CD1	2.28	0.64
3:B:1801:B12:N23	4:D:1500:5AD:H4'	2.13	0.64
1:B:171:VAL:HG23	1:B:209:ILE:HD13	1.80	0.63
1:A:153:ARG:HD2	6:A:783:HOH:O	1.97	0.63
1:B:13:LEU:HD13	1:B:91:ILE:HG22	1.80	0.63
1:D:649:VAL:HG23	6:D:943:HOH:O	1.96	0.63
1:B:301:ASN:O	1:B:305:MET:CE	2.46	0.63
1:B:541:ILE:CD1	1:B:554:VAL:HG23	2.27	0.63
2:H:25:ARG:HA	2:H:28:GLU:HG2	1.80	0.63
1:A:43:MET:HE2	6:A:803:HOH:O	1.97	0.63
1:B:246:ALA:O	1:B:250:ILE:HG22	1.98	0.63
1:B:88:GLU:OE2	1:B:498:ARG:HD2	1.99	0.63
1:B:43:MET:CE	1:B:72:PRO:HB3	2.28	0.63
1:D:736:ARG:HD3	6:D:849:HOH:O	1.99	0.63
1:C:335:THR:HG22	1:C:348:ASN:HA	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:445:MET:CE	1:D:471:LEU:HD23	2.28	0.63
1:B:7:LEU:HB2	6:B:940:HOH:O	1.98	0.63
1:D:301:ASN:O	1:D:305:MET:HE3	1.98	0.62
2:H:54:LEU:HA	2:H:57:MET:HE2	1.80	0.62
1:A:41:LEU:CD2	1:A:43:MET:HE2	2.29	0.62
1:A:445:MET:HE1	1:A:447:PRO:CB	2.25	0.62
1:C:660:LYS:HG3	1:C:660:LYS:O	1.98	0.62
1:A:392:MET:HE1	2:E:30:ALA:HB2	1.82	0.62
1:D:668:THR:CG2	1:D:668:THR:O	2.47	0.62
1:B:7:LEU:CD2	1:B:146:LEU:HB3	2.29	0.62
1:A:629:LYS:HZ1	5:C:767:Z98:H4A	1.60	0.62
1:B:73:GLN:HE21	1:B:153:ARG:HH22	1.46	0.61
3:A:1801:B12:N22	4:C:1500:5AD:H5'1	2.13	0.61
1:B:86:ARG:NE	1:B:125:GLN:NE2	2.48	0.61
3:B:1801:B12:C47	3:B:1801:B12:H492	2.30	0.61
1:B:445:MET:HE2	1:B:446:ALA:C	2.21	0.61
1:C:13:LEU:HD22	1:C:18:ILE:HD11	1.81	0.61
1:C:597:ILE:CD1	1:C:726:ILE:HD11	2.31	0.61
1:A:464:LEU:CD2	1:A:471:LEU:HD13	2.31	0.61
1:C:153:ARG:HD2	6:C:791:HOH:O	1.99	0.61
1:C:123:THR:O	1:C:498:ARG:NH2	2.32	0.61
1:A:568:ILE:HG22	1:A:570:LEU:HD12	1.83	0.61
2:G:94:ILE:HD12	2:G:98:GLU:HB3	1.83	0.61
1:B:207:LYS:HZ2	1:B:217:GLN:NE2	1.99	0.60
1:B:511:ILE:CG2	1:B:580:ILE:HD11	2.30	0.60
1:B:511:ILE:HG21	1:B:580:ILE:HD11	1.83	0.60
1:B:623:ARG:HD3	1:D:115:HIS:CE1	2.37	0.60
1:D:574:VAL:HG13	1:D:576:PHE:CE1	2.36	0.60
3:B:1801:B12:H473	3:B:1801:B12:H492	1.83	0.60
1:C:626:ILE:O	1:C:634:GLU:HB2	2.01	0.60
1:C:616:ASP:N	6:C:806:HOH:O	2.33	0.60
1:A:43:MET:HE1	1:A:72:PRO:HA	1.84	0.60
1:B:80:THR:OG1	1:B:348:ASN:ND2	2.30	0.60
1:C:7:LEU:HD21	1:C:95:ARG:NH2	2.16	0.60
1:A:606:LEU:HD12	1:A:662:ASP:OD2	2.01	0.60
1:B:39:GLU:OE1	1:B:39:GLU:HA	2.02	0.60
2:H:98:GLU:HG3	6:H:490:HOH:O	2.02	0.60
1:C:668:THR:CG2	1:C:676:HIS:HB2	2.32	0.59
1:A:629:LYS:HZ1	5:C:767:Z98:C4A	2.15	0.59
1:A:703:THR:O	1:A:721:ARG:NH1	2.35	0.59
1:B:509:SER:N	6:B:925:HOH:O	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:207:LYS:HZ2	1:C:217:GLN:HE22	1.48	0.59
3:B:1801:B12:H301	3:B:1801:B12:H203	1.84	0.59
1:A:664:ILE:O	1:A:665:LEU:HD23	2.03	0.59
1:C:445:MET:CE	1:C:447:PRO:HA	2.32	0.59
1:D:736:ARG:CD	6:D:849:HOH:O	2.50	0.59
1:B:264:LEU:HD21	1:B:291:PHE:CD1	2.37	0.59
1:B:15:VAL:HG22	6:B:913:HOH:O	2.01	0.59
1:C:525:LEU:HB3	1:C:570:LEU:HD12	1.84	0.59
1:A:459:GLN:HG3	1:A:460:TYR:CD2	2.38	0.59
1:B:18:ILE:O	1:B:142:LYS:NZ	2.33	0.59
1:B:513:PRO:O	1:B:521:GLY:HA2	2.03	0.58
3:C:1801:B12:H552	3:C:1801:B12:H531	1.83	0.58
1:D:427:GLN:HG3	6:D:824:HOH:O	2.03	0.58
1:A:79:THR:HB	1:A:332:SER:HA	1.86	0.58
1:B:689:GLU:O	1:B:689:GLU:HG2	2.04	0.58
1:A:546:LYS:HZ2	1:C:578:ILE:HD11	1.67	0.58
1:B:738:GLU:CG	1:B:738:GLU:O	2.51	0.58
1:C:202:ASP:OD2	2:G:48:SER:OG	2.16	0.58
1:D:160:TYR:OH	5:D:767:Z98:HB	2.04	0.58
1:A:726:ILE:HG23	1:A:727:HIS:CD2	2.38	0.58
1:C:668:THR:HG23	1:C:676:HIS:CB	2.32	0.58
1:A:608:ILE:HD13	1:A:638:VAL:CG1	2.34	0.58
1:D:389:VAL:HG13	2:H:29:MET:CE	2.33	0.58
1:A:302:THR:HG21	1:A:334:ILE:HD12	1.86	0.57
1:A:580:ILE:CD1	1:C:535:VAL:HG11	2.34	0.57
1:B:540:ALA:HB1	1:B:570:LEU:HD11	1.85	0.57
1:B:82:ILE:HG22	1:B:90:ASP:HB3	1.85	0.57
1:C:687:ALA:HB3	1:C:693:ARG:HD3	1.85	0.57
1:D:668:THR:HG23	1:D:676:HIS:CB	2.30	0.57
1:B:123:THR:O	1:B:494:ASN:HA	2.05	0.57
1:C:41:LEU:HD23	1:C:43:MET:HE1	1.84	0.57
1:A:200:PHE:CD2	2:E:37:LEU:HD13	2.39	0.57
1:C:596:GLU:CB	6:C:826:HOH:O	2.52	0.57
1:D:389:VAL:HG13	2:H:29:MET:HE1	1.86	0.57
1:C:445:MET:CE	1:C:447:PRO:N	2.67	0.57
1:D:172:MET:HE2	1:D:173:PHE:N	2.19	0.57
1:D:608:ILE:HG13	1:D:663:ALA:HB3	1.86	0.57
1:A:164:VAL:HG13	1:A:194:ILE:HG12	1.87	0.57
1:A:464:LEU:CD2	1:A:471:LEU:CD1	2.83	0.57
1:B:266:THR:O	1:B:266:THR:HG23	2.03	0.57
1:B:668:THR:HG22	1:B:668:THR:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1500:5AD:C4'	3:D:1801:B12:N23	2.67	0.57
1:B:445:MET:HE1	1:B:447:PRO:CA	2.35	0.57
1:B:629:LYS:HE2	5:D:767:Z98:H4A	1.81	0.57
1:B:416:TYR:CD1	1:B:417:PRO:HA	2.40	0.56
1:B:445:MET:HA	1:B:455:ASN:OD1	2.05	0.56
1:B:668:THR:CG2	1:B:676:HIS:CB	2.80	0.56
1:C:537:GLU:CG	1:C:554:VAL:HG21	2.35	0.56
1:C:234:ALA:O	1:C:237:VAL:HG12	2.06	0.56
1:C:668:THR:HG23	1:C:676:HIS:HB2	1.87	0.56
1:B:393:GLU:OE2	2:F:25:ARG:NH1	2.32	0.56
1:D:41:LEU:HD23	1:D:43:MET:HE1	1.85	0.56
1:D:591:ILE:HG23	1:D:591:ILE:O	2.05	0.56
1:B:504:GLU:CB	6:B:840:HOH:O	2.52	0.56
1:B:445:MET:CE	1:B:471:LEU:HD23	2.35	0.56
1:C:7:LEU:HD22	1:C:150:GLU:OE2	2.05	0.56
1:C:233:GLU:HG2	1:C:235:TRP:CH2	2.41	0.56
1:C:615:GLU:C	6:C:806:HOH:O	2.43	0.56
1:A:269:PRO:HB2	1:A:270:THR:HG23	1.89	0.56
1:A:613:VAL:HG21	1:A:649:VAL:CG2	2.36	0.56
1:B:43:MET:HE1	6:B:892:HOH:O	2.05	0.56
1:C:428:ILE:HG21	6:C:778:HOH:O	2.06	0.56
1:D:181:ALA:HB3	1:D:210:MET:HE3	1.87	0.56
1:D:344:TRP:O	1:D:345:HIS:C	2.41	0.56
1:D:204:CYS:HB3	1:D:452:PHE:CD2	2.41	0.55
1:B:120:ILE:HG13	1:B:133:THR:HG22	1.87	0.55
1:C:612:THR:HB	1:C:645:THR:HG22	1.89	0.55
1:A:41:LEU:CD2	1:A:43:MET:HE3	2.35	0.55
1:C:13:LEU:CD2	1:C:18:ILE:HD11	2.37	0.55
3:B:1801:B12:C36	3:B:1801:B12:C35	2.79	0.55
1:D:509:SER:N	6:D:988:HOH:O	2.40	0.55
1:D:610:ALA:HA	1:D:665:LEU:O	2.06	0.55
3:B:1801:B12:H3	3:B:1801:B12:O28	2.06	0.55
1:C:161:VAL:O	1:C:161:VAL:HG12	2.06	0.55
1:D:445:MET:HE3	1:D:471:LEU:HD23	1.88	0.55
1:D:574:VAL:CG1	1:D:576:PHE:CE1	2.90	0.55
1:D:172:MET:HE2	1:D:173:PHE:HD1	1.71	0.55
3:D:1801:B12:C47	3:D:1801:B12:H492	2.36	0.55
1:D:605:PRO:O	1:D:736:ARG:NH2	2.39	0.55
1:B:207:LYS:NZ	1:B:217:GLN:NE2	2.55	0.55
1:C:594:GLU:CB	6:C:819:HOH:O	2.55	0.55
3:A:1801:B12:H531	3:A:1801:B12:H552	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:449:THR:OG1	1:D:478:GLU:OE2	2.16	0.54
1:A:613:VAL:HG21	1:A:649:VAL:HG23	1.89	0.54
4:A:1500:5AD:C4'	3:C:1801:B12:N23	2.70	0.54
1:B:207:LYS:HZ2	1:B:217:GLN:HE22	1.53	0.54
1:B:580:ILE:HD13	1:B:580:ILE:N	2.22	0.54
1:A:464:LEU:HD23	1:A:471:LEU:HD13	1.89	0.54
2:E:6:ASP:N	6:E:410:HOH:O	2.40	0.54
1:A:543:PHE:CE1	1:C:578:ILE:HD13	2.42	0.54
1:B:649:VAL:CB	1:B:683:ILE:CD1	2.83	0.54
1:D:26:THR:HG22	1:D:27:PRO:HD2	1.88	0.54
1:A:392:MET:CE	2:E:30:ALA:HB2	2.38	0.54
2:E:74:ARG:HD2	2:E:113:ILE:HD11	1.88	0.54
1:B:668:THR:HG23	1:B:676:HIS:HB3	1.87	0.54
1:C:392:MET:HE1	2:G:30:ALA:HB2	1.90	0.54
3:B:1801:B12:H531	3:B:1801:B12:C55	2.22	0.53
1:C:445:MET:CE	1:C:471:LEU:HD23	2.39	0.53
1:D:172:MET:HE1	1:D:173:PHE:HD1	1.72	0.53
2:E:53:VAL:O	2:E:57:MET:HG3	2.09	0.53
1:A:41:LEU:HD23	1:A:43:MET:CE	2.38	0.53
1:D:607:LYS:C	1:D:608:ILE:HD12	2.28	0.53
1:A:53:THR:HG23	1:A:54:PRO:HD2	1.90	0.53
1:A:7:LEU:HB2	6:A:834:HOH:O	2.08	0.53
1:B:506:ARG:HH11	1:B:518:GLN:HE22	1.56	0.53
1:B:610:ALA:HB1	1:B:622:LEU:HD21	1.91	0.53
1:C:41:LEU:CD2	1:C:43:MET:HE1	2.38	0.53
1:C:82:ILE:HG22	1:C:90:ASP:HB3	1.90	0.53
1:D:172:MET:C	1:D:172:MET:HE2	2.26	0.53
2:G:7:PHE:CZ	2:G:11:ARG:HD2	2.43	0.53
1:B:445:MET:CE	1:B:447:PRO:HB3	2.27	0.53
1:A:369:VAL:CG1	1:C:369:VAL:CG1	2.87	0.53
1:C:7:LEU:CD2	1:C:95:ARG:NH2	2.72	0.53
1:A:5:LEU:O	1:A:6:GLN:CB	2.56	0.53
1:A:713:GLN:HA	1:A:713:GLN:HE21	1.73	0.53
1:C:607:LYS:NZ	6:C:815:HOH:O	2.31	0.53
1:D:606:LEU:HD11	1:D:608:ILE:HD11	1.91	0.53
1:B:629:LYS:NZ	1:D:226:ASN:OD1	2.40	0.53
1:C:6:GLN:HG2	1:C:7:LEU:N	2.24	0.53
1:D:399:GLY:HA3	1:D:403:ASN:HD22	1.73	0.53
1:D:669:ILE:N	1:D:669:ILE:HD13	2.24	0.53
1:C:232:ARG:HA	1:C:232:ARG:HH11	1.74	0.52
1:C:305:MET:HE2	6:C:829:HOH:O	2.05	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:GLY:O	1:A:127:ILE:HD13	2.10	0.52
5:B:767:Z98:C4A	1:D:629:LYS:HZ1	2.12	0.52
2:F:86:TYR:O	2:F:89:ALA:HB3	2.09	0.52
1:A:123:THR:O	1:A:498:ARG:NH2	2.42	0.52
1:B:415:TYR:O	1:B:416:TYR:C	2.48	0.52
1:B:149:GLU:CG	6:B:795:HOH:O	2.56	0.52
1:A:370:GLN:NE2	1:C:370:GLN:OE1	2.40	0.52
1:D:596:GLU:CB	6:D:960:HOH:O	2.56	0.52
1:A:445:MET:HE2	1:A:446:ALA:C	2.30	0.52
1:C:389:VAL:HG13	2:G:29:MET:HE1	1.92	0.52
3:A:1801:B12:C6	4:C:1500:5AD:H5'1	2.39	0.52
1:A:134:ARG:NH1	1:A:175:GLU:OE2	2.34	0.52
1:A:623:ARG:HD3	1:C:115:HIS:CE1	2.44	0.52
1:C:7:LEU:HD12	1:C:146:LEU:HB3	1.91	0.52
1:D:123:THR:O	1:D:498:ARG:NH2	2.42	0.52
4:B:1500:5AD:H4'	3:D:1801:B12:N23	2.25	0.52
1:B:267:VAL:HG22	1:B:299:GLN:HB3	1.91	0.52
1:A:709:VAL:O	1:A:712:LYS:HB3	2.09	0.52
1:C:15:VAL:HG23	1:C:499:MET:CE	2.40	0.52
1:A:710:ALA:O	1:A:715:VAL:HG23	2.10	0.51
1:B:234:ALA:O	1:B:237:VAL:HG12	2.10	0.51
1:C:392:MET:CE	2:G:30:ALA:HB2	2.39	0.51
1:D:445:MET:HE1	1:D:471:LEU:HD23	1.92	0.51
2:G:20:GLU:HB3	6:G:725:HOH:O	2.10	0.51
2:E:92:LYS:HB2	2:E:94:ILE:HG12	1.92	0.51
1:A:57:ASN:HB3	1:A:99:TRP:CH2	2.45	0.51
1:B:628:ILE:HD12	1:D:424:ILE:HD11	1.92	0.51
1:C:580:ILE:O	1:C:580:ILE:HG22	2.11	0.51
1:D:340:ARG:HG2	1:D:555:ILE:HD12	1.93	0.51
1:A:201:ILE:HD13	2:E:44:ASN:HB2	1.91	0.51
1:B:207:LYS:NZ	1:B:217:GLN:HE22	2.09	0.51
1:C:608:ILE:CD1	1:C:663:ALA:HB3	2.39	0.51
4:A:1500:5AD:H4'	3:C:1801:B12:N23	2.24	0.51
1:C:445:MET:HE2	1:C:447:PRO:CA	2.40	0.51
1:C:207:LYS:NZ	1:C:217:GLN:NE2	2.59	0.51
2:E:85:VAL:HG22	2:E:103:LEU:HD12	1.93	0.51
1:A:200:PHE:CE2	2:E:37:LEU:HD13	2.45	0.51
2:F:55:LEU:HD23	2:F:59:PHE:O	2.11	0.51
1:B:541:ILE:HD12	1:B:552:VAL:HG12	1.93	0.51
1:C:660:LYS:CG	1:C:660:LYS:O	2.59	0.51
1:D:172:MET:CE	1:D:173:PHE:N	2.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:103:LEU:HD23	2:F:107:LYS:O	2.11	0.51
1:B:301:ASN:O	1:B:305:MET:HE3	2.11	0.51
1:C:96:MET:HE1	1:C:345:HIS:HB3	1.91	0.51
1:D:266:THR:O	1:D:266:THR:HG23	2.10	0.51
3:A:1801:B12:N23	4:C:1500:5AD:H4'	2.26	0.50
2:F:45:THR:OG1	2:F:46:THR:N	2.43	0.50
1:C:506:ARG:HH11	1:C:518:GLN:HE22	1.60	0.50
1:A:87:PHE:HE1	1:A:139:ALA:CB	2.23	0.50
1:C:445:MET:HE1	1:C:447:PRO:HA	1.91	0.50
1:D:541:ILE:CD1	1:D:554:VAL:HG23	2.41	0.50
1:B:607:LYS:C	1:B:608:ILE:HD12	2.32	0.50
1:C:123:THR:HG23	1:C:135:LYS:HD3	1.93	0.50
1:D:301:ASN:O	1:D:305:MET:HE2	2.09	0.50
1:D:445:MET:CE	1:D:447:PRO:CA	2.87	0.50
1:D:302:THR:HA	1:D:305:MET:HE3	1.94	0.50
1:B:668:THR:HG23	1:B:676:HIS:HB2	1.85	0.50
3:D:1801:B12:H601	3:D:1801:B12:H252	1.93	0.50
1:A:512:LYS:HB2	1:A:513:PRO:CD	2.42	0.50
1:B:295:ARG:HD3	6:B:898:HOH:O	2.11	0.50
1:D:88:GLU:OE2	1:D:498:ARG:HD2	2.12	0.50
1:A:392:MET:HE2	2:E:26:PHE:CE1	2.47	0.49
1:A:540:ALA:HB1	1:A:570:LEU:HD11	1.93	0.49
1:B:132:ILE:HA	1:B:136:GLN:OE1	2.12	0.49
1:B:42:GLN:NE2	1:B:44:GLY:O	2.45	0.49
1:B:445:MET:CE	1:B:447:PRO:CA	2.90	0.49
1:D:416:TYR:CG	1:D:417:PRO:HA	2.46	0.49
1:D:445:MET:CE	1:D:447:PRO:CB	2.88	0.49
1:C:161:VAL:CG1	1:C:161:VAL:O	2.60	0.49
2:F:95:SER:OG	2:F:98:GLU:HG3	2.12	0.49
2:H:54:LEU:HD23	2:H:57:MET:HE1	1.90	0.49
1:D:611:ALA:HB1	1:D:647:VAL:HG21	1.94	0.49
1:B:233:GLU:HG2	1:B:235:TRP:CZ2	2.47	0.49
1:C:512:LYS:HB2	1:C:513:PRO:HD2	1.94	0.49
1:B:130:VAL:HG13	6:B:774:HOH:O	2.13	0.49
1:D:723:SER:O	3:D:1801:B12:H5R1	2.12	0.49
1:D:269:PRO:HD2	1:D:280:ASP:CG	2.33	0.49
1:A:710:ALA:O	1:A:715:VAL:CG2	2.61	0.49
1:C:346:ILE:HG23	6:C:891:HOH:O	2.11	0.49
1:C:525:LEU:HD21	1:C:547:MET:CE	2.43	0.49
3:D:1801:B12:C35	3:D:1801:B12:C36	2.80	0.49
1:D:123:THR:O	1:D:494:ASN:HA	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:543:PHE:CZ	1:C:578:ILE:HD13	2.47	0.49
1:D:264:LEU:HD12	1:D:264:LEU:N	2.28	0.49
1:C:213:ALA:HB3	1:C:215:MET:HG3	1.94	0.49
3:D:1801:B12:C47	3:D:1801:B12:C49	2.91	0.49
1:D:729:ALA:O	1:D:733:VAL:HG22	2.12	0.49
1:A:629:LYS:HE2	5:C:767:Z98:H4A	1.94	0.49
1:A:546:LYS:NZ	1:C:578:ILE:HD11	2.28	0.48
1:B:161:VAL:O	1:B:161:VAL:HG12	2.12	0.48
1:D:654:ASP:HA	1:D:657:ILE:HD12	1.94	0.48
2:F:110:ASP:O	2:F:114:GLN:HB2	2.13	0.48
1:B:19:LEU:HD12	1:B:499:MET:HE1	1.95	0.48
1:C:224:ALA:HB3	1:C:245:HIS:CE1	2.48	0.48
1:D:631:GLY:O	1:D:725:GLY:HA3	2.13	0.48
1:A:389:VAL:HG21	2:E:22:LEU:HD11	1.95	0.48
3:D:1801:B12:H473	3:D:1801:B12:H492	1.95	0.48
1:D:592:LEU:CD2	6:D:960:HOH:O	2.56	0.48
1:D:654:ASP:OD1	1:D:690:LYS:NZ	2.47	0.48
1:B:364:GLY:O	1:B:365:LEU:C	2.49	0.48
1:B:204:CYS:HB3	1:B:452:PHE:CD2	2.49	0.48
1:B:506:ARG:HH11	1:B:518:GLN:NE2	2.12	0.48
3:C:1801:B12:H2B	3:C:1801:B12:O7R	2.14	0.48
1:B:224:ALA:HB3	1:B:245:HIS:CE1	2.49	0.48
1:C:616:ASP:HA	6:C:806:HOH:O	2.13	0.48
1:C:649:VAL:CG1	1:C:686:LEU:HD12	2.43	0.48
1:D:13:LEU:HD13	1:D:91:ILE:HG22	1.95	0.48
1:A:172:MET:CE	1:A:176:GLU:HG3	2.44	0.48
1:A:238:MET:HA	1:A:241:LEU:HD12	1.95	0.48
1:A:369:VAL:HG13	1:C:369:VAL:CG1	2.44	0.48
1:A:513:PRO:HA	1:C:529:LEU:HD23	1.95	0.48
1:A:608:ILE:HD13	1:A:638:VAL:HG11	1.96	0.48
1:B:526:THR:HG23	1:B:569:GLU:HG2	1.95	0.48
1:B:633:ILE:HD12	1:B:638:VAL:HG11	1.96	0.48
1:C:132:ILE:HA	1:C:136:GLN:OE1	2.14	0.48
1:D:445:MET:HE2	1:D:446:ALA:C	2.34	0.48
1:B:301:ASN:O	1:B:305:MET:HE1	2.13	0.47
1:A:161:VAL:O	1:A:161:VAL:HG12	2.15	0.47
1:C:207:LYS:HZ2	1:C:217:GLN:NE2	2.11	0.47
1:C:415:TYR:O	1:C:416:TYR:C	2.53	0.47
1:D:117:ASP:HA	1:D:164:VAL:HG23	1.95	0.47
1:D:711:VAL:CG1	1:D:711:VAL:O	2.59	0.47
1:A:426:ARG:HA	6:A:871:HOH:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:522:THR:HA	1:C:572:GLY:O	2.15	0.47
1:C:616:ASP:CA	6:C:806:HOH:O	2.62	0.47
1:B:377:LEU:O	1:B:381:VAL:HG23	2.15	0.47
1:B:670:ILE:HG23	3:B:1801:B12:O34	2.14	0.47
1:D:79:THR:HA	1:D:104:HIS:HB3	1.97	0.47
1:A:82:ILE:HG22	1:A:90:ASP:HB3	1.96	0.47
1:B:201:ILE:HD13	1:B:437:VAL:HG13	1.97	0.47
1:C:684:HIS:O	1:C:688:VAL:HG23	2.14	0.47
1:D:224:ALA:CB	1:D:245:HIS:CE1	2.98	0.47
2:F:23:GLN:O	2:F:26:PHE:HB3	2.15	0.47
2:H:54:LEU:CD2	2:H:57:MET:CE	2.87	0.47
1:C:612:THR:HG22	1:C:616:ASP:HB3	1.96	0.47
1:A:475:CYS:HB2	2:E:56:ARG:O	2.15	0.47
1:B:391:PHE:HA	1:B:416:TYR:CZ	2.50	0.47
1:B:649:VAL:HG12	1:B:686:LEU:CD1	2.45	0.47
1:C:373:ARG:HA	1:C:377:LEU:HD23	1.97	0.47
1:D:269:PRO:HD2	1:D:280:ASP:OD1	2.15	0.47
2:H:57:MET:HE1	2:H:82:GLY:HA2	1.97	0.47
1:B:80:THR:HG1	1:B:348:ASN:HD22	1.57	0.47
1:C:200:PHE:CE2	2:G:37:LEU:HD13	2.50	0.47
1:C:26:THR:HG22	1:C:27:PRO:CD	2.43	0.47
1:A:668:THR:HG21	1:A:676:HIS:CA	2.36	0.47
1:C:479:VAL:O	1:C:481:GLU:N	2.48	0.47
1:A:335:THR:HG22	1:A:348:ASN:HA	1.97	0.46
1:B:233:GLU:CG	1:B:235:TRP:CH2	2.98	0.46
1:B:416:TYR:CG	1:B:417:PRO:HA	2.50	0.46
1:A:172:MET:HE2	1:A:176:GLU:CG	2.46	0.46
1:A:459:GLN:HG3	1:A:460:TYR:CE2	2.51	0.46
1:A:694:ASP:C	1:A:694:ASP:OD1	2.54	0.46
1:B:428:ILE:CG2	1:B:429:ASN:N	2.78	0.46
3:B:1801:B12:C47	3:B:1801:B12:C49	2.90	0.46
1:C:15:VAL:HG23	1:C:499:MET:HE1	1.96	0.46
2:E:20:GLU:H	2:E:20:GLU:CD	2.18	0.46
6:A:768:HOH:O	2:E:87:LYS:CB	2.64	0.46
1:C:387:ARG:NH1	1:C:416:TYR:O	2.43	0.46
1:C:7:LEU:HD21	1:C:95:ARG:CZ	2.45	0.46
1:D:123:THR:OG1	1:D:495:VAL:HG12	2.16	0.46
1:B:672:HIS:O	1:B:675:ILE:HG22	2.15	0.46
1:C:189:VAL:HG12	1:C:426:ARG:HG3	1.98	0.46
1:C:416:TYR:CG	1:C:417:PRO:HA	2.51	0.46
1:D:600:ASP:OD2	1:D:736:ARG:NH1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:59:PHE:CE1	2:H:100:GLY:HA3	2.51	0.46
1:A:341:ASN:ND2	1:A:342:VAL:O	2.43	0.46
1:B:57:ASN:HB3	1:B:99:TRP:CH2	2.51	0.46
1:C:282:PRO:HG3	1:C:377:LEU:HD12	1.97	0.46
1:C:43:MET:HE1	1:C:54:PRO:HG3	1.98	0.46
1:B:158:HIS:HA	1:B:180:GLY:O	2.16	0.46
1:A:236:LYS:HG2	1:A:415:TYR:HB2	1.98	0.46
1:B:7:LEU:HD23	1:B:146:LEU:HB3	1.96	0.46
1:A:426:ARG:NH1	1:C:634:GLU:OE2	2.31	0.46
1:C:77:VAL:CG1	1:C:104:HIS:HB2	2.46	0.46
3:A:1801:B12:C25	3:A:1801:B12:N29	2.76	0.46
1:B:649:VAL:HG21	1:B:683:ILE:CD1	2.39	0.46
3:C:1801:B12:N29	3:C:1801:B12:H251	2.31	0.46
1:D:85:GLY:HA2	1:D:129:GLY:O	2.16	0.45
1:D:649:VAL:HG13	1:D:683:ILE:HG13	1.97	0.45
1:D:606:LEU:CD1	1:D:608:ILE:CD1	2.94	0.45
2:G:114:GLN:C	6:G:125:HOH:O	2.54	0.45
1:A:43:MET:CE	6:A:803:HOH:O	2.60	0.45
1:B:607:LYS:O	1:B:608:ILE:HD12	2.17	0.45
1:C:15:VAL:HG23	1:C:16:GLU:N	2.30	0.45
1:C:305:MET:HE3	6:C:829:HOH:O	2.12	0.45
1:A:344:TRP:CD1	1:A:515:VAL:HB	2.52	0.45
1:A:445:MET:HE1	1:A:447:PRO:CA	2.46	0.45
1:B:268:PRO:HA	1:B:269:PRO:HD3	1.81	0.45
1:C:468:PRO:O	1:C:471:LEU:HB2	2.15	0.45
1:D:267:VAL:HG22	1:D:299:GLN:HB3	1.98	0.45
1:A:289:GLU:CD	1:A:373:ARG:HH21	2.19	0.45
1:A:649:VAL:O	1:A:653:VAL:HG23	2.16	0.45
1:A:75:LEU:N	1:A:76:PRO:CD	2.80	0.45
1:B:315:THR:HB	6:B:852:HOH:O	2.15	0.45
1:D:210:MET:HG2	1:D:215:MET:CE	2.46	0.45
1:D:302:THR:HG23	6:D:973:HOH:O	2.17	0.45
1:A:271:ALA:O	1:A:274:ALA:HB3	2.17	0.45
1:A:504:GLU:HA	6:A:868:HOH:O	2.17	0.45
1:B:90:ASP:O	1:B:94:MET:HG3	2.17	0.45
1:D:593:SER:O	1:D:597:ILE:HG13	2.17	0.45
1:D:82:ILE:HG22	1:D:90:ASP:HB3	1.98	0.45
2:G:53:VAL:O	2:G:57:MET:HG3	2.17	0.45
1:A:671:SER:HB2	1:A:676:HIS:ND1	2.32	0.45
2:E:54:LEU:HD12	2:E:68:VAL:HG23	1.99	0.45
1:A:697:MET:HE1	1:A:736:ARG:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1801:B12:H601	3:C:1801:B12:H252	1.98	0.45
1:C:581:ASN:C	1:C:583:LEU:H	2.20	0.45
1:D:416:TYR:CD1	1:D:417:PRO:HA	2.52	0.45
3:C:1801:B12:C35	3:C:1801:B12:C36	2.84	0.45
1:D:445:MET:HE2	1:D:447:PRO:HA	1.95	0.45
1:A:138:ARG:O	1:A:139:ALA:C	2.54	0.45
1:B:729:ALA:O	1:B:733:VAL:HG13	2.17	0.45
1:C:679:ASN:O	1:C:683:ILE:CG1	2.58	0.45
1:D:224:ALA:HB3	1:D:245:HIS:CE1	2.52	0.45
3:A:1801:B12:H2B	3:A:1801:B12:O7R	2.17	0.44
1:B:224:ALA:CB	1:B:245:HIS:CE1	3.00	0.44
1:C:615:GLU:O	1:C:646:SER:OG	2.34	0.44
1:D:43:MET:HE3	1:D:72:PRO:HB3	1.98	0.44
1:A:609:VAL:HG21	1:A:656:ALA:HB2	1.99	0.44
1:D:459:GLN:HE22	2:H:83:HIS:CE1	2.35	0.44
1:A:542:GLU:HG3	1:C:583:LEU:CD2	2.47	0.44
1:B:541:ILE:HD13	1:B:570:LEU:CD2	2.47	0.44
3:A:1801:B12:O7R	3:A:1801:B12:C2B	2.65	0.44
1:A:608:ILE:HG13	1:A:663:ALA:HB3	1.99	0.44
1:D:197:ILE:HG22	1:D:437:VAL:HG21	1.99	0.44
1:C:728:VAL:CG2	3:C:1801:B12:HM61	2.47	0.44
1:D:13:LEU:HD11	1:D:147:ILE:HD11	2.00	0.44
1:D:5:LEU:HD12	6:D:987:HOH:O	2.17	0.44
3:B:1801:B12:N23	4:D:1500:5AD:C4'	2.75	0.44
1:D:701:GLY:HA2	1:D:719:PHE:O	2.18	0.44
1:A:735:LYS:O	1:A:738:GLU:N	2.49	0.44
3:C:1801:B12:H253	3:C:1801:B12:H301	1.81	0.44
3:B:1801:B12:H261	4:D:1500:5AD:H5'3	2.00	0.44
1:A:153:ARG:HA	1:A:154:PRO:HD3	1.90	0.44
1:A:445:MET:CE	1:A:447:PRO:CA	2.96	0.44
1:A:613:VAL:HG22	1:A:614:GLY:H	1.82	0.44
1:A:668:THR:HB	1:A:676:HIS:HB2	1.99	0.44
5:A:767:Z98:H4A	1:C:629:LYS:HE3	1.87	0.44
1:C:13:LEU:HD22	1:C:18:ILE:CD1	2.47	0.44
1:C:445:MET:HE1	1:C:471:LEU:HD23	2.00	0.44
2:H:40:LEU:HD23	2:H:40:LEU:HA	1.72	0.44
1:A:320:LEU:HD13	1:A:358:ALA:HB3	1.99	0.44
1:A:606:LEU:CD2	1:A:732:LEU:HD13	2.39	0.44
3:B:1801:B12:H473	3:B:1801:B12:C49	2.33	0.44
1:B:225:HIS:HE2	5:B:767:Z98:HB	1.83	0.44
1:B:250:ILE:O	1:B:251:PHE:C	2.54	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:292:GLU:HG3	6:B:944:HOH:O	2.18	0.44
3:D:1801:B12:H203	3:D:1801:B12:H301	2.00	0.44
1:D:668:THR:HG23	1:D:668:THR:O	2.17	0.44
1:A:568:ILE:CG2	1:A:570:LEU:HD11	2.48	0.43
1:C:597:ILE:HD13	1:C:726:ILE:CD1	2.47	0.43
1:D:611:ALA:HB2	1:D:643:LEU:HB2	2.00	0.43
1:A:389:VAL:HG13	2:E:29:MET:HE1	2.00	0.43
1:C:460:TYR:O	1:C:461:ASP:HB2	2.17	0.43
1:D:667:SER:OG	1:D:669:ILE:HD11	2.18	0.43
1:B:377:LEU:HB2	1:D:368:MET:HG2	2.00	0.43
1:B:79:THR:HB	1:B:332:SER:HA	2.00	0.43
1:C:13:LEU:CD1	1:C:91:ILE:HG22	2.48	0.43
1:A:542:GLU:HG3	1:C:583:LEU:HD23	2.01	0.43
1:B:687:ALA:HB3	1:B:693:ARG:HD3	2.00	0.43
1:A:369:VAL:CG1	1:C:369:VAL:HG13	2.48	0.43
1:D:196:MET:SD	1:D:402:PHE:CD1	3.11	0.43
1:B:623:ARG:CZ	1:D:432:ILE:HD12	2.49	0.43
1:C:268:PRO:HA	1:C:269:PRO:HD3	1.83	0.43
1:C:6:GLN:CG	1:C:7:LEU:N	2.80	0.43
1:D:428:ILE:HB	6:D:882:HOH:O	2.18	0.43
1:A:484:VAL:HG12	1:A:486:ILE:CD1	2.49	0.43
1:A:160:TYR:CE1	5:A:767:Z98:HG	2.53	0.43
3:B:1801:B12:C6	4:D:1500:5AD:H5'1	2.48	0.43
1:C:574:VAL:HG13	1:C:576:PHE:CE1	2.54	0.43
1:A:461:ASP:O	1:A:462:GLU:C	2.56	0.43
1:A:713:GLN:NE2	1:A:713:GLN:HA	2.34	0.43
1:A:184:ASP:HA	1:A:185:PRO:HD2	1.90	0.43
1:A:188:ASN:HB3	1:A:194:ILE:HB	2.01	0.43
1:B:658:GLU:HG2	6:B:966:HOH:O	2.17	0.43
1:C:270:THR:HG21	1:C:279:LEU:HD13	2.01	0.43
1:D:250:ILE:HG23	2:H:34:VAL:HG21	2.01	0.43
1:B:730:THR:HG22	1:B:734:LYS:HD2	2.01	0.43
1:A:580:ILE:HD12	1:C:535:VAL:HG11	2.00	0.43
1:D:116:TYR:HE2	1:D:120:ILE:HD13	1.84	0.43
1:D:281:LEU:HB3	1:D:282:PRO:HD3	2.00	0.43
1:D:668:THR:C	1:D:669:ILE:HD13	2.38	0.43
1:A:422:ASP:OD1	1:A:422:ASP:N	2.51	0.42
1:A:445:MET:HE2	1:A:446:ALA:O	2.19	0.42
1:B:161:VAL:O	1:B:161:VAL:CG1	2.67	0.42
1:C:631:GLY:O	1:C:725:GLY:HA3	2.19	0.42
1:A:344:TRP:CG	1:A:515:VAL:HB	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1801:B12:C36	3:A:1801:B12:C35	2.84	0.42
1:A:512:LYS:HB2	1:A:513:PRO:HD2	2.00	0.42
1:A:717:ALA:HB2	1:A:731:PHE:CE1	2.54	0.42
1:B:322:ILE:HD13	1:B:322:ILE:HA	1.87	0.42
1:A:7:LEU:HD23	1:A:7:LEU:HA	1.75	0.42
1:C:5:LEU:O	1:C:5:LEU:HD23	2.19	0.42
1:C:668:THR:CG2	1:C:668:THR:O	2.68	0.42
1:B:604:THR:O	1:B:736:ARG:NH2	2.37	0.42
1:A:629:LYS:NZ	1:C:226:ASN:OD1	2.49	0.42
1:D:424:ILE:HG21	1:D:426:ARG:CZ	2.50	0.42
2:G:89:ALA:HB2	2:G:99:ALA:HB2	2.01	0.42
3:A:1801:B12:H473	3:A:1801:B12:H481	0.99	0.42
1:B:15:VAL:HG23	1:B:499:MET:CE	2.49	0.42
1:B:649:VAL:CG1	1:B:686:LEU:HD12	2.50	0.42
3:C:1801:B12:H473	3:C:1801:B12:H481	1.52	0.42
1:C:359:LEU:HA	1:C:359:LEU:HD23	1.98	0.42
1:D:649:VAL:CG1	1:D:683:ILE:HG13	2.49	0.42
1:A:541:ILE:O	1:A:545:LYS:HG2	2.20	0.42
1:C:626:ILE:HD13	1:C:640:VAL:HG11	2.00	0.42
1:C:79:THR:HB	6:C:790:HOH:O	2.19	0.42
2:F:25:ARG:O	2:F:29:MET:HG2	2.20	0.42
1:A:415:TYR:O	1:A:416:TYR:C	2.58	0.42
1:A:485:TYR:C	1:A:486:ILE:HD12	2.40	0.42
1:A:711:VAL:HA	1:A:715:VAL:O	2.20	0.42
1:B:22:LEU:HB2	6:B:864:HOH:O	2.18	0.42
1:D:268:PRO:HA	1:D:269:PRO:HD3	1.74	0.42
1:A:172:MET:HE2	1:A:176:GLU:HG3	2.01	0.42
3:A:1801:B12:H601	3:A:1801:B12:H252	2.02	0.42
3:D:1801:B12:H471	3:D:1801:B12:H492	2.01	0.42
1:D:668:THR:HG22	1:D:668:THR:O	2.18	0.42
1:D:95:ARG:O	1:D:98:ALA:HB3	2.20	0.42
1:D:475:CYS:HB2	2:H:56:ARG:O	2.20	0.42
1:A:515:VAL:HG23	1:A:516:GLU:HG2	2.02	0.41
1:A:688:VAL:HG22	1:A:693:ARG:HG2	2.02	0.41
1:B:282:PRO:HG3	1:B:377:LEU:CD1	2.50	0.41
1:B:513:PRO:O	1:B:521:GLY:CA	2.68	0.41
1:C:443:ASP:O	2:G:83:HIS:CE1	2.73	0.41
1:D:266:THR:HG23	6:D:777:HOH:O	2.20	0.41
1:A:123:THR:HG23	1:A:135:LYS:HD3	2.03	0.41
1:A:724:LYS:HB2	1:A:726:ILE:HG22	2.01	0.41
1:B:528:PHE:C	1:B:528:PHE:CD2	2.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:109:ARG:NH2	1:C:114:SER:OG	2.54	0.41
1:C:577:SER:O	1:C:578:ILE:HD12	2.20	0.41
1:D:606:LEU:HD12	1:D:608:ILE:CD1	2.50	0.41
1:A:161:VAL:HG23	1:A:181:ALA:HB1	2.02	0.41
1:D:335:THR:O	1:D:338:GLU:HB2	2.21	0.41
1:D:578:ILE:HD13	1:D:578:ILE:HA	1.78	0.41
1:B:123:THR:OG1	1:B:488:GLU:OE2	2.33	0.41
1:B:612:THR:HB	1:B:645:THR:HG22	2.03	0.41
3:C:1801:B12:C2B	3:C:1801:B12:O7R	2.68	0.41
1:C:185:PRO:HB3	1:C:203:ALA:HB2	2.02	0.41
1:C:410:PHE:C	1:C:411:VAL:HG23	2.39	0.41
1:D:301:ASN:HB2	6:D:926:HOH:O	2.19	0.41
1:C:200:PHE:CD2	2:G:37:LEU:HD13	2.55	0.41
1:C:444:TYR:CD2	1:C:444:TYR:C	2.93	0.41
1:C:122:GLY:HA2	1:C:487:ASP:O	2.20	0.41
1:C:617:GLU:HB2	3:C:1801:B12:C43	2.51	0.41
1:C:657:ILE:CG1	1:C:692:ILE:HD13	2.51	0.41
1:D:736:ARG:HD2	6:D:849:HOH:O	2.17	0.41
1:B:410:PHE:C	1:B:411:VAL:HG23	2.40	0.41
1:A:568:ILE:HG22	1:A:570:LEU:HD11	2.00	0.41
3:B:1801:B12:H471	3:B:1801:B12:H492	2.01	0.41
1:B:688:VAL:HG12	1:B:689:GLU:N	2.35	0.41
1:C:344:TRP:CD1	1:C:515:VAL:HB	2.56	0.41
1:C:82:ILE:CG2	1:C:90:ASP:HB3	2.51	0.41
2:G:76:LEU:HB3	2:G:84:ILE:HD11	2.02	0.41
1:A:608:ILE:HD13	1:A:638:VAL:HG13	2.03	0.41
1:B:279:LEU:HD11	1:D:46:PHE:CE1	2.55	0.41
1:B:663:ALA:HA	1:B:697:MET:O	2.21	0.41
2:G:16:ASN:HD22	2:G:16:ASN:HA	1.73	0.41
1:A:164:VAL:CG1	1:A:194:ILE:HG12	2.50	0.41
1:C:15:VAL:CG2	1:C:499:MET:HE3	2.51	0.41
1:D:233:GLU:HG2	1:D:235:TRP:CH2	2.56	0.41
1:A:349:ILE:N	1:A:349:ILE:CD1	2.84	0.41
1:B:201:ILE:HD13	1:B:437:VAL:CG1	2.51	0.41
1:B:679:ASN:O	1:B:683:ILE:HD13	2.20	0.41
1:A:371:LEU:HD23	1:C:369:VAL:HG22	2.03	0.41
1:D:26:THR:HG22	1:D:27:PRO:CD	2.49	0.41
1:D:428:ILE:HG23	6:D:873:HOH:O	2.21	0.41
2:G:57:MET:HB2	2:G:57:MET:HE2	1.76	0.41
1:B:19:LEU:HD12	1:B:499:MET:CE	2.51	0.40
1:B:610:ALA:HA	1:B:665:LEU:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:MET:HB2	1:C:96:MET:HE2	1.90	0.40
1:A:618:HIS:CD2	3:A:1801:B12:H482	2.57	0.40
1:A:225:HIS:HE2	5:A:767:Z98:HB	1.86	0.40
3:B:1801:B12:H481	3:B:1801:B12:H473	1.86	0.40
1:C:197:ILE:HG22	1:C:201:ILE:HD11	2.03	0.40
1:C:335:THR:HA	1:C:336:PRO:HD3	1.91	0.40
1:D:608:ILE:CG1	1:D:663:ALA:HB3	2.50	0.40
1:D:495:VAL:O	1:D:499:MET:HG2	2.21	0.40
1:A:266:THR:O	1:A:266:THR:HG23	2.22	0.40
1:A:613:VAL:CG2	1:A:649:VAL:HG23	2.51	0.40
1:B:552:VAL:CG1	1:B:570:LEU:HD23	2.51	0.40
1:A:224:ALA:HB3	1:A:245:HIS:CE1	2.57	0.40
1:B:238:MET:SD	1:B:283:TYR:HB2	2.62	0.40
1:B:445:MET:CE	1:B:447:PRO:CB	2.92	0.40
1:C:8:ARG:HD3	1:C:11:GLU:CD	2.42	0.40
1:C:259:LYS:HA	1:C:262:ILE:HD12	2.02	0.40
1:C:15:VAL:CG2	1:C:499:MET:CE	3.00	0.40
1:D:185:PRO:O	1:D:189:VAL:HG23	2.21	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	722/763 (95%)	674 (93%)	42 (6%)	6 (1%)	22	33
1	B	722/763 (95%)	683 (95%)	32 (4%)	7 (1%)	18	26
1	C	722/763 (95%)	691 (96%)	22 (3%)	9 (1%)	15	21
1	D	722/763 (95%)	690 (96%)	30 (4%)	2 (0%)	44	60
2	E	107/121 (88%)	101 (94%)	5 (5%)	1 (1%)	20	29
2	F	107/121 (88%)	103 (96%)	3 (3%)	1 (1%)	20	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	G	107/121 (88%)	105 (98%)	2 (2%)	0	100	100
2	H	107/121 (88%)	106 (99%)	1 (1%)	0	100	100
All	All	3316/3536 (94%)	3153 (95%)	137 (4%)	26 (1%)	22	33

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	462	GLU
1	B	7	LEU
1	B	739	MET
1	C	6	GLN
1	C	505	PHE
2	E	93	ASN
1	B	6	GLN
1	B	689	GLU
1	C	461	ASP
1	B	69	ASP
1	C	582	SER
1	A	487	ASP
1	A	736	ARG
1	C	480	PRO
1	C	487	ASP
1	A	7	LEU
2	F	15	ALA
1	C	7	LEU
1	B	16	GLU
1	C	688	VAL
1	D	461	ASP
1	B	411	VAL
1	C	411	VAL
1	D	411	VAL
1	A	411	VAL

### 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	598/644 (93%)	568 (95%)	30 (5%)	28	45
1	B	604/644 (94%)	577 (96%)	27 (4%)	32	50
1	C	600/644 (93%)	573 (96%)	27 (4%)	32	50
1	D	602/644 (94%)	566 (94%)	36 (6%)	22	35
2	E	89/100 (89%)	83 (93%)	6 (7%)	19	30
2	F	90/100 (90%)	85 (94%)	5 (6%)	25	39
2	G	89/100 (89%)	84 (94%)	5 (6%)	25	39
2	H	89/100 (89%)	86 (97%)	3 (3%)	42	63
All	All	2761/2976 (93%)	2622 (95%)	139 (5%)	28	45

All (139) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	7	LEU
1	A	18	ILE
1	A	24	LYS
1	A	28	LYS
1	A	69	ASP
1	A	172	MET
1	A	232	ARG
1	A	250	ILE
1	A	341	ASN
1	A	349	ILE
1	A	391	PHE
1	A	418	GLU
1	A	449	THR
1	A	471	LEU
1	A	506	ARG
1	A	533	LYS
1	A	541	ILE
1	A	557	ARG
1	A	574	VAL
1	A	578	ILE
1	A	604	THR
1	A	651	LYS
1	A	668	THR
1	A	689	GLU
1	A	694	ASP
1	A	696	ILE

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Mol	Chain	Res	Type
1	A	706	THR
1	A	712	LYS
1	A	738	GLU
2	E	20	GLU
2	E	42	LYS
2	E	73	ASP
2	E	76	LEU
2	E	93	ASN
2	E	114	GLN
1	B	6	GLN
1	B	18	ILE
1	B	24	LYS
1	B	49	LYS
1	B	168	ASP
1	B	172	MET
1	B	232	ARG
1	B	306	GLU
1	B	338	GLU
1	B	341	ASN
1	B	349	ILE
1	B	391	PHE
1	B	428	ILE
1	B	445	MET
1	B	458	LYS
1	B	464	LEU
1	B	471	LEU
1	B	557	ARG
1	B	592	LEU
1	B	603	LYS
1	B	613	VAL
1	B	651	LYS
1	B	668	THR
1	B	676	HIS
1	B	696	ILE
1	B	703	THR
1	B	736	ARG
2	F	20	GLU
2	F	31	GLU
2	F	76	LEU
2	F	101	LEU
2	F	104	SER
1	C	6	GLN

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Mol	Chain	Res	Type
1	C	7	LEU
1	C	13	LEU
1	C	20	LYS
1	C	39	GLU
1	C	79	THR
1	C	164	VAL
1	C	168	ASP
1	C	232	ARG
1	C	301	ASN
1	C	306	GLU
1	C	341	ASN
1	C	391	PHE
1	C	428	ILE
1	C	464	LEU
1	C	471	LEU
1	C	570	LEU
1	C	576	PHE
1	C	604	THR
1	C	613	VAL
1	C	651	LYS
1	C	668	THR
1	C	683	ILE
1	C	694	ASP
1	C	696	ILE
1	C	731	PHE
1	C	736	ARG
2	G	9	GLN
2	G	39	ASP
2	G	76	LEU
2	G	90	LYS
2	G	101	LEU
1	D	5	LEU
1	D	6	GLN
1	D	8	ARG
1	D	24	LYS
1	D	26	THR
1	D	28	LYS
1	D	127	ILE
1	D	172	MET
1	D	232	ARG
1	D	258	LYS
1	D	290	MET

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Mol	Chain	Res	Type
1	D	306	GLU
1	D	349	ILE
1	D	370	GLN
1	D	391	PHE
1	D	427	GLN
1	D	449	THR
1	D	471	LEU
1	D	491	GLU
1	D	501	GLU
1	D	546	LYS
1	D	557	ARG
1	D	577	SER
1	D	591	ILE
1	D	604	THR
1	D	606	LEU
1	D	613	VAL
1	D	615	GLU
1	D	657	ILE
1	D	660	LYS
1	D	668	THR
1	D	682	ARG
1	D	683	ILE
1	D	694	ASP
1	D	696	ILE
1	D	736	ARG
2	H	6	ASP
2	H	76	LEU
2	H	93	ASN

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

Mol	Chain	Res	Type
1	A	331	GLN
1	A	370	GLN
1	A	672	HIS
1	A	704	GLN
1	A	713	GLN
2	E	16	ASN
2	E	114	GLN
1	B	36	GLN
1	B	73	GLN
1	B	125	GLN

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Mol	Chain	Res	Type
1	B	217	GLN
1	B	331	GLN
1	B	370	GLN
1	B	518	GLN
1	C	36	GLN
1	C	217	GLN
1	C	301	ASN
1	C	331	GLN
1	C	370	GLN
1	C	518	GLN
1	C	581	ASN
2	G	8	GLN
2	G	16	ASN
2	G	93	ASN
1	D	370	GLN
1	D	429	ASN
1	D	459	GLN
1	D	518	GLN
2	H	16	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](#)

12 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	$\# Z  > 2$
4	5AD	A	1500	3	17,20,20	1.74	5 (29%)	13,30,30	3.05	6 (46%)
3	B12	A	1801	1,4	73,101,101	1.14	5 (6%)	111,166,166	2.35	20 (18%)
5	Z98	A	767	-	18,23,23	2.01	8 (44%)	25,32,32	2.43	6 (24%)
4	5AD	B	1500	3	17,20,20	1.57	3 (17%)	13,30,30	2.44	2 (15%)
3	B12	B	1801	1,4	73,101,101	1.20	5 (6%)	111,166,166	2.28	20 (18%)
5	Z98	B	767	-	18,23,23	1.72	4 (22%)	25,32,32	1.95	6 (24%)
4	5AD	C	1500	3	17,20,20	1.38	3 (17%)	13,30,30	2.84	5 (38%)
3	B12	C	1801	1,4	73,101,101	1.11	5 (6%)	111,166,166	2.23	20 (18%)
5	Z98	C	767	-	18,23,23	1.59	3 (16%)	25,32,32	1.85	5 (20%)
4	5AD	D	1500	3	17,20,20	1.62	4 (23%)	13,30,30	3.35	4 (30%)
3	B12	D	1801	1,4	73,101,101	1.13	4 (5%)	111,166,166	2.18	20 (18%)
5	Z98	D	767	-	18,23,23	1.63	5 (27%)	25,32,32	1.62	3 (12%)

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
4	5AD	A	1500	3	1/1/4/4	0/0/20/20	0/3/3/3
3	B12	A	1801	1,4	1/1/36/38	0/51/223/223	0/3/11/11
5	Z98	A	767	-	-	1/13/17/17	0/1/1/1
4	5AD	B	1500	3	-	0/0/20/20	0/3/3/3
3	B12	B	1801	1,4	1/1/36/38	0/51/223/223	0/3/11/11
5	Z98	B	767	-	-	1/13/17/17	0/1/1/1
4	5AD	C	1500	3	-	0/0/20/20	0/3/3/3
3	B12	C	1801	1,4	1/1/36/38	0/51/223/223	0/3/11/11
5	Z98	C	767	-	-	0/13/17/17	0/1/1/1
4	5AD	D	1500	3	1/1/4/4	0/0/20/20	0/3/3/3
3	B12	D	1801	1,4	-	0/51/223/223	0/3/11/11
5	Z98	D	767	-	-	1/13/17/17	0/1/1/1

All (54) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1801	B12	C11-C10	-5.83	1.30	1.41
3	A	1801	B12	C8B-N1B	-4.44	1.32	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1801	B12	C11-C10	-4.21	1.33	1.41
3	A	1801	B12	C11-C10	-4.02	1.34	1.41
4	A	1500	5AD	C2'-C1'	-3.99	1.47	1.53
5	B	767	Z98	C3-C2	-3.72	1.38	1.40
3	D	1801	B12	C8B-N1B	-3.68	1.33	1.38
5	A	767	Z98	C4-C4A	-3.60	1.40	1.46
5	A	767	Z98	OP4-C5A	-3.53	1.31	1.44
5	B	767	Z98	C4-C4A	-3.13	1.40	1.46
3	B	1801	B12	C8B-N1B	-3.06	1.34	1.38
3	D	1801	B12	C11-C10	-3.05	1.35	1.41
5	D	767	Z98	C4-C4A	-2.48	1.42	1.46
3	C	1801	B12	C2-C3	-2.45	1.54	1.58
4	A	1500	5AD	C3'-C2'	-2.43	1.47	1.53
3	A	1801	B12	C2-C3	-2.38	1.54	1.58
5	D	767	Z98	C3-C2	-2.26	1.39	1.40
4	D	1500	5AD	C2'-C1'	-2.26	1.50	1.53
3	C	1801	B12	C4B-C9B	-2.25	1.38	1.41
5	A	767	Z98	C4-C5	-2.23	1.39	1.42
5	C	767	Z98	C4-C4A	-2.20	1.42	1.46
5	A	767	Z98	P-OP1	-2.01	1.46	1.54
5	D	767	Z98	CG-ND	2.00	1.51	1.46
4	A	1500	5AD	C2-N3	2.08	1.35	1.32
3	C	1801	B12	C6B-C5B	2.19	1.46	1.41
5	A	767	Z98	C4A-ND	2.19	1.33	1.27
4	C	1500	5AD	C2-N3	2.26	1.36	1.32
5	A	767	Z98	P-OP3	2.32	1.64	1.54
4	A	1500	5AD	O4'-C1'	2.38	1.44	1.41
4	D	1500	5AD	C2-N3	2.47	1.36	1.32
4	C	1500	5AD	O4'-C1'	2.49	1.44	1.41
3	B	1801	B12	O6R-C1R	2.53	1.44	1.41
5	D	767	Z98	C2A-C2	2.53	1.55	1.50
5	C	767	Z98	C4A-ND	2.56	1.34	1.27
5	B	767	Z98	P-OP2	2.59	1.59	1.50
4	B	1500	5AD	C2-N3	2.71	1.36	1.32
5	D	767	Z98	C4A-ND	2.74	1.35	1.27
4	D	1500	5AD	C5-C4	2.83	1.46	1.40
3	C	1801	B12	C8B-C9B	2.93	1.46	1.40
5	B	767	Z98	C4A-ND	2.96	1.36	1.27
3	B	1801	B12	C6B-C5B	2.99	1.48	1.41
5	A	767	Z98	C2A-C2	3.10	1.56	1.50
3	A	1801	B12	C6B-C5B	3.10	1.48	1.41
3	D	1801	B12	C6B-C5B	3.14	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1500	5AD	C5-C4	3.21	1.47	1.40
4	A	1500	5AD	C5-C4	3.25	1.47	1.40
3	A	1801	B12	C8B-C9B	3.33	1.47	1.40
5	A	767	Z98	P-OP2	3.37	1.62	1.50
4	C	1500	5AD	C5-C4	3.56	1.48	1.40
5	C	767	Z98	P-OP2	3.68	1.63	1.50
4	B	1500	5AD	O4'-C1'	3.75	1.46	1.41
4	D	1500	5AD	O4'-C1'	4.01	1.46	1.41
3	D	1801	B12	C8B-C9B	4.22	1.48	1.40
3	B	1801	B12	C8B-C9B	4.76	1.49	1.40

All (117) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1801	B12	C20-C1-C19	-11.50	98.19	109.34
3	A	1801	B12	C20-C1-C19	-10.00	99.64	109.34
3	C	1801	B12	C20-C1-C19	-9.30	100.33	109.34
4	D	1500	5AD	N3-C2-N1	-8.42	121.53	128.86
3	D	1801	B12	C20-C1-C19	-7.87	101.72	109.34
4	B	1500	5AD	N3-C2-N1	-7.73	122.13	128.86
4	A	1500	5AD	N3-C2-N1	-7.48	122.34	128.86
4	C	1500	5AD	N3-C2-N1	-7.33	122.47	128.86
3	A	1801	B12	C13-C12-C11	-7.30	91.01	100.87
5	A	767	Z98	OP3-P-OP4	-7.19	87.60	106.73
3	D	1801	B12	C13-C12-C11	-6.74	91.75	100.87
3	D	1801	B12	C46-C12-C13	-6.64	85.78	112.75
3	C	1801	B12	C13-C12-C11	-6.58	91.98	100.87
3	A	1801	B12	C46-C12-C13	-6.44	86.59	112.75
3	B	1801	B12	C13-C12-C11	-5.72	93.13	100.87
3	C	1801	B12	C46-C12-C13	-5.54	90.25	112.75
3	A	1801	B12	C47-C12-C13	-5.36	90.97	112.75
3	B	1801	B12	C46-C12-C13	-5.32	91.13	112.75
3	D	1801	B12	C25-C2-C1	-4.85	106.43	113.78
4	D	1500	5AD	C4-C5-N7	-4.34	105.22	109.41
3	C	1801	B12	C9-C10-C11	-4.31	119.34	131.90
3	B	1801	B12	C47-C12-C13	-3.94	96.75	112.75
3	B	1801	B12	C9-C10-C11	-3.94	120.42	131.90
3	D	1801	B12	C47-C12-C13	-3.90	96.91	112.75
3	B	1801	B12	C25-C2-C3	-3.74	109.80	115.56
3	B	1801	B12	C20-C1-C2	-3.68	107.01	113.32
4	A	1500	5AD	O2'-C2'-C3'	-3.66	100.09	111.83
3	C	1801	B12	C47-C12-C13	-3.64	97.96	112.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1801	B12	C20-C1-C2	-3.41	107.48	113.32
3	D	1801	B12	C9-C10-C11	-3.28	122.34	131.90
4	A	1500	5AD	C4-C5-N7	-3.10	106.42	109.41
3	A	1801	B12	C9-C10-C11	-3.03	123.08	131.90
3	B	1801	B12	C54-C17-C18	-2.94	108.37	112.94
4	C	1500	5AD	C4-C5-N7	-2.93	106.58	109.41
3	C	1801	B12	C20-C1-N21	-2.88	99.96	108.23
5	C	767	Z98	C4-C4A-ND	-2.88	110.66	124.66
3	C	1801	B12	C7B-C8B-C9B	-2.87	117.71	120.54
3	A	1801	B12	C54-C17-C18	-2.85	108.51	112.94
4	C	1500	5AD	C5'-C4'-C3'	-2.83	112.72	115.70
3	A	1801	B12	C3-C4-C5	-2.80	122.14	131.85
3	C	1801	B12	C5R-C4R-C3R	-2.76	105.89	114.89
5	C	767	Z98	CB-CG-ND	-2.69	104.94	110.87
5	B	767	Z98	OP3-P-OP2	-2.63	100.23	110.50
4	B	1500	5AD	C4-C5-N7	-2.59	106.91	109.41
3	A	1801	B12	C20-C1-C2	-2.54	108.96	113.32
3	C	1801	B12	C25-C2-C3	-2.42	111.83	115.56
3	A	1801	B12	C25-C2-C1	-2.41	110.13	113.78
5	B	767	Z98	C3-C4-C4A	-2.41	115.91	120.52
4	D	1500	5AD	C5'-C4'-C3'	-2.40	113.18	115.70
3	C	1801	B12	C2P-C1P-N59	-2.38	109.55	112.96
4	A	1500	5AD	C5'-C4'-C3'	-2.33	113.26	115.70
3	D	1801	B12	C3-C4-C5	-2.32	123.80	131.85
5	C	767	Z98	C2A-C2-C3	-2.25	118.27	120.96
3	D	1801	B12	C2P-C1P-N59	-2.22	109.78	112.96
3	D	1801	B12	C54-C17-C18	-2.20	109.53	112.94
3	D	1801	B12	C4B-C9B-C8B	-2.09	118.96	121.10
3	C	1801	B12	C13-C14-C15	-2.06	124.69	131.85
3	B	1801	B12	C13-C14-C15	-2.05	124.73	131.85
3	A	1801	B12	C56-C55-C17	2.03	119.59	115.56
5	B	767	Z98	C4-C4A-ND	2.04	134.57	124.66
3	A	1801	B12	C37-C7-C8	2.05	113.86	108.30
5	C	767	Z98	CG-CB-CA	2.10	117.98	112.72
3	D	1801	B12	C3R-C2R-C1R	2.12	104.70	99.95
3	A	1801	B12	C53-C15-C16	2.12	120.61	117.85
5	B	767	Z98	C5-C4-C4A	2.22	124.68	121.36
5	A	767	Z98	C2A-C2-C3	2.24	123.63	120.96
3	A	1801	B12	C35-C5-C6	2.26	120.80	117.85
3	B	1801	B12	C60-C18-C19	2.27	120.69	114.65
3	D	1801	B12	C35-C5-C6	2.28	120.82	117.85
5	A	767	Z98	C5A-C5-C4	2.37	125.80	121.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1801	B12	C36-C7-C37	2.38	114.85	110.80
3	B	1801	B12	O3-C2P-C1P	2.43	111.83	106.91
3	C	1801	B12	C35-C5-C6	2.47	121.08	117.85
3	B	1801	B12	C48-C13-C12	2.53	123.80	116.59
4	A	1500	5AD	O3'-C3'-C4'	2.57	116.77	110.47
3	D	1801	B12	C4R-O6R-C1R	2.68	112.62	109.77
3	C	1801	B12	C26-C2-C1	2.79	114.32	110.01
5	D	767	Z98	CG-ND-C4A	2.83	127.25	119.03
5	B	767	Z98	C5A-C5-C4	2.88	126.70	121.66
3	C	1801	B12	O6R-C4R-C5R	2.94	115.46	109.16
3	A	1801	B12	C18-C17-C16	2.96	104.38	100.57
3	C	1801	B12	C18-C17-C16	3.00	104.44	100.57
5	A	767	Z98	CB-CG-ND	3.01	117.50	110.87
3	D	1801	B12	C2-C1-C19	3.05	123.50	118.60
3	D	1801	B12	C18-C17-C16	3.28	104.81	100.57
3	B	1801	B12	C18-C17-C16	3.36	104.90	100.57
3	B	1801	B12	C35-C5-C6	3.46	122.36	117.85
5	A	767	Z98	CG-ND-C4A	3.54	129.30	119.03
5	D	767	Z98	OP4-C5A-C5	3.58	116.52	109.32
4	C	1500	5AD	O2'-C2'-C3'	3.73	123.76	111.83
3	B	1801	B12	C47-C12-C46	3.73	117.89	109.66
4	C	1500	5AD	O2'-C2'-C1'	3.90	123.82	111.61
5	D	767	Z98	OP1-P-OP4	3.92	117.16	106.73
3	C	1801	B12	C2-C1-C19	4.31	125.52	118.60
3	A	1801	B12	C2-C1-C19	4.43	125.72	118.60
3	D	1801	B12	C47-C12-C46	4.50	119.59	109.66
3	A	1801	B12	C47-C12-C46	4.76	120.18	109.66
4	A	1500	5AD	O2'-C2'-C1'	4.91	126.98	111.61
3	A	1801	B12	C26-C2-C1	5.00	117.73	110.01
3	C	1801	B12	C1-C19-C18	5.40	130.90	121.90
3	B	1801	B12	C1-C19-C18	5.45	130.98	121.90
5	B	767	Z98	CG-ND-C4A	5.49	134.98	119.03
3	B	1801	B12	C2-C1-C19	5.61	127.62	118.60
3	C	1801	B12	C47-C12-C46	5.96	122.83	109.66
3	D	1801	B12	C1-C19-C18	6.29	132.38	121.90
4	D	1500	5AD	O2'-C2'-C1'	6.39	131.62	111.61
5	C	767	Z98	CG-ND-C4A	6.58	138.15	119.03
5	A	767	Z98	OP1-P-OP4	6.61	124.33	106.73
3	A	1801	B12	C19-C1-N21	6.71	108.86	102.16
3	C	1801	B12	C1-C19-N24	7.04	114.28	106.24
3	A	1801	B12	C1-C19-C18	7.11	133.76	121.90
3	B	1801	B12	C1-C19-N24	7.26	114.52	106.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1801	B12	C19-C1-N21	7.46	109.61	102.16
3	B	1801	B12	C19-C1-N21	7.50	109.65	102.16
3	C	1801	B12	C19-C1-N21	8.37	110.52	102.16
3	D	1801	B12	C1-C19-N24	8.85	116.34	106.24
3	A	1801	B12	C1-C19-N24	9.15	116.69	106.24

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	1801	B12	C19
3	C	1801	B12	C19
3	A	1801	B12	C19
4	D	1500	5AD	C2'
4	A	1500	5AD	C2'

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	767	Z98	C4-C4A-ND-CG
5	A	767	Z98	C4-C4A-ND-CG
5	D	767	Z98	C4-C4A-ND-CG

There are no ring outliers.

12 monomers are involved in 99 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1500	5AD	2	0
3	A	1801	B12	15	0
5	A	767	Z98	10	0
4	B	1500	5AD	2	0
3	B	1801	B12	19	0
5	B	767	Z98	9	0
4	C	1500	5AD	3	0
3	C	1801	B12	16	0
5	C	767	Z98	8	0
4	D	1500	5AD	4	0
3	D	1801	B12	14	0
5	D	767	Z98	8	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	728/763 (95%)	0.03	24 (3%) 47 45	13, 27, 68, 84	0
1	B	728/763 (95%)	-0.26	1 (0%) 95 95	10, 22, 42, 56	0
1	C	728/763 (95%)	-0.17	2 (0%) 93 93	12, 28, 49, 66	0
1	D	728/763 (95%)	-0.14	4 (0%) 90 89	10, 23, 50, 65	0
2	E	109/121 (90%)	0.07	1 (0%) 84 82	17, 32, 46, 50	0
2	F	109/121 (90%)	-0.06	1 (0%) 84 82	15, 24, 37, 45	0
2	G	109/121 (90%)	0.20	6 (5%) 26 24	24, 35, 50, 55	0
2	H	109/121 (90%)	-0.04	0 100 100	15, 27, 45, 61	0
All	All	3348/3536 (94%)	-0.11	39 (1%) 79 77	10, 26, 54, 84	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	683	ILE	4.1
1	D	692	ILE	3.4
1	A	717	ALA	3.2
1	C	511	ILE	3.0
1	A	705	VAL	3.0
1	A	715	VAL	2.9
2	E	94	ILE	2.9
1	D	688	VAL	2.8
1	A	680	MET	2.8
1	A	679	ASN	2.7
1	A	592	LEU	2.6
1	A	728	VAL	2.5
1	A	714	GLY	2.5
2	G	107	LYS	2.5
1	A	694	ASP	2.5
1	A	649	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
2	G	108	TYR	2.5
2	G	84	ILE	2.4
2	G	89	ALA	2.4
1	A	673	ASP	2.4
1	A	446	ALA	2.3
2	G	80	GLY	2.3
1	A	698	ILE	2.3
1	A	710	ALA	2.3
1	D	694	ASP	2.3
1	A	616	ASP	2.2
1	A	663	ALA	2.2
1	A	671	SER	2.2
1	D	683	ILE	2.2
1	B	8	ARG	2.1
1	A	670	ILE	2.1
1	C	683	ILE	2.1
2	G	88	ILE	2.1
1	A	733	VAL	2.1
2	F	85	VAL	2.1
1	A	699	GLY	2.1
1	A	697	MET	2.0
1	A	686	LEU	2.0
1	A	622	LEU	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	5AD	A	1500	18/18	0.89	0.22	2.70	39,43,47,47	0
5	Z98	A	767	23/23	0.96	0.16	2.06	21,32,42,43	0
5	Z98	C	767	23/23	0.95	0.17	1.90	26,34,43,44	0
5	Z98	D	767	23/23	0.97	0.15	1.88	19,24,46,46	0
5	Z98	B	767	23/23	0.96	0.16	1.88	18,23,33,34	0
4	5AD	D	1500	18/18	0.90	0.20	1.74	38,40,45,45	0
4	5AD	B	1500	18/18	0.92	0.17	0.98	25,38,42,42	0
3	B12	D	1801	91/91	0.95	0.19	0.10	19,29,40,43	0
3	B12	A	1801	91/91	0.95	0.22	-0.00	27,43,50,54	0
3	B12	C	1801	91/91	0.97	0.15	-0.05	12,23,31,34	0
3	B12	B	1801	91/91	0.97	0.14	-0.40	14,21,29,35	0
4	5AD	C	1500	18/18	0.87	0.22	-	53,54,55,57	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.