



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 1, 2017 – 11:07 PM EDT

PDB ID : 1XWF  
Title : K185N mutated S-adenosylhomocysteine hydrolase  
Authors : Yamada, T.; Takata, Y.; Komoto, J.; Gomi, T.; Ogawa, H.; Fujioka, M.; Takusagawa, F.  
Deposited on : unknown  
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](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 : rb-20030345  
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) : rb-20030345

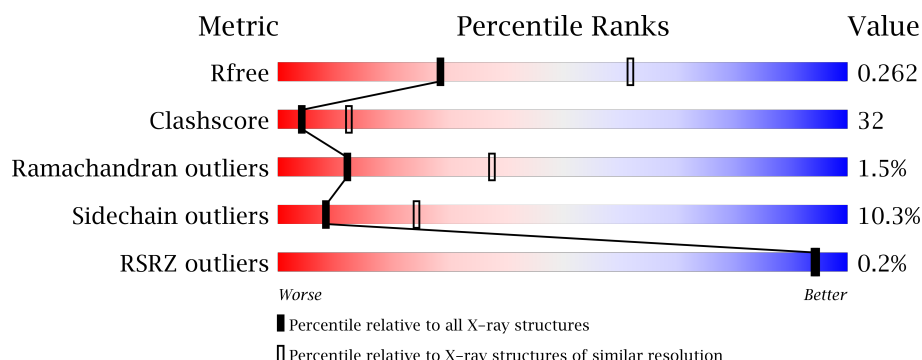
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	431	<div> <div>48%</div> <div>45%</div> <div>6%</div> </div>
1	B	431	<div> <div>49%</div> <div>44%</div> <div>7%</div> </div>
1	C	431	<div> <div>46%</div> <div>46%</div> <div>7%</div> </div>
1	D	431	<div> <div>47%</div> <div>47%</div> <div>6%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13564 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 Adenosylhomocysteinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	430	Total	C	N	O	S	0	0	0
			3318	2106	571	616	25			
1	B	430	Total	C	N	O	S	0	0	0
			3318	2106	571	616	25			
1	C	430	Total	C	N	O	S	0	0	0
			3318	2106	571	616	25			
1	D	430	Total	C	N	O	S	0	0	0
			3318	2106	571	616	25			

There are 4 discrepancies between the modelled and reference sequences:

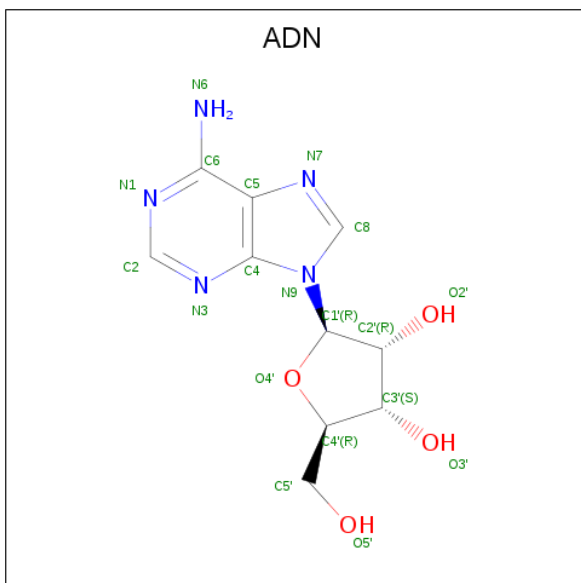
Chain	Residue	Modelled	Actual	Comment	Reference
A	185	ASN	LYS	ENGINEERED	UNP P10760
B	185	ASN	LYS	ENGINEERED	UNP P10760
C	185	ASN	LYS	ENGINEERED	UNP P10760
D	185	ASN	LYS	ENGINEERED	UNP P10760

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C<sub>21</sub>H<sub>27</sub>N<sub>7</sub>O<sub>14</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	B	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	C	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	D	1	Total 44	C 21	N 7	O 14	P 2	0	0

- Molecule 3 is ADENOSINE (three-letter code: ADN) (formula:  $\text{C}_{10}\text{H}_{13}\text{N}_5\text{O}_4$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			19	10	5	4		
3	B	1	Total	C	N	O	0	0
			19	10	5	4		
3	C	1	Total	C	N	O	0	0
			19	10	5	4		
3	D	1	Total	C	N	O	0	0
			19	10	5	4		

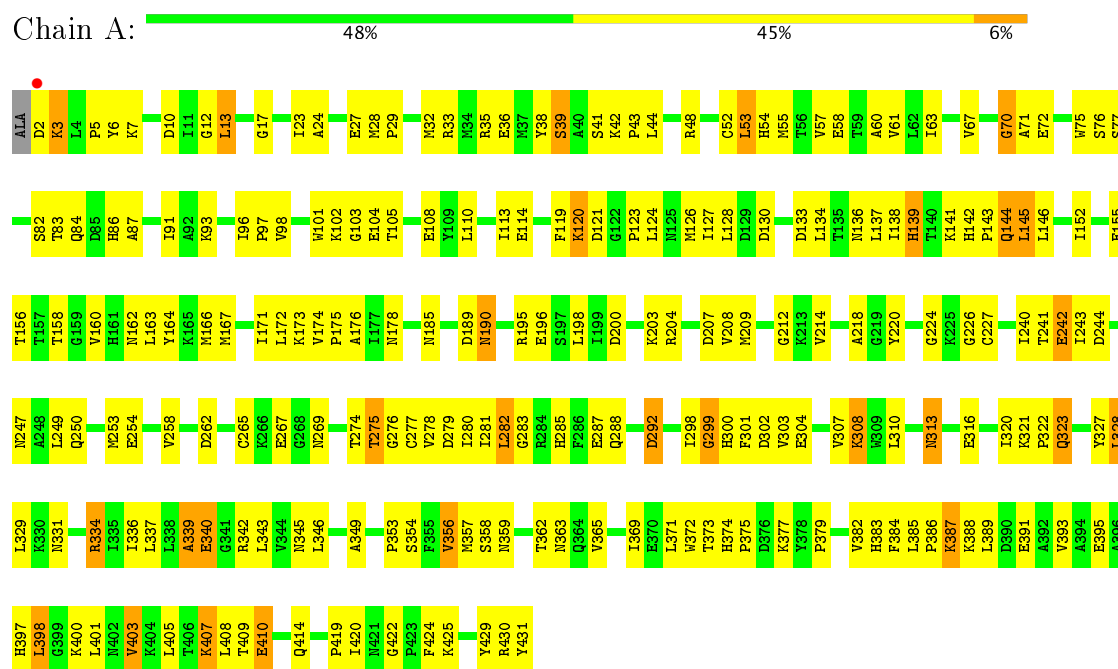
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	9	Total	O	0	0
			9	9		
4	B	12	Total	O	0	0
			12	12		
4	C	11	Total	O	0	0
			11	11		
4	D	8	Total	O	0	0
			8	8		

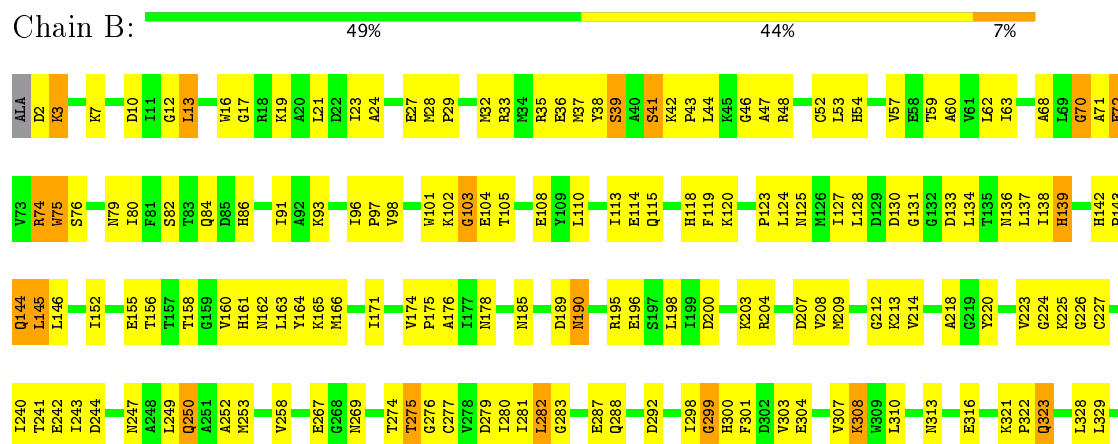
### 3 Residue-property plots

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: Adenosylhomocysteinase



#### • Molecule 1: Adenosylhomocysteinase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.34Å 109.37Å 104.07Å 90.00° 115.50° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80 20.01 – 2.79	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.80) 98.8 (20.01-2.79)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.28 (at 2.79Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.225 , 0.286 0.207 , 0.262	Depositor DCC
$R_{free}$ test set	4526 reflections (10.08%)	DCC
Wilson B-factor (Å <sup>2</sup> )	48.4	Xtriage
Anisotropy	0.417	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.16 , -1.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.208 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	13564	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% 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: ADN, NAD

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	0.43	0/3383	0.65	0/4579
1	B	0.43	0/3383	0.65	0/4579
1	C	0.42	0/3383	0.65	0/4579
1	D	0.43	0/3383	0.65	0/4579
All	All	0.43	0/13532	0.65	0/18316

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3318	0	3334	227	0
1	B	3318	0	3334	220	0
1	C	3318	0	3334	233	0
1	D	3318	0	3334	245	0
2	A	44	0	26	4	0
2	B	44	0	26	4	0
2	C	44	0	26	5	0
2	D	44	0	26	5	0
3	A	19	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	19	0	13	0	0
3	C	19	0	13	0	0
3	D	19	0	13	0	0
4	A	9	0	0	1	0
4	B	12	0	0	4	0
4	C	11	0	0	4	0
4	D	8	0	0	0	0
All	All	13564	0	13492	874	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 32.

All (874) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:419:PRO:HG2	1:C:422:GLY:HA3	1.36	1.06
1:A:419:PRO:HG2	1:A:422:GLY:HA3	1.38	1.03
1:B:419:PRO:HG2	1:B:422:GLY:HA3	1.40	1.03
1:D:419:PRO:HG2	1:D:422:GLY:HA3	1.42	0.99
1:D:353:PRO:HD2	1:D:356:VAL:HG11	1.44	0.99
1:A:127:ILE:HG23	1:A:134:LEU:HD12	1.45	0.98
1:A:214:VAL:H	1:A:269:ASN:HD22	1.11	0.97
1:A:247:ASN:HD21	1:B:425:LYS:HE2	1.31	0.96
1:B:353:PRO:HD2	1:B:356:VAL:HG11	1.46	0.95
1:B:136:ASN:HD21	1:B:162:ASN:HD21	1.15	0.95
1:C:127:ILE:HG23	1:C:134:LEU:HD12	1.46	0.94
1:C:41:SER:HB2	1:C:43:PRO:HD3	1.49	0.94
1:B:214:VAL:H	1:B:269:ASN:HD22	1.16	0.93
1:C:247:ASN:HD21	1:D:425:LYS:HE2	1.32	0.93
1:D:143:PRO:HA	1:D:146:LEU:HD23	1.50	0.92
1:D:41:SER:HB2	1:D:43:PRO:HD3	1.51	0.92
1:C:353:PRO:HD2	1:C:356:VAL:HG11	1.53	0.91
1:B:35:ARG:O	1:B:39:SER:HB2	1.69	0.91
1:C:247:ASN:HA	1:C:250:GLN:HE21	1.36	0.90
1:B:323:GLN:HG3	1:B:339:ALA:HA	1.54	0.90
1:C:214:VAL:H	1:C:269:ASN:HD22	1.19	0.89
1:A:323:GLN:HG3	1:A:339:ALA:HA	1.52	0.88
1:D:127:ILE:HG23	1:D:134:LEU:HD12	1.53	0.88
1:B:127:ILE:HG23	1:B:134:LEU:HD12	1.53	0.88
1:C:323:GLN:HG3	1:C:339:ALA:HA	1.53	0.88
1:D:247:ASN:HA	1:D:250:GLN:HE21	1.39	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:ASN:HA	1:A:250:GLN:HE21	1.37	0.86
1:D:385:LEU:HD12	1:D:386:PRO:HD2	1.58	0.86
1:C:343:LEU:HD23	1:C:346:LEU:HD12	1.58	0.86
1:B:143:PRO:HA	1:B:146:LEU:HD23	1.57	0.86
1:A:136:ASN:HD21	1:A:162:ASN:HD21	1.24	0.85
1:D:323:GLN:HG3	1:D:339:ALA:HA	1.58	0.85
1:A:353:PRO:HD2	1:A:356:VAL:HG11	1.57	0.85
1:A:35:ARG:O	1:A:39:SER:HB2	1.76	0.84
1:B:142:HIS:HB3	1:B:145:LEU:HD12	1.59	0.84
1:A:419:PRO:CG	1:A:422:GLY:HA3	2.07	0.84
1:A:143:PRO:HA	1:A:146:LEU:HD23	1.59	0.83
1:D:35:ARG:O	1:D:39:SER:HB2	1.78	0.83
1:D:343:LEU:HD23	1:D:346:LEU:HD12	1.59	0.83
1:C:110:LEU:O	1:C:114:GLU:HG3	1.79	0.82
1:A:60:ALA:HA	1:A:91:ILE:HD11	1.62	0.82
1:D:136:ASN:HD21	1:D:162:ASN:HD21	1.28	0.82
1:D:214:VAL:H	1:D:269:ASN:HD22	1.28	0.82
1:D:353:PRO:O	1:D:356:VAL:HG13	1.80	0.81
1:B:247:ASN:HA	1:B:250:GLN:HE21	1.45	0.81
1:A:425:LYS:HE2	1:B:247:ASN:HD21	1.46	0.81
1:B:161:HIS:HB2	4:B:443:HOH:O	1.81	0.81
1:B:343:LEU:HD23	1:B:346:LEU:HD12	1.63	0.80
1:C:143:PRO:HA	1:C:146:LEU:HD23	1.61	0.80
1:C:136:ASN:HD21	1:C:162:ASN:HD21	1.29	0.80
1:B:419:PRO:CG	1:B:422:GLY:HA3	2.11	0.80
1:C:419:PRO:CG	1:C:422:GLY:HA3	2.10	0.79
1:A:142:HIS:HB3	1:A:145:LEU:HD12	1.64	0.79
1:C:385:LEU:HD12	1:C:386:PRO:HD2	1.63	0.79
1:B:156:THR:HA	4:B:435:HOH:O	1.83	0.78
1:B:385:LEU:HD12	1:B:386:PRO:HD2	1.64	0.78
1:A:41:SER:HB2	1:A:43:PRO:HD3	1.65	0.78
1:D:60:ALA:HA	1:D:91:ILE:HD11	1.66	0.78
1:A:430:ARG:HD3	1:B:430:ARG:HA	1.66	0.77
1:C:244:ASP:HB3	1:C:247:ASN:HD22	1.50	0.77
1:C:419:PRO:HG2	1:C:422:GLY:CA	2.13	0.77
1:D:419:PRO:CG	1:D:422:GLY:HA3	2.15	0.77
1:A:156:THR:O	1:A:160:VAL:HG23	1.85	0.77
1:B:142:HIS:HB3	1:B:145:LEU:CD1	2.15	0.76
1:C:292:ASP:OD1	1:C:336:ILE:HD11	1.85	0.76
1:A:292:ASP:OD1	1:A:336:ILE:HD11	1.84	0.76
1:C:60:ALA:HA	1:C:91:ILE:HD11	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:LEU:O	1:A:114:GLU:HG3	1.86	0.76
1:C:35:ARG:O	1:C:39:SER:HB2	1.86	0.75
1:A:419:PRO:HG2	1:A:422:GLY:CA	2.14	0.75
1:B:292:ASP:OD1	1:B:336:ILE:HD11	1.87	0.74
1:A:385:LEU:HD12	1:A:386:PRO:HD2	1.70	0.74
1:B:130:ASP:O	1:B:156:THR:HG21	1.86	0.74
1:B:393:VAL:O	1:B:397:HIS:HD2	1.70	0.73
1:B:60:ALA:HA	1:B:91:ILE:HD11	1.70	0.73
1:D:353:PRO:HD2	1:D:356:VAL:CG1	2.17	0.73
1:B:41:SER:HB2	1:B:43:PRO:HD3	1.70	0.73
1:B:57:VAL:HG23	1:B:84:GLN:NE2	2.04	0.72
1:B:75:TRP:HH2	1:B:128:LEU:HD13	1.54	0.72
1:D:419:PRO:HG2	1:D:422:GLY:CA	2.16	0.72
1:A:142:HIS:HB3	1:A:145:LEU:CD1	2.18	0.72
1:C:190:ASN:HD22	1:C:190:ASN:N	1.88	0.71
1:A:398:LEU:HG	1:A:403:VAL:CG2	2.21	0.71
1:C:247:ASN:ND2	1:D:425:LYS:HE2	2.05	0.71
1:D:275:THR:HG22	1:D:276:GLY:H	1.56	0.71
1:D:343:LEU:CD2	1:D:346:LEU:HD12	2.21	0.70
1:B:398:LEU:HG	1:B:403:VAL:CG2	2.21	0.70
1:B:203:LYS:O	1:B:207:ASP:N	2.24	0.70
1:C:353:PRO:O	1:C:356:VAL:HG13	1.91	0.70
1:C:258:VAL:HB	1:D:403:VAL:HB	1.74	0.70
1:C:105:THR:OG1	1:C:108:GLU:HG3	1.91	0.70
1:B:110:LEU:O	1:B:114:GLU:HG3	1.92	0.69
1:B:419:PRO:HG2	1:B:422:GLY:CA	2.19	0.69
1:A:430:ARG:HA	1:B:430:ARG:HD3	1.73	0.69
1:D:220:TYR:CD1	1:D:240:ILE:HD13	2.28	0.69
1:D:292:ASP:OD1	1:D:336:ILE:HD11	1.93	0.69
1:B:213:LYS:NZ	4:B:436:HOH:O	2.25	0.69
1:C:247:ASN:HA	1:C:250:GLN:NE2	2.07	0.69
1:C:308:LYS:HD2	1:C:308:LYS:H	1.57	0.69
1:C:386:PRO:HG2	1:C:389:LEU:HD12	1.75	0.69
1:C:425:LYS:HE2	1:D:247:ASN:HD21	1.57	0.69
1:A:353:PRO:O	1:A:356:VAL:HG13	1.93	0.68
1:B:300:HIS:HA	1:B:343:LEU:HD11	1.75	0.68
1:A:220:TYR:CD1	1:A:240:ILE:HD13	2.29	0.68
1:D:142:HIS:HB3	1:D:145:LEU:HD12	1.76	0.68
1:D:185:ASN:ND2	1:D:360:SER:HB2	2.09	0.67
1:D:247:ASN:HA	1:D:250:GLN:NE2	2.10	0.67
1:B:386:PRO:HG2	1:B:389:LEU:HD12	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:ASN:ND2	1:B:425:LYS:HE2	2.07	0.67
1:D:10:ASP:HB3	1:D:13:LEU:HD23	1.77	0.67
1:B:209:MET:CE	1:D:196:GLU:HG3	2.25	0.67
1:D:142:HIS:HB3	1:D:145:LEU:CD1	2.24	0.67
1:A:343:LEU:HD23	1:A:346:LEU:HD12	1.77	0.66
1:A:275:THR:HG21	2:A:432:NAD:C8A	2.25	0.66
1:B:308:LYS:HD2	1:B:308:LYS:H	1.60	0.66
1:B:283:GLY:O	1:B:287:GLU:HG3	1.96	0.66
1:B:353:PRO:HD2	1:B:356:VAL:CG1	2.24	0.66
1:A:393:VAL:O	1:A:397:HIS:HD2	1.79	0.66
1:A:105:THR:OG1	1:A:108:GLU:HG3	1.95	0.65
1:A:127:ILE:CG2	1:A:134:LEU:HD12	2.24	0.65
1:A:17:GLY:HA2	1:A:86:HIS:HD2	1.61	0.65
1:A:398:LEU:CD2	1:A:405:LEU:HD22	2.27	0.65
1:D:57:VAL:HG23	1:D:84:GLN:NE2	2.12	0.64
1:A:3:LYS:O	4:A:440:HOH:O	2.15	0.64
1:B:142:HIS:N	1:B:143:PRO:CD	2.61	0.64
1:D:53:LEU:HG	1:D:130:ASP:HB2	1.78	0.64
1:C:275:THR:HG21	2:C:432:NAD:C8A	2.27	0.64
1:C:220:TYR:CD1	1:C:240:ILE:HD13	2.33	0.64
1:C:334:ARG:HD3	1:C:334:ARG:N	2.12	0.64
1:A:275:THR:O	1:A:304:GLU:OE2	2.16	0.64
1:B:101:TRP:NE1	1:B:104:GLU:HB3	2.13	0.64
1:B:105:THR:OG1	1:B:108:GLU:HG3	1.97	0.64
1:B:275:THR:HG22	1:B:276:GLY:H	1.63	0.64
1:A:300:HIS:HA	1:A:343:LEU:HD11	1.81	0.63
1:A:247:ASN:HA	1:A:250:GLN:NE2	2.10	0.63
1:A:301:PHE:C	1:A:303:VAL:H	2.00	0.63
1:B:298:ILE:HG12	1:B:298:ILE:O	1.99	0.63
1:C:142:HIS:N	1:C:143:PRO:CD	2.60	0.63
1:D:155:GLU:O	1:D:155:GLU:HG2	1.98	0.63
1:B:321:LYS:HB2	1:B:322:PRO:HD2	1.81	0.63
1:A:254:GLU:HG2	4:B:444:HOH:O	1.98	0.63
1:B:420:ILE:HG12	1:B:420:ILE:O	1.99	0.63
1:C:343:LEU:CD2	1:C:346:LEU:HD12	2.27	0.63
1:B:353:PRO:O	1:B:356:VAL:HG13	1.98	0.63
1:C:142:HIS:HB3	1:C:145:LEU:CD1	2.28	0.63
1:B:275:THR:HG21	2:B:432:NAD:C8A	2.29	0.63
1:A:190:ASN:HD22	1:A:190:ASN:N	1.95	0.62
1:C:398:LEU:HG	1:C:403:VAL:CG2	2.28	0.62
1:B:398:LEU:HG	1:B:403:VAL:HG22	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:LYS:HD2	1:A:308:LYS:H	1.63	0.62
1:D:44:LEU:HB3	1:D:71:ALA:HB2	1.81	0.62
1:A:386:PRO:HG2	1:A:389:LEU:HD12	1.82	0.62
1:C:152:ILE:HD11	1:C:174:VAL:HB	1.82	0.62
1:A:244:ASP:HB3	1:A:247:ASN:HD22	1.65	0.62
1:B:281:ILE:C	1:B:282:LEU:HD13	2.20	0.62
1:D:288:GLN:OE1	1:D:288:GLN:HA	2.00	0.62
1:C:72:GLU:HB3	1:C:119:PHE:CE2	2.35	0.62
1:D:142:HIS:N	1:D:143:PRO:CD	2.63	0.62
1:D:203:LYS:O	1:D:207:ASP:N	2.33	0.62
1:A:142:HIS:N	1:A:143:PRO:CD	2.61	0.62
1:A:275:THR:HG22	1:A:276:GLY:H	1.63	0.62
1:B:190:ASN:N	1:B:190:ASN:HD22	1.96	0.62
1:C:142:HIS:HB3	1:C:145:LEU:HD12	1.81	0.62
1:C:321:LYS:HB2	1:C:322:PRO:HD2	1.81	0.62
1:D:110:LEU:O	1:D:114:GLU:HG3	2.00	0.62
1:C:123:PRO:CB	1:C:145:LEU:HD22	2.30	0.61
1:C:28:MET:HB3	1:C:358:SER:HB2	1.82	0.61
1:C:38:TYR:HD1	1:C:43:PRO:HG3	1.65	0.61
1:C:57:VAL:HG23	1:C:84:GLN:NE2	2.15	0.61
1:C:38:TYR:CD1	1:C:43:PRO:HG3	2.36	0.61
1:D:398:LEU:HG	1:D:403:VAL:CG2	2.30	0.61
1:C:53:LEU:HG	1:C:130:ASP:HB2	1.82	0.61
1:A:243:ILE:HG21	1:B:408:LEU:HD13	1.81	0.61
1:B:124:LEU:H	1:B:124:LEU:HD23	1.65	0.61
1:B:53:LEU:HG	1:B:130:ASP:HB2	1.82	0.61
1:B:334:ARG:N	1:B:334:ARG:HD3	2.14	0.61
1:D:321:LYS:HB2	1:D:322:PRO:HD2	1.82	0.61
1:D:334:ARG:HD3	1:D:334:ARG:N	2.16	0.61
1:D:54:HIS:HB3	1:D:82:SER:OG	2.00	0.61
1:A:321:LYS:HB2	1:A:322:PRO:HD2	1.83	0.61
1:B:247:ASN:HA	1:B:250:GLN:NE2	2.16	0.61
1:C:188:PHE:CE1	1:D:249:LEU:HD21	2.36	0.61
1:D:299:GLY:O	2:D:432:NAD:H2N	2.01	0.61
1:A:53:LEU:HG	1:A:130:ASP:HB2	1.81	0.61
1:A:247:ASN:HD21	1:B:425:LYS:CE	2.10	0.61
1:C:142:HIS:N	1:C:143:PRO:HD3	2.15	0.61
1:D:105:THR:OG1	1:D:108:GLU:HG3	2.00	0.60
1:D:240:ILE:O	1:D:258:VAL:HA	2.00	0.60
1:C:54:HIS:HB3	1:C:82:SER:OG	2.01	0.60
1:B:343:LEU:CD2	1:B:346:LEU:HD12	2.30	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:298:ILE:HG12	1:D:298:ILE:O	2.01	0.60
1:B:166:MET:HA	1:B:171:ILE:HD12	1.84	0.60
1:B:185:ASN:ND2	1:B:360:SER:HB2	2.16	0.60
1:B:57:VAL:HG23	1:B:84:GLN:HE22	1.67	0.60
1:A:321:LYS:HB2	1:A:322:PRO:CD	2.31	0.60
1:D:275:THR:O	1:D:304:GLU:OE2	2.19	0.60
1:A:203:LYS:O	1:A:207:ASP:N	2.34	0.60
1:B:17:GLY:HA2	1:B:86:HIS:HD2	1.67	0.60
1:C:130:ASP:O	1:C:156:THR:HG21	2.01	0.60
1:D:190:ASN:HD22	1:D:190:ASN:N	1.98	0.60
1:B:200:ASP:O	1:B:204:ARG:HG3	2.02	0.59
1:A:55:MET:HB3	1:A:83:THR:HG23	1.84	0.59
1:B:162:ASN:O	1:B:166:MET:HG3	2.03	0.59
1:B:393:VAL:O	1:B:397:HIS:CD2	2.55	0.59
1:C:398:LEU:CD2	1:C:405:LEU:HD22	2.33	0.59
1:C:127:ILE:CG2	1:C:134:LEU:HD12	2.28	0.59
1:C:139:HIS:CE1	1:C:146:LEU:HD11	2.37	0.59
1:A:398:LEU:HG	1:A:403:VAL:HG22	1.83	0.59
1:C:284:ARG:HD2	4:C:440:HOH:O	2.02	0.59
1:D:308:LYS:HD2	1:D:308:LYS:H	1.67	0.59
1:C:178:ASN:HD22	1:C:384:PHE:HE1	1.51	0.59
1:D:393:VAL:O	1:D:397:HIS:HD2	1.85	0.59
1:D:42:LYS:N	1:D:43:PRO:CD	2.65	0.59
1:C:203:LYS:O	1:C:207:ASP:N	2.35	0.59
1:D:321:LYS:HB2	1:D:322:PRO:CD	2.32	0.59
1:D:301:PHE:C	1:D:303:VAL:H	2.06	0.59
1:B:308:LYS:HD2	1:B:308:LYS:N	2.18	0.58
1:C:244:ASP:CB	1:C:247:ASN:HD22	2.15	0.58
1:A:403:VAL:HB	1:B:258:VAL:HB	1.84	0.58
1:B:389:LEU:O	1:B:392:ALA:HB3	2.02	0.58
1:B:321:LYS:HB2	1:B:322:PRO:CD	2.32	0.58
1:C:275:THR:HB	1:C:277:CYS:H	1.68	0.58
1:A:123:PRO:CB	1:A:145:LEU:HD22	2.32	0.58
1:B:299:GLY:O	2:B:432:NAD:H2N	2.04	0.58
1:C:249:LEU:HD21	1:D:188:PHE:CE1	2.39	0.58
1:D:300:HIS:HA	1:D:343:LEU:HD11	1.84	0.58
1:C:245:PRO:HG2	1:D:391:GLU:HB3	1.86	0.58
1:B:136:ASN:HD21	1:B:162:ASN:ND2	1.92	0.58
1:B:240:ILE:O	1:B:258:VAL:HA	2.03	0.58
1:C:42:LYS:N	1:C:43:PRO:CD	2.67	0.58
1:C:218:ALA:HA	1:C:241:THR:OG1	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:53:LEU:O	1:B:54:HIS:C	2.41	0.58
1:A:334:ARG:HD3	1:A:334:ARG:N	2.18	0.57
1:C:300:HIS:HA	1:C:343:LEU:HD11	1.86	0.57
1:C:53:LEU:O	1:C:54:HIS:C	2.41	0.57
1:A:320:ILE:HG22	1:A:321:LYS:HG2	1.85	0.57
1:B:52:CYS:HA	1:B:76:SER:O	2.04	0.57
1:D:275:THR:HG21	2:D:432:NAD:C8A	2.34	0.57
1:B:10:ASP:HB3	1:B:13:LEU:HD23	1.85	0.57
1:B:75:TRP:CH2	1:B:128:LEU:HD13	2.36	0.57
1:B:277:CYS:O	1:B:304:GLU:HG2	2.04	0.57
1:C:430:ARG:HD3	1:D:430:ARG:HA	1.87	0.57
1:B:44:LEU:HB3	1:B:71:ALA:HB2	1.86	0.57
1:B:160:VAL:O	1:B:163:LEU:HB2	2.05	0.57
1:C:162:ASN:O	1:C:166:MET:HG3	2.04	0.57
1:C:328:LEU:HD12	1:C:329:LEU:N	2.19	0.57
1:B:101:TRP:HD1	1:B:102:LYS:O	1.86	0.57
1:A:382:VAL:HG13	1:A:382:VAL:O	2.03	0.57
1:C:283:GLY:O	1:C:287:GLU:HG3	2.04	0.57
1:C:301:PHE:C	1:C:303:VAL:H	2.07	0.57
1:C:72:GLU:HB3	1:C:119:PHE:HE2	1.68	0.57
1:D:48:ARG:HB2	1:D:125:ASN:ND2	2.18	0.57
1:D:195:ARG:HG3	1:D:226:GLY:O	2.05	0.57
1:D:283:GLY:O	1:D:287:GLU:HG3	2.05	0.57
1:A:299:GLY:O	2:A:432:NAD:H2N	2.05	0.57
1:D:178:ASN:HD22	1:D:384:PHE:HE1	1.52	0.57
1:D:13:LEU:HB3	1:D:86:HIS:HA	1.87	0.57
1:C:10:ASP:HB3	1:C:13:LEU:HD23	1.86	0.56
1:D:134:LEU:O	1:D:138:ILE:HG13	2.05	0.56
1:B:178:ASN:HD22	1:B:384:PHE:HE1	1.53	0.56
1:A:10:ASP:HB3	1:A:13:LEU:HD23	1.87	0.56
1:A:57:VAL:HG23	1:A:84:GLN:NE2	2.20	0.56
1:C:321:LYS:HB2	1:C:322:PRO:CD	2.35	0.56
1:D:389:LEU:O	1:D:392:ALA:HB3	2.05	0.56
1:C:160:VAL:O	1:C:163:LEU:HB2	2.05	0.56
1:B:279:ASP:HA	1:B:282:LEU:HD11	1.88	0.56
1:A:166:MET:HA	1:A:171:ILE:HD12	1.88	0.56
1:C:155:GLU:HG2	1:C:155:GLU:O	2.05	0.56
1:C:240:ILE:O	1:C:258:VAL:HA	2.05	0.56
1:A:164:TYR:CE1	1:A:382:VAL:HG11	2.40	0.56
1:A:276:GLY:O	1:B:415:TYR:HE2	1.88	0.56
1:B:155:GLU:O	1:B:155:GLU:HG2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:298:ILE:O	1:B:298:ILE:CG1	2.52	0.56
1:B:220:TYR:CD1	1:B:240:ILE:HD13	2.41	0.56
1:C:308:LYS:HD2	1:C:308:LYS:N	2.21	0.56
1:D:101:TRP:NE1	1:D:104:GLU:HB3	2.21	0.56
1:D:307:VAL:O	1:D:310:LEU:HB2	2.05	0.56
1:B:139:HIS:CE1	1:B:146:LEU:HD11	2.42	0.55
1:D:398:LEU:HG	1:D:403:VAL:HG22	1.87	0.55
1:B:308:LYS:CD	1:B:308:LYS:H	2.15	0.55
1:C:110:LEU:HD22	1:C:110:LEU:O	2.06	0.55
1:C:353:PRO:HD2	1:C:356:VAL:CG1	2.32	0.55
1:C:373:THR:HG22	1:C:374:HIS:CE1	2.42	0.55
1:D:398:LEU:CD2	1:D:405:LEU:HD22	2.37	0.55
1:D:123:PRO:CB	1:D:145:LEU:HD22	2.36	0.55
1:A:54:HIS:HB3	1:A:82:SER:OG	2.06	0.55
1:B:144:GLN:H	1:B:144:GLN:CD	2.10	0.55
1:C:188:PHE:HE1	1:D:249:LEU:HD21	1.72	0.55
1:B:142:HIS:CB	1:B:145:LEU:HD12	2.34	0.55
1:C:126:MET:CE	1:C:372:TRP:HB2	2.36	0.55
1:C:113:ILE:HG23	1:C:134:LEU:HD23	1.89	0.55
1:C:44:LEU:HB3	1:C:71:ALA:HB2	1.88	0.55
1:D:249:LEU:O	1:D:253:MET:HG2	2.07	0.55
1:A:195:ARG:HG3	1:A:226:GLY:O	2.07	0.55
1:C:37:MET:HE2	1:C:38:TYR:CE2	2.42	0.55
1:D:353:PRO:O	1:D:356:VAL:CG1	2.54	0.55
1:A:160:VAL:O	1:A:163:LEU:HB2	2.07	0.55
1:D:60:ALA:CA	1:D:91:ILE:HD11	2.37	0.55
1:B:198:LEU:HD22	1:B:227:CYS:HB3	1.88	0.55
1:B:301:PHE:C	1:B:303:VAL:H	2.09	0.55
1:B:38:TYR:CD1	1:B:43:PRO:HG3	2.41	0.55
1:B:407:LYS:CD	1:B:420:ILE:HD11	2.36	0.55
1:C:307:VAL:O	1:C:310:LEU:HB2	2.06	0.55
1:B:209:MET:HA	1:D:196:GLU:OE1	2.07	0.55
1:A:101:TRP:NE1	1:A:104:GLU:HB3	2.22	0.54
1:B:301:PHE:HB2	1:B:303:VAL:HG22	1.88	0.54
1:D:3:LYS:N	1:D:3:LYS:HD2	2.21	0.54
1:B:142:HIS:N	1:B:143:PRO:HD3	2.21	0.54
1:A:307:VAL:O	1:A:310:LEU:HB2	2.07	0.54
1:A:42:LYS:N	1:A:43:PRO:CD	2.70	0.54
1:C:308:LYS:CD	1:C:308:LYS:H	2.16	0.54
1:C:408:LEU:HD13	1:D:243:ILE:HG21	1.87	0.54
1:D:38:TYR:CD1	1:D:43:PRO:HG3	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:LEU:N	1:B:124:LEU:HD23	2.21	0.54
1:C:301:PHE:HB2	1:C:303:VAL:HG22	1.90	0.54
1:C:63:ILE:HD12	1:C:91:ILE:HD13	1.90	0.54
1:B:398:LEU:HG	1:B:403:VAL:HG21	1.90	0.54
1:C:249:LEU:HD21	1:D:188:PHE:HE1	1.73	0.54
1:A:142:HIS:N	1:A:143:PRO:HD3	2.21	0.54
1:A:277:CYS:HB3	1:A:280:ILE:HD11	1.90	0.54
1:A:374:HIS:N	1:A:375:PRO:CD	2.70	0.54
1:B:369:ILE:O	1:B:373:THR:HB	2.08	0.54
1:C:299:GLY:O	2:C:432:NAD:H2N	2.09	0.54
1:D:28:MET:HA	1:D:358:SER:HB2	1.90	0.54
1:A:155:GLU:HG2	1:A:155:GLU:O	2.08	0.53
1:B:358:SER:OG	1:B:397:HIS:HE1	1.91	0.53
1:D:53:LEU:O	1:D:54:HIS:C	2.46	0.53
1:A:224:GLY:HA2	1:A:274:THR:HG21	1.90	0.53
1:C:398:LEU:HG	1:C:403:VAL:HG22	1.90	0.53
1:D:386:PRO:HG2	1:D:389:LEU:HD12	1.90	0.53
1:A:277:CYS:O	1:A:304:GLU:HG2	2.08	0.53
1:A:44:LEU:HB3	1:A:71:ALA:HB2	1.89	0.53
1:D:194:CYS:SG	1:D:223:VAL:HG13	2.48	0.53
1:B:209:MET:HE2	1:D:196:GLU:HG3	1.89	0.53
1:C:279:ASP:OD2	1:D:411:LYS:HD3	2.09	0.53
1:D:190:ASN:ND2	2:D:432:NAD:H5N	2.23	0.53
1:B:16:TRP:O	1:B:19:LYS:HB2	2.07	0.53
1:C:139:HIS:ND1	1:C:146:LEU:HD11	2.24	0.53
1:D:185:ASN:HB2	1:D:363:ASN:ND2	2.23	0.53
1:D:52:CYS:HA	1:D:76:SER:O	2.09	0.53
1:A:27:GLU:C	1:A:29:PRO:HD3	2.29	0.53
1:A:343:LEU:CD2	1:A:346:LEU:HD12	2.38	0.53
1:A:369:ILE:O	1:A:373:THR:HB	2.08	0.53
1:C:200:ASP:O	1:C:204:ARG:HG3	2.09	0.53
1:A:75:TRP:HH2	1:A:128:LEU:HD13	1.74	0.53
1:A:136:ASN:HD21	1:A:162:ASN:ND2	2.00	0.53
1:B:123:PRO:CB	1:B:145:LEU:HD22	2.38	0.53
1:D:273:THR:OG1	1:D:297:ASN:OD1	2.27	0.53
1:D:277:CYS:O	1:D:304:GLU:HG2	2.09	0.53
1:C:275:THR:HG22	1:C:276:GLY:H	1.74	0.53
1:A:24:ALA:O	1:A:28:MET:HG3	2.09	0.53
1:A:178:ASN:N	1:A:383:HIS:O	2.41	0.53
1:A:275:THR:HG23	2:A:432:NAD:O4B	2.08	0.53
1:C:298:ILE:O	1:C:299:GLY:O	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:372:TRP:O	1:D:372:TRP:CG	2.61	0.53
1:A:52:CYS:HA	1:A:76:SER:O	2.09	0.52
1:B:288:GLN:OE1	1:B:288:GLN:HA	2.09	0.52
1:A:298:ILE:O	1:A:298:ILE:HG12	2.10	0.52
1:D:38:TYR:HD1	1:D:43:PRO:HG3	1.74	0.52
1:D:425:LYS:HD3	1:D:429:TYR:CE2	2.45	0.52
1:C:179:VAL:HG13	1:C:363:ASN:HB3	1.90	0.52
1:D:281:ILE:C	1:D:282:LEU:HD13	2.30	0.52
1:A:353:PRO:HD2	1:A:356:VAL:CG1	2.33	0.52
1:C:75:TRP:HH2	1:C:128:LEU:HD13	1.75	0.52
1:D:130:ASP:O	1:D:156:THR:HG21	2.10	0.52
1:A:337:LEU:C	1:A:337:LEU:HD13	2.30	0.52
1:C:279:ASP:HA	1:C:282:LEU:HD11	1.90	0.52
1:A:313:ASN:N	1:A:313:ASN:HD22	2.07	0.52
1:B:10:ASP:OD1	1:B:12:GLY:N	2.42	0.52
1:C:320:ILE:HG22	1:C:321:LYS:HG2	1.91	0.52
1:D:57:VAL:HG23	1:D:84:GLN:HE22	1.74	0.52
1:A:283:GLY:O	1:A:287:GLU:HG3	2.09	0.52
1:A:38:TYR:CD1	1:A:43:PRO:HG3	2.44	0.52
1:A:3:LYS:N	1:A:3:LYS:HD2	2.25	0.52
1:A:398:LEU:HG	1:A:403:VAL:HG21	1.91	0.52
1:B:130:ASP:C	1:B:156:THR:HG21	2.30	0.52
1:B:190:ASN:ND2	2:B:432:NAD:H5N	2.25	0.52
1:C:224:GLY:HA2	1:C:274:THR:HG21	1.91	0.52
1:C:316:GLU:HG3	1:C:328:LEU:HB3	1.90	0.52
1:A:212:GLY:HA2	1:D:252:ALA:O	2.09	0.52
1:A:72:GLU:HB3	1:A:119:PHE:CE2	2.44	0.52
1:B:277:CYS:HB3	1:B:280:ILE:HD11	1.90	0.52
1:D:387:LYS:HE2	1:D:431:TYR:OH	2.09	0.52
1:A:398:LEU:HD23	1:A:405:LEU:HD22	1.92	0.52
1:C:156:THR:O	1:C:160:VAL:HG23	2.10	0.52
1:C:401:LEU:HD12	1:C:403:VAL:HG13	1.91	0.52
1:A:362:THR:HB	1:A:393:VAL:HG13	1.93	0.51
1:B:42:LYS:N	1:B:43:PRO:CD	2.73	0.51
1:C:152:ILE:CD1	1:C:174:VAL:HB	2.41	0.51
1:A:142:HIS:CB	1:A:145:LEU:HD12	2.37	0.51
1:B:38:TYR:HD1	1:B:43:PRO:HG3	1.73	0.51
1:C:16:TRP:O	1:C:19:LYS:HB2	2.10	0.51
1:C:80:ILE:HG13	1:C:81:PHE:CD2	2.45	0.51
1:A:17:GLY:HA2	1:A:86:HIS:CD2	2.43	0.51
1:B:337:LEU:C	1:B:337:LEU:HD13	2.31	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:298:ILE:O	1:D:299:GLY:O	2.29	0.51
1:A:126:MET:HE1	1:A:372:TRP:HB2	1.93	0.51
1:C:101:TRP:NE1	1:C:104:GLU:HB3	2.24	0.51
1:B:124:LEU:H	1:B:124:LEU:CD2	2.23	0.51
1:B:209:MET:HE3	1:D:196:GLU:HG3	1.92	0.51
1:B:244:ASP:HB3	1:B:247:ASN:HD22	1.76	0.51
1:C:301:PHE:N	4:C:434:HOH:O	2.36	0.51
1:D:308:LYS:CD	1:D:308:LYS:H	2.22	0.51
1:D:17:GLY:HA2	1:D:86:HIS:HD2	1.76	0.51
1:A:113:ILE:HG23	1:A:134:LEU:HD23	1.91	0.51
1:C:166:MET:HA	1:C:171:ILE:HD12	1.92	0.51
1:C:323:GLN:CG	1:C:339:ALA:HA	2.35	0.51
1:D:328:LEU:HD12	1:D:329:LEU:N	2.25	0.51
1:A:162:ASN:O	1:A:166:MET:HG3	2.11	0.51
1:A:323:GLN:N	1:A:323:GLN:HE21	2.09	0.51
1:C:425:LYS:HE2	1:D:247:ASN:ND2	2.26	0.51
1:A:328:LEU:HD12	1:A:329:LEU:N	2.26	0.51
1:B:139:HIS:ND1	1:B:146:LEU:HD11	2.25	0.51
1:C:190:ASN:N	1:C:190:ASN:ND2	2.57	0.51
1:C:52:CYS:HA	1:C:76:SER:O	2.11	0.51
1:A:53:LEU:O	1:A:54:HIS:C	2.48	0.50
1:B:382:VAL:O	1:B:382:VAL:HG13	2.11	0.50
1:C:288:GLN:OE1	1:C:288:GLN:HA	2.11	0.50
1:D:163:LEU:HD13	1:D:176:ALA:CB	2.41	0.50
1:D:96:ILE:O	1:D:98:VAL:HG23	2.11	0.50
1:D:101:TRP:HD1	1:D:102:LYS:O	1.93	0.50
1:D:353:PRO:CD	1:D:356:VAL:HG11	2.29	0.50
1:D:59:THR:O	1:D:62:LEU:HB3	2.11	0.50
1:A:124:LEU:N	1:A:124:LEU:HD23	2.27	0.50
1:A:379:PRO:O	1:A:383:HIS:HE1	1.94	0.50
1:B:79:ASN:HB3	1:B:82:SER:OG	2.11	0.50
1:D:275:THR:HG22	1:D:276:GLY:N	2.25	0.50
1:D:401:LEU:HD12	1:D:403:VAL:HG13	1.94	0.50
1:A:155:GLU:HG3	1:A:185:ASN:HD21	1.77	0.50
1:A:301:PHE:HB2	1:A:303:VAL:HG22	1.93	0.50
1:B:127:ILE:CG2	1:B:134:LEU:HD12	2.34	0.50
1:C:275:THR:O	1:C:304:GLU:OE2	2.30	0.50
1:C:27:GLU:C	1:C:29:PRO:HD3	2.32	0.50
1:C:374:HIS:N	1:C:375:PRO:CD	2.74	0.50
1:A:262:ASP:O	1:A:265:CYS:SG	2.66	0.50
1:A:395:GLU:HA	1:A:398:LEU:HD22	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:185:ASN:HB2	1:C:363:ASN:ND2	2.27	0.50
1:C:28:MET:CB	1:C:358:SER:HB2	2.41	0.50
1:C:386:PRO:CG	1:C:389:LEU:HD12	2.40	0.50
1:C:276:GLY:O	1:D:415:TYR:HE2	1.93	0.50
1:B:28:MET:HA	1:B:358:SER:HB2	1.93	0.50
1:C:101:TRP:HD1	1:C:102:LYS:O	1.95	0.50
1:C:398:LEU:HG	1:C:403:VAL:HG21	1.93	0.50
1:D:407:LYS:HD3	1:D:420:ILE:HD11	1.93	0.50
1:B:134:LEU:O	1:B:138:ILE:HG13	2.12	0.50
1:B:152:ILE:HD11	1:B:174:VAL:HB	1.93	0.50
1:B:307:VAL:O	1:B:310:LEU:HB2	2.12	0.50
1:B:60:ALA:CA	1:B:91:ILE:HD11	2.40	0.50
1:C:28:MET:HA	1:C:358:SER:HB2	1.94	0.50
1:C:63:ILE:HD11	1:C:75:TRP:CG	2.47	0.50
1:A:28:MET:HB3	1:A:358:SER:HB2	1.93	0.50
1:C:164:TYR:CE1	1:C:382:VAL:HG11	2.47	0.50
1:C:195:ARG:HG3	1:C:226:GLY:O	2.12	0.50
1:C:13:LEU:HB3	1:C:86:HIS:HA	1.93	0.50
1:D:281:ILE:HA	1:D:285:HIS:ND1	2.27	0.50
1:D:419:PRO:HB2	1:D:422:GLY:H	1.76	0.50
1:A:190:ASN:ND2	2:A:432:NAD:H5N	2.27	0.49
1:B:165:LYS:NZ	1:B:165:LYS:HB2	2.27	0.49
1:C:275:THR:HG23	2:C:432:NAD:O4B	2.11	0.49
1:D:113:ILE:HG23	1:D:134:LEU:HD23	1.94	0.49
1:D:279:ASP:HA	1:D:282:LEU:HD11	1.93	0.49
1:A:298:ILE:O	1:A:299:GLY:O	2.28	0.49
1:B:208:VAL:HG22	1:B:209:MET:N	2.27	0.49
1:B:398:LEU:CD2	1:B:405:LEU:HD22	2.43	0.49
1:C:273:THR:OG1	1:C:297:ASN:HB2	2.11	0.49
1:C:403:VAL:HB	1:D:258:VAL:HB	1.94	0.49
1:A:323:GLN:CG	1:A:339:ALA:HA	2.36	0.49
1:A:164:TYR:CD1	1:A:382:VAL:HG11	2.48	0.49
1:B:224:GLY:HA2	1:B:274:THR:HG21	1.94	0.49
1:C:3:LYS:N	1:C:3:LYS:HD2	2.28	0.49
1:D:278:VAL:HG12	1:D:303:VAL:HB	1.93	0.49
1:D:407:LYS:HE3	1:D:408:LEU:O	2.13	0.49
1:A:340:GLU:HB3	1:A:342:ARG:NH2	2.28	0.49
1:A:258:VAL:HB	1:B:403:VAL:HB	1.94	0.49
1:D:27:GLU:C	1:D:29:PRO:HD3	2.32	0.49
1:A:429:TYR:HD2	1:A:431:TYR:CE1	2.30	0.49
1:D:407:LYS:CD	1:D:420:ILE:HD11	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:275:THR:O	1:B:304:GLU:OE2	2.30	0.49
1:C:32:MET:O	1:C:36:GLU:HG3	2.12	0.49
1:D:16:TRP:O	1:D:19:LYS:HB2	2.12	0.49
1:A:409:THR:O	1:A:410:GLU:C	2.51	0.49
1:C:185:ASN:ND2	1:C:360:SER:HB2	2.27	0.49
1:A:101:TRP:HD1	1:A:102:LYS:O	1.96	0.49
1:B:185:ASN:HB2	1:B:363:ASN:ND2	2.28	0.49
1:B:47:ALA:HB2	1:B:372:TRP:CE2	2.48	0.49
1:B:96:ILE:O	1:B:98:VAL:HG23	2.13	0.49
1:D:369:ILE:O	1:D:373:THR:HB	2.12	0.49
1:D:425:LYS:HD3	1:D:429:TYR:CD2	2.47	0.49
1:B:249:LEU:O	1:B:253:MET:HG2	2.14	0.48
1:B:316:GLU:HG3	1:B:328:LEU:HB3	1.95	0.48
1:C:164:TYR:CD1	1:C:382:VAL:HG11	2.48	0.48
1:D:174:VAL:CG1	1:D:175:PRO:HD2	2.43	0.48
1:A:17:GLY:HA3	1:A:86:HIS:O	2.13	0.48
1:A:301:PHE:HB3	1:A:303:VAL:HG13	1.95	0.48
1:C:17:GLY:HA2	1:C:86:HIS:HD2	1.78	0.48
1:D:28:MET:HB3	1:D:358:SER:HB2	1.93	0.48
1:B:189:ASP:C	1:B:190:ASN:HD22	2.16	0.48
1:D:183:VAL:HG21	1:D:431:TYR:CE1	2.48	0.48
1:A:275:THR:HB	1:A:277:CYS:H	1.78	0.48
1:B:13:LEU:HB3	1:B:86:HIS:HA	1.95	0.48
1:A:48:ARG:NH1	1:A:123:PRO:O	2.45	0.48
1:B:113:ILE:HG23	1:B:134:LEU:HD23	1.94	0.48
1:C:249:LEU:CD2	1:D:188:PHE:HE1	2.26	0.48
1:C:292:ASP:OD1	1:C:336:ILE:CD1	2.58	0.48
1:D:72:GLU:HB3	1:D:119:PHE:CE2	2.49	0.48
1:D:124:LEU:N	1:D:124:LEU:HD23	2.29	0.48
1:D:127:ILE:CG2	1:D:134:LEU:HD12	2.33	0.48
1:D:220:TYR:CZ	1:D:225:LYS:HG2	2.48	0.48
1:D:374:HIS:N	1:D:375:PRO:CD	2.76	0.48
1:D:393:VAL:O	1:D:397:HIS:CD2	2.67	0.48
1:B:196:GLU:HG3	1:D:209:MET:CE	2.43	0.48
1:C:242:GLU:O	1:D:405:LEU:HD12	2.14	0.48
1:A:152:ILE:HD11	1:A:174:VAL:HB	1.96	0.48
1:C:281:ILE:C	1:C:282:LEU:HD13	2.34	0.48
1:D:308:LYS:HD2	1:D:308:LYS:N	2.28	0.48
1:C:181:ASP:OD1	1:D:428:HIS:CE1	2.67	0.48
1:A:178:ASN:HD22	1:A:384:PHE:HE1	1.59	0.47
1:B:379:PRO:O	1:B:383:HIS:HE1	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:27:GLU:O	1:C:29:PRO:HD3	2.14	0.47
1:C:57:VAL:HG23	1:C:84:GLN:HE22	1.78	0.47
1:A:301:PHE:C	1:A:303:VAL:N	2.68	0.47
1:B:27:GLU:O	1:B:355:PHE:HA	2.14	0.47
1:C:206:THR:OG1	1:C:208:VAL:HG12	2.14	0.47
1:A:139:HIS:CE1	1:A:146:LEU:HD11	2.49	0.47
1:A:13:LEU:HB3	1:A:86:HIS:HA	1.97	0.47
1:A:292:ASP:OD1	1:A:336:ILE:CD1	2.58	0.47
1:D:298:ILE:CG1	1:D:298:ILE:O	2.61	0.47
1:A:174:VAL:CG1	1:A:175:PRO:HD2	2.43	0.47
1:B:419:PRO:HB2	1:B:422:GLY:H	1.79	0.47
1:B:48:ARG:H	1:B:125:ASN:CG	2.15	0.47
1:C:144:GLN:H	1:C:144:GLN:CD	2.16	0.47
1:C:410:GLU:O	1:C:414:GLN:HB2	2.15	0.47
1:D:241:THR:HG22	1:D:259:THR:O	2.15	0.47
1:C:243:ILE:HG21	1:D:408:LEU:HD13	1.96	0.47
1:B:345:ASN:O	1:B:349:ALA:HB3	2.15	0.47
1:B:374:HIS:N	1:B:375:PRO:CD	2.77	0.47
1:B:275:THR:HB	1:B:277:CYS:H	1.79	0.47
1:B:164:TYR:CE1	1:B:382:VAL:HG11	2.50	0.47
1:A:130:ASP:C	1:A:156:THR:HG21	2.35	0.47
1:A:44:LEU:C	1:A:70:GLY:O	2.53	0.47
1:C:393:VAL:O	1:C:397:HIS:HD2	1.98	0.47
1:A:420:ILE:HG12	1:A:420:ILE:O	2.15	0.47
1:B:27:GLU:C	1:B:29:PRO:HD3	2.35	0.47
1:C:395:GLU:HA	1:C:398:LEU:HD22	1.96	0.46
1:D:156:THR:O	1:D:160:VAL:HG23	2.15	0.46
1:C:415:TYR:HE2	1:D:276:GLY:O	1.98	0.46
1:A:145:LEU:HG	1:A:145:LEU:H	1.45	0.46
1:B:143:PRO:CA	1:B:146:LEU:HD23	2.37	0.46
1:B:212:GLY:HA2	1:C:252:ALA:O	2.15	0.46
1:D:178:ASN:N	1:D:383:HIS:O	2.44	0.46
1:A:10:ASP:HB3	1:A:13:LEU:CD2	2.46	0.46
1:A:208:VAL:HG22	1:A:209:MET:N	2.30	0.46
1:C:136:ASN:HD21	1:C:162:ASN:ND2	2.04	0.46
1:B:209:MET:HG3	1:D:196:GLU:OE1	2.16	0.46
1:A:189:ASP:C	1:A:190:ASN:HD22	2.18	0.46
1:A:279:ASP:HA	1:A:282:LEU:HD11	1.97	0.46
1:C:372:TRP:O	1:C:372:TRP:CG	2.68	0.46
1:D:10:ASP:HB3	1:D:13:LEU:CD2	2.43	0.46
1:A:218:ALA:HA	1:A:241:THR:OG1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:63:ILE:HD11	1:B:75:TRP:CG	2.50	0.46
1:C:337:LEU:HD13	1:C:337:LEU:C	2.36	0.46
1:A:72:GLU:HB3	1:A:119:PHE:HE2	1.81	0.46
1:A:139:HIS:ND1	1:A:146:LEU:HD11	2.31	0.46
1:B:373:THR:HG22	1:B:374:HIS:CE1	2.51	0.46
1:B:68:ALA:C	1:B:70:GLY:H	2.19	0.46
1:A:196:GLU:HG3	1:C:209:MET:CE	2.46	0.46
1:D:334:ARG:HH11	1:D:334:ARG:HG2	1.81	0.46
1:D:407:LYS:HE2	1:D:407:LYS:HB3	1.58	0.46
1:D:44:LEU:C	1:D:70:GLY:O	2.54	0.46
1:A:387:LYS:O	1:A:391:GLU:HG3	2.15	0.46
1:C:430:ARG:O	1:C:431:TYR:C	2.54	0.46
1:D:167:MET:HB2	1:D:172:LEU:HD22	1.98	0.46
1:D:316:GLU:HG3	1:D:328:LEU:HB3	1.98	0.46
1:C:48:ARG:NH1	1:C:123:PRO:O	2.49	0.46
1:C:174:VAL:CG1	1:C:175:PRO:HD2	2.45	0.46
1:C:189:ASP:C	1:C:190:ASN:HD22	2.19	0.46
1:D:17:GLY:HA2	1:D:86:HIS:CD2	2.50	0.46
1:A:164:TYR:CE1	1:A:382:VAL:CG1	2.99	0.46
1:B:407:LYS:HD3	1:B:420:ILE:HD11	1.97	0.46
1:D:21:LEU:N	1:D:21:LEU:HD23	2.31	0.46
1:D:53:LEU:HG	1:D:130:ASP:CB	2.45	0.46
1:D:60:ALA:CB	1:D:91:ILE:HD11	2.46	0.46
1:A:126:MET:CE	1:A:372:TRP:HB2	2.45	0.45
1:B:220:TYR:CZ	1:B:225:LYS:HG2	2.51	0.45
1:B:387:LYS:HG2	1:B:423:PRO:HB3	1.97	0.45
1:C:48:ARG:HG2	1:C:119:PHE:CD2	2.52	0.45
1:D:152:ILE:HD11	1:D:174:VAL:HB	1.98	0.45
1:A:288:GLN:OE1	1:A:288:GLN:HA	2.17	0.45
1:B:10:ASP:HB3	1:B:13:LEU:CD2	2.46	0.45
1:B:59:THR:O	1:B:62:LEU:HB3	2.16	0.45
1:B:74:ARG:HG3	1:B:97:PRO:HB2	1.98	0.45
1:C:298:ILE:O	1:C:298:ILE:HG12	2.15	0.45
1:D:224:GLY:HA2	1:D:274:THR:HG21	1.97	0.45
1:A:244:ASP:CB	1:A:247:ASN:HD22	2.28	0.45
1:A:38:TYR:HD1	1:A:43:PRO:HG3	1.81	0.45
1:B:60:ALA:CB	1:B:91:ILE:HD11	2.47	0.45
1:D:46:GLY:O	1:D:372:TRP:CH2	2.69	0.45
1:D:398:LEU:HG	1:D:403:VAL:HG21	1.98	0.45
1:A:393:VAL:O	1:A:397:HIS:CD2	2.66	0.45
1:C:151:GLY:HA3	1:C:371:LEU:HG	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:301:PHE:HB3	1:C:303:VAL:HG13	1.99	0.45
1:C:416:LEU:HD11	1:D:277:CYS:SG	2.56	0.45
1:C:74:ARG:HG3	1:C:97:PRO:HB2	1.98	0.45
1:A:407:LYS:CD	1:A:420:ILE:HD11	2.46	0.45
1:B:275:THR:HG23	2:B:432:NAD:O4B	2.17	0.45
1:D:285:HIS:O	1:D:288:GLN:HB2	2.16	0.45
1:D:275:THR:HG23	2:D:432:NAD:O4B	2.15	0.45
1:B:178:ASN:N	1:B:383:HIS:O	2.46	0.45
1:C:28:MET:HA	1:C:358:SER:CB	2.46	0.45
1:D:2:ASP:C	1:D:3:LYS:HD2	2.37	0.45
1:D:318:VAL:HG22	1:D:326:ARG:O	2.17	0.45
1:A:407:LYS:HE2	1:A:407:LYS:HB3	1.50	0.45
1:B:275:THR:HG22	1:B:276:GLY:N	2.31	0.45
1:B:48:ARG:NH1	1:B:123:PRO:O	2.49	0.45
1:C:164:TYR:CE1	1:C:382:VAL:CG1	3.00	0.45
1:C:83:THR:HG22	1:C:84:GLN:N	2.31	0.45
1:A:124:LEU:H	1:A:124:LEU:HD23	1.81	0.45
1:A:134:LEU:O	1:A:138:ILE:HG13	2.17	0.45
1:A:374:HIS:O	1:A:377:LYS:HB2	2.16	0.45
1:B:17:GLY:HA2	1:B:86:HIS:CD2	2.48	0.45
1:C:138:ILE:O	1:C:139:HIS:C	2.55	0.45
1:D:320:ILE:HG22	1:D:321:LYS:HG2	1.98	0.45
1:A:137:LEU:HD12	1:A:141:LYS:HD2	1.98	0.45
1:A:163:LEU:HD13	1:A:176:ALA:CB	2.47	0.45
1:A:408:LEU:HD13	1:B:243:ILE:HG21	1.99	0.45
1:B:156:THR:O	1:B:160:VAL:HG23	2.16	0.45
1:B:328:LEU:HD12	1:B:329:LEU:N	2.31	0.45
1:C:313:ASN:HD22	1:C:313:ASN:N	2.15	0.45
1:A:240:ILE:O	1:A:258:VAL:HA	2.16	0.45
1:B:72:GLU:HB3	1:B:119:PHE:CE2	2.51	0.45
1:B:195:ARG:HG3	1:B:226:GLY:O	2.17	0.45
1:B:21:LEU:N	1:B:21:LEU:HD23	2.32	0.45
1:A:242:GLU:O	1:B:406:THR:HB	2.17	0.45
1:D:337:LEU:C	1:D:337:LEU:HD13	2.37	0.45
1:A:308:LYS:HD2	1:A:308:LYS:N	2.31	0.44
1:D:174:VAL:HG12	1:D:175:PRO:HD2	2.00	0.44
1:A:190:ASN:ND2	1:A:190:ASN:N	2.62	0.44
1:B:24:ALA:O	1:B:28:MET:HG3	2.17	0.44
1:D:218:ALA:HA	1:D:241:THR:OG1	2.17	0.44
1:A:152:ILE:O	1:A:176:ALA:HA	2.17	0.44
1:A:63:ILE:HG12	1:A:75:TRP:CE3	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:127:ILE:HD11	1:B:138:ILE:HD12	1.99	0.44
1:C:111:TRP:O	1:C:115:GLN:HG2	2.18	0.44
1:C:194:CYS:SG	1:C:223:VAL:HG13	2.57	0.44
1:D:243:ILE:HG13	1:D:244:ASP:N	2.32	0.44
1:C:278:VAL:HG13	1:D:415:TYR:CE2	2.52	0.44
1:A:389:LEU:O	1:A:393:VAL:HG23	2.18	0.44
1:A:84:GLN:O	1:A:87:ALA:HB3	2.18	0.44
1:C:74:ARG:HB3	1:C:116:THR:CB	2.48	0.44
1:D:75:TRP:HH2	1:D:128:LEU:HD13	1.81	0.44
1:A:198:LEU:HD22	1:A:227:CYS:HB3	2.00	0.44
1:A:374:HIS:N	1:A:375:PRO:HD2	2.32	0.44
1:B:218:ALA:HA	1:B:241:THR:OG1	2.17	0.44
1:C:21:LEU:N	1:C:21:LEU:HD23	2.31	0.44
1:D:189:ASP:O	1:D:189:ASP:OD2	2.36	0.44
1:D:63:ILE:HD11	1:D:75:TRP:CG	2.52	0.44
1:A:386:PRO:CG	1:A:389:LEU:HD12	2.46	0.44
1:A:54:HIS:HA	1:A:77:SER:OG	2.18	0.44
1:B:27:GLU:OE2	1:B:400:LYS:HE2	2.18	0.44
1:A:209:MET:HG3	1:C:196:GLU:OE1	2.17	0.44
1:C:278:VAL:HG12	1:C:303:VAL:HB	2.00	0.44
1:C:184:THR:HB	1:C:359:ASN:HD22	1.83	0.44
1:D:425:LYS:HD3	1:D:429:TYR:CZ	2.53	0.44
1:B:189:ASP:OD2	1:B:189:ASP:O	2.36	0.44
1:B:79:ASN:OD1	1:B:80:ILE:N	2.51	0.44
1:A:345:ASN:O	1:A:349:ALA:HB3	2.17	0.44
1:B:46:GLY:O	1:B:372:TRP:CH2	2.71	0.44
1:B:409:THR:O	1:B:410:GLU:C	2.56	0.44
1:B:410:GLU:O	1:B:414:GLN:HB2	2.18	0.44
1:C:17:GLY:HA2	1:C:86:HIS:CD2	2.53	0.44
1:C:369:ILE:O	1:C:373:THR:HB	2.17	0.44
1:D:387:LYS:O	1:D:391:GLU:HG3	2.18	0.44
1:A:373:THR:HG22	1:A:374:HIS:CE1	2.53	0.44
1:A:91:ILE:HG22	1:A:98:VAL:HG21	2.00	0.44
1:A:5:PRO:O	1:A:97:PRO:HA	2.18	0.44
1:B:190:ASN:N	1:B:190:ASN:ND2	2.64	0.44
1:D:142:HIS:N	1:D:143:PRO:HD3	2.32	0.44
1:D:37:MET:HE2	1:D:37:MET:HB3	1.79	0.44
1:C:243:ILE:HD13	1:D:408:LEU:HD22	2.00	0.44
1:B:48:ARG:H	1:B:125:ASN:ND2	2.16	0.43
1:C:391:GLU:HB3	1:D:245:PRO:HG2	1.99	0.43
1:D:165:LYS:NZ	1:D:165:LYS:HB2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:27:GLU:O	1:D:355:PHE:HA	2.18	0.43
1:A:313:ASN:N	1:A:313:ASN:ND2	2.67	0.43
1:D:275:THR:HB	1:D:277:CYS:H	1.84	0.43
1:D:306:ASP:CG	1:D:309:TRP:HB2	2.38	0.43
1:A:387:LYS:HE2	1:A:431:TYR:OH	2.17	0.43
1:C:398:LEU:HD23	1:C:405:LEU:HD22	1.98	0.43
1:D:80:ILE:HG13	1:D:81:PHE:CD2	2.53	0.43
1:C:128:LEU:HD21	1:C:364:GLN:HG2	2.00	0.43
1:C:389:LEU:O	1:C:392:ALA:HB3	2.18	0.43
1:C:190:ASN:ND2	2:C:432:NAD:H5N	2.34	0.43
1:A:96:ILE:O	1:A:98:VAL:HG23	2.19	0.43
1:C:220:TYR:CZ	1:C:225:LYS:HG2	2.54	0.43
1:C:373:THR:O	1:C:373:THR:HG22	2.19	0.43
1:C:430:ARG:HA	1:D:430:ARG:HD3	2.00	0.43
1:D:55:MET:HE1	1:D:75:TRP:CD1	2.54	0.43
1:A:185:ASN:HB2	1:A:363:ASN:ND2	2.34	0.43
1:B:164:TYR:CD1	1:B:382:VAL:HG11	2.53	0.43
1:D:136:ASN:ND2	1:D:162:ASN:HD21	2.08	0.43
1:D:336:ILE:HD12	1:D:336:ILE:N	2.33	0.43
1:D:142:HIS:HB3	1:D:145:LEU:HD11	2.00	0.43
1:D:299:GLY:HA3	1:D:304:GLU:OE2	2.19	0.43
1:D:124:LEU:H	1:D:124:LEU:HD23	1.83	0.43
1:C:259:THR:HA	1:D:404:LYS:HB2	2.01	0.43
1:A:91:ILE:CG2	1:A:98:VAL:HG21	2.49	0.43
1:D:385:LEU:CD1	1:D:386:PRO:HD2	2.40	0.43
1:A:124:LEU:H	1:A:124:LEU:CD2	2.31	0.43
1:C:126:MET:HE1	1:C:372:TRP:HB2	2.01	0.43
1:C:393:VAL:O	1:C:397:HIS:CD2	2.71	0.43
1:D:334:ARG:NH1	1:D:334:ARG:HG2	2.33	0.43
1:A:281:ILE:C	1:A:282:LEU:HD13	2.39	0.42
1:C:145:LEU:H	1:C:145:LEU:HG	1.51	0.42
1:C:152:ILE:O	1:C:176:ALA:HA	2.18	0.42
1:C:277:CYS:O	1:C:304:GLU:HG2	2.19	0.42
1:D:145:LEU:HG	1:D:145:LEU:H	1.45	0.42
1:D:373:THR:O	1:D:373:THR:HG22	2.18	0.42
1:C:174:VAL:HG12	1:C:175:PRO:HD2	2.00	0.42
1:C:407:LYS:HE2	1:C:407:LYS:HB3	1.46	0.42
1:D:301:PHE:HB2	1:D:303:VAL:HG22	2.01	0.42
1:D:385:LEU:HA	1:D:385:LEU:HD12	1.88	0.42
1:B:174:VAL:CG1	1:B:175:PRO:HD2	2.48	0.42
1:C:10:ASP:HB3	1:C:13:LEU:CD2	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:74:ARG:HB3	1:C:116:THR:HB	2.01	0.42
1:D:21:LEU:HD23	1:D:57:VAL:HG13	1.99	0.42
1:B:313:ASN:N	1:B:313:ASN:HD22	2.17	0.42
1:B:63:ILE:HD12	1:B:91:ILE:HD13	2.01	0.42
1:C:7:LYS:HD2	1:C:7:LYS:HA	1.79	0.42
1:D:48:ARG:NH1	1:D:123:PRO:O	2.52	0.42
1:D:72:GLU:HB3	1:D:119:PHE:HE2	1.82	0.42
1:A:167:MET:HB2	1:A:172:LEU:HD22	2.01	0.42
1:A:67:VAL:O	1:A:70:GLY:N	2.51	0.42
1:D:184:THR:HB	1:D:359:ASN:HD22	1.84	0.42
1:D:310:LEU:HD13	1:D:327:TYR:CD1	2.55	0.42
1:D:28:MET:CB	1:D:358:SER:HB2	2.49	0.42
1:D:73:VAL:CG1	1:D:75:TRP:HE3	2.32	0.42
1:A:298:ILE:CG1	1:A:298:ILE:O	2.68	0.42
1:A:429:TYR:HD2	1:A:431:TYR:CD1	2.37	0.42
1:A:63:ILE:HD11	1:A:75:TRP:CG	2.53	0.42
1:A:63:ILE:HD12	1:A:91:ILE:HD13	2.00	0.42
1:B:301:PHE:HB3	1:B:303:VAL:HG13	2.01	0.42
1:C:388:LYS:HE3	4:C:443:HOH:O	2.19	0.42
1:D:177:ILE:HG22	1:D:177:ILE:O	2.19	0.42
1:D:360:SER:HA	1:D:363:ASN:HD22	1.84	0.42
1:D:7:LYS:HD2	1:D:7:LYS:HA	1.81	0.42
1:A:373:THR:O	1:A:373:THR:HG22	2.18	0.42
1:A:407:LYS:HE3	1:A:408:LEU:O	2.20	0.42
1:D:274:THR:O	2:D:432:NAD:H51N	2.19	0.42
1:D:373:THR:HG22	1:D:374:HIS:CE1	2.55	0.42
1:A:10:ASP:OD1	1:A:12:GLY:N	2.52	0.42
1:A:171:ILE:O	1:A:173:LYS:HG3	2.20	0.42
1:A:310:LEU:HD13	1:A:327:TYR:CD1	2.55	0.42
1:B:279:ASP:CA	1:B:282:LEU:HD11	2.49	0.42
1:B:298:ILE:O	1:B:299:GLY:O	2.36	0.42
1:D:370:GLU:OE2	1:D:378:TYR:OH	2.23	0.42
1:B:118:HIS:CE1	1:B:123:PRO:HB3	2.55	0.42
1:B:143:PRO:HA	1:B:146:LEU:CD2	2.38	0.42
1:B:282:LEU:N	1:B:282:LEU:HD13	2.34	0.42
1:B:44:LEU:C	1:B:70:GLY:O	2.57	0.42
1:C:284:ARG:CD	4:C:440:HOH:O	2.66	0.42
1:C:408:LEU:HD12	1:C:408:LEU:HA	1.86	0.42
1:C:48:ARG:H	1:C:125:ASN:CG	2.23	0.42
1:D:74:ARG:HB3	1:D:116:THR:CB	2.49	0.42
1:D:55:MET:HB3	1:D:83:THR:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:VAL:O	1:A:359:ASN:HB2	2.20	0.42
1:B:105:THR:O	1:B:108:GLU:N	2.53	0.42
1:B:124:LEU:HD11	1:B:138:ILE:CD1	2.50	0.42
1:B:37:MET:HE1	1:B:38:TYR:CE2	2.55	0.42
1:B:53:LEU:HG	1:B:130:ASP:CB	2.48	0.42
1:C:407:LYS:HE3	1:C:408:LEU:O	2.20	0.42
1:D:371:LEU:HD12	1:D:371:LEU:HA	1.78	0.42
1:C:124:LEU:HD23	1:C:124:LEU:N	2.35	0.41
1:C:220:TYR:HB3	1:C:247:ASN:HB3	2.01	0.41
1:D:162:ASN:O	1:D:166:MET:HG3	2.20	0.41
1:D:189:ASP:C	1:D:190:ASN:HD22	2.23	0.41
1:D:296:CYS:HB3	1:D:338:LEU:HD12	2.01	0.41
1:A:249:LEU:O	1:A:253:MET:HG2	2.20	0.41
1:A:27:GLU:OE2	1:A:400:LYS:HE2	2.20	0.41
1:B:145:LEU:HG	1:B:145:LEU:H	1.48	0.41
1:B:17:GLY:HA3	1:B:86:HIS:O	2.20	0.41
1:B:32:MET:O	1:B:36:GLU:HG3	2.20	0.41
1:C:153:SER:OG	1:C:368:GLN:NE2	2.53	0.41
1:C:91:ILE:O	1:C:96:ILE:HB	2.19	0.41
1:C:96:ILE:O	1:C:98:VAL:HG23	2.19	0.41
1:D:146:LEU:HA	1:D:146:LEU:HD13	1.93	0.41
1:D:208:VAL:HG22	1:D:209:MET:N	2.35	0.41
1:D:301:PHE:HB3	1:D:303:VAL:HG13	2.02	0.41
1:A:75:TRP:CH2	1:A:128:LEU:HD13	2.54	0.41
1:A:424:PHE:O	1:A:425:LYS:HG2	2.20	0.41
1:B:7:LYS:HD2	1:B:7:LYS:HA	1.80	0.41
1:D:150:ARG:HD2	1:D:372:TRP:HA	2.02	0.41
1:D:13:LEU:HD12	1:D:16:TRP:HE3	1.86	0.41
1:D:200:ASP:OD2	1:D:204:ARG:NH2	2.53	0.41
1:D:28:MET:HA	1:D:358:SER:CB	2.50	0.41
1:A:144:GLN:CD	1:A:144:GLN:H	2.23	0.41
1:B:101:TRP:CE2	1:B:104:GLU:HB3	2.55	0.41
1:C:13:LEU:HD12	1:C:16:TRP:CE3	2.55	0.41
1:C:425:LYS:CD	1:C:429:TYR:CE2	3.03	0.41
1:D:13:LEU:HD12	1:D:16:TRP:CE3	2.55	0.41
1:D:190:ASN:ND2	1:D:190:ASN:N	2.67	0.41
1:B:80:ILE:O	1:B:103:GLY:N	2.54	0.41
1:B:152:ILE:O	1:B:176:ALA:HA	2.20	0.41
1:C:60:ALA:CA	1:C:91:ILE:HD11	2.46	0.41
1:D:134:LEU:HD13	1:D:134:LEU:O	2.21	0.41
1:D:48:ARG:HG2	1:D:119:PHE:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:329:LEU:HB2	1:A:331:ASN:OD1	2.19	0.41
1:A:91:ILE:HG22	1:A:98:VAL:CG2	2.50	0.41
1:B:136:ASN:O	1:B:137:LEU:C	2.59	0.41
1:B:401:LEU:HD12	1:B:403:VAL:HG13	2.03	0.41
1:C:329:LEU:HB2	1:C:331:ASN:OD1	2.21	0.41
1:C:409:THR:O	1:C:410:GLU:C	2.59	0.41
1:D:313:ASN:N	1:D:313:ASN:HD22	2.18	0.41
1:D:379:PRO:O	1:D:383:HIS:HE1	2.03	0.41
1:D:55:MET:SD	1:D:91:ILE:HD12	2.61	0.41
1:A:142:HIS:HB3	1:A:145:LEU:HD11	2.00	0.41
1:A:278:VAL:HG12	1:A:303:VAL:HB	2.03	0.41
1:C:188:PHE:HE1	1:D:249:LEU:CD2	2.33	0.41
1:C:59:THR:O	1:C:62:LEU:HB3	2.20	0.41
1:D:395:GLU:HA	1:D:398:LEU:HD22	2.02	0.41
1:A:120:LYS:HD2	1:A:121:ASP:CG	2.42	0.41
1:A:160:VAL:HG12	1:A:164:TYR:CE2	2.56	0.41
1:A:200:ASP:O	1:A:204:ARG:HG3	2.21	0.41
1:A:7:LYS:HD2	1:A:7:LYS:HA	1.92	0.41
1:B:371:LEU:HA	1:B:371:LEU:HD12	1.91	0.41
1:C:108:GLU:O	1:C:111:TRP:HB3	2.21	0.41
1:C:299:GLY:HA3	1:C:304:GLU:OE2	2.21	0.41
2:C:432:NAD:H3B	1:D:425:LYS:NZ	2.36	0.41
1:D:63:ILE:HD12	1:D:91:ILE:HD13	2.02	0.41
1:A:379:PRO:O	1:A:383:HIS:CE1	2.74	0.41
1:B:340:GLU:HB3	1:B:342:ARG:NH2	2.36	0.41
1:B:72:GLU:HB3	1:B:119:PHE:HE2	1.86	0.41
1:B:79:ASN:HB3	1:B:82:SER:HG	1.85	0.41
1:C:373:THR:O	1:C:373:THR:CG2	2.69	0.41
1:A:32:MET:O	1:A:36:GLU:HG3	2.21	0.41
1:A:365:VAL:O	1:A:369:ILE:HG13	2.21	0.41
1:A:58:GLU:HG2	1:A:354:SER:HA	2.01	0.41
1:B:3:LYS:HD2	1:B:3:LYS:N	2.36	0.41
1:C:109:TYR:CE2	1:C:113:ILE:HD11	2.56	0.41
1:C:403:VAL:CG2	1:C:403:VAL:O	2.67	0.41
1:A:137:LEU:CD1	1:A:141:LYS:HD2	2.50	0.40
1:A:316:GLU:HG3	1:A:328:LEU:HB3	2.03	0.40
1:B:252:ALA:O	1:C:212:GLY:HA2	2.22	0.40
1:B:292:ASP:OD1	1:B:336:ILE:CD1	2.62	0.40
1:B:353:PRO:CD	1:B:356:VAL:HG11	2.33	0.40
1:B:399:GLY:O	1:B:400:LYS:C	2.58	0.40
1:C:285:HIS:O	1:C:288:GLN:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:379:PRO:O	1:C:383:HIS:CE1	2.74	0.40
1:C:44:LEU:C	1:C:70:GLY:O	2.59	0.40
1:D:329:LEU:C	1:D:331:ASN:H	2.24	0.40
1:D:74:ARG:HB3	1:D:116:THR:HB	2.03	0.40
1:D:17:GLY:HA3	1:D:86:HIS:O	2.22	0.40
1:A:353:PRO:O	1:A:356:VAL:CG1	2.65	0.40
1:B:310:LEU:HA	1:B:310:LEU:HD23	1.92	0.40
1:C:183:VAL:HG21	1:C:431:TYR:CE1	2.56	0.40
1:C:73:VAL:CG1	1:C:75:TRP:HE3	2.34	0.40
1:C:5:PRO:O	1:C:97:PRO:HA	2.21	0.40
1:A:281:ILE:HA	1:A:285:HIS:ND1	2.35	0.40
1:A:57:VAL:O	1:A:61:VAL:HG23	2.22	0.40
1:B:223:VAL:HG12	1:B:274:THR:HG22	2.04	0.40
1:D:96:ILE:HA	1:D:97:PRO:HD3	1.96	0.40
1:A:275:THR:HG22	1:A:276:GLY:N	2.33	0.40
1:A:5:PRO:O	1:A:6:TYR:HB3	2.22	0.40
1:B:74:ARG:NH1	1:B:115:GLN:O	2.54	0.40
1:C:367:ALA:O	1:C:371:LEU:HB2	2.21	0.40
1:D:244:ASP:OD2	1:D:244:ASP:C	2.60	0.40
1:D:301:PHE:C	1:D:303:VAL:N	2.74	0.40
1:A:136:ASN:O	1:A:137:LEU:C	2.59	0.40
1:A:143:PRO:CA	1:A:146:LEU:HD23	2.40	0.40
1:A:174:VAL:HG12	1:A:175:PRO:HD2	2.04	0.40
1:A:320:ILE:O	1:A:321:LYS:HB3	2.21	0.40
1:A:407:LYS:CE	1:A:420:ILE:HD11	2.52	0.40
1:A:209:MET:HA	1:C:196:GLU:OE1	2.22	0.40
1:C:389:LEU:O	1:C:393:VAL:HG23	2.22	0.40
1:D:279:ASP:CA	1:D:282:LEU:HD11	2.52	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	428/431 (99%)	378 (88%)	43 (10%)	7 (2%)	11	36
1	B	428/431 (99%)	377 (88%)	45 (10%)	6 (1%)	13	39
1	C	428/431 (99%)	374 (87%)	48 (11%)	6 (1%)	13	39
1	D	428/431 (99%)	370 (86%)	52 (12%)	6 (1%)	13	39
All	All	1712/1724 (99%)	1499 (88%)	188 (11%)	25 (2%)	12	37

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	299	GLY
1	B	103	GLY
1	B	299	GLY
1	C	299	GLY
1	C	339	ALA
1	D	103	GLY
1	D	299	GLY
1	D	339	ALA
1	A	13	LEU
1	B	339	ALA
1	A	302	ASP
1	A	339	ALA
1	B	13	LEU
1	B	70	GLY
1	B	131	GLY
1	D	70	GLY
1	A	70	GLY
1	C	70	GLY
1	C	131	GLY
1	D	131	GLY
1	A	103	GLY
1	A	410	GLU
1	D	268	GLY
1	C	103	GLY
1	C	315	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	353/353 (100%)	318 (90%)	35 (10%)	9	26
1	B	353/353 (100%)	317 (90%)	36 (10%)	8	25
1	C	353/353 (100%)	315 (89%)	38 (11%)	7	22
1	D	353/353 (100%)	317 (90%)	36 (10%)	8	25
All	All	1412/1412 (100%)	1267 (90%)	145 (10%)	8	24

All (145) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ASP
1	A	3	LYS
1	A	23	ILE
1	A	33	ARG
1	A	39	SER
1	A	53	LEU
1	A	93	LYS
1	A	120	LYS
1	A	133	ASP
1	A	139	HIS
1	A	144	GLN
1	A	145	LEU
1	A	158	THR
1	A	190	ASN
1	A	242	GLU
1	A	267	GLU
1	A	275	THR
1	A	282	LEU
1	A	292	ASP
1	A	308	LYS
1	A	313	ASN
1	A	323	GLN
1	A	328	LEU
1	A	334	ARG
1	A	340	GLU
1	A	356	VAL
1	A	357	MET
1	A	371	LEU
1	A	387	LYS
1	A	388	LYS
1	A	398	LEU

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Mol	Chain	Res	Type
1	A	401	LEU
1	A	403	VAL
1	A	407	LYS
1	A	414	GLN
1	B	2	ASP
1	B	3	LYS
1	B	23	ILE
1	B	33	ARG
1	B	39	SER
1	B	41	SER
1	B	72	GLU
1	B	74	ARG
1	B	75	TRP
1	B	93	LYS
1	B	120	LYS
1	B	133	ASP
1	B	139	HIS
1	B	144	GLN
1	B	145	LEU
1	B	158	THR
1	B	190	ASN
1	B	242	GLU
1	B	250	GLN
1	B	267	GLU
1	B	275	THR
1	B	282	LEU
1	B	308	LYS
1	B	323	GLN
1	B	334	ARG
1	B	340	GLU
1	B	356	VAL
1	B	357	MET
1	B	371	LEU
1	B	387	LYS
1	B	388	LYS
1	B	401	LEU
1	B	403	VAL
1	B	407	LYS
1	B	414	GLN
1	B	420	ILE
1	C	3	LYS
1	C	33	ARG

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Mol	Chain	Res	Type
1	C	39	SER
1	C	41	SER
1	C	53	LEU
1	C	72	GLU
1	C	74	ARG
1	C	75	TRP
1	C	93	LYS
1	C	120	LYS
1	C	133	ASP
1	C	139	HIS
1	C	144	GLN
1	C	145	LEU
1	C	158	THR
1	C	190	ASN
1	C	250	GLN
1	C	267	GLU
1	C	275	THR
1	C	282	LEU
1	C	297	ASN
1	C	308	LYS
1	C	323	GLN
1	C	334	ARG
1	C	340	GLU
1	C	356	VAL
1	C	357	MET
1	C	371	LEU
1	C	376	ASP
1	C	387	LYS
1	C	388	LYS
1	C	398	LEU
1	C	401	LEU
1	C	403	VAL
1	C	407	LYS
1	C	408	LEU
1	C	414	GLN
1	C	420	ILE
1	D	3	LYS
1	D	23	ILE
1	D	33	ARG
1	D	39	SER
1	D	41	SER
1	D	53	LEU

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Mol	Chain	Res	Type
1	D	72	GLU
1	D	75	TRP
1	D	93	LYS
1	D	120	LYS
1	D	130	ASP
1	D	133	ASP
1	D	139	HIS
1	D	144	GLN
1	D	145	LEU
1	D	158	THR
1	D	190	ASN
1	D	242	GLU
1	D	250	GLN
1	D	275	THR
1	D	282	LEU
1	D	308	LYS
1	D	323	GLN
1	D	334	ARG
1	D	340	GLU
1	D	356	VAL
1	D	357	MET
1	D	371	LEU
1	D	376	ASP
1	D	387	LYS
1	D	388	LYS
1	D	401	LEU
1	D	403	VAL
1	D	407	LYS
1	D	408	LEU
1	D	414	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (64) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	84	GLN
1	A	86	HIS
1	A	136	ASN
1	A	190	ASN
1	A	247	ASN
1	A	250	GLN
1	A	269	ASN
1	A	300	HIS

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Mol	Chain	Res	Type
1	A	313	ASN
1	A	323	GLN
1	A	352	HIS
1	A	359	ASN
1	A	363	ASN
1	A	368	GLN
1	A	374	HIS
1	A	383	HIS
1	A	397	HIS
1	A	412	GLN
1	B	84	GLN
1	B	86	HIS
1	B	136	ASN
1	B	190	ASN
1	B	247	ASN
1	B	250	GLN
1	B	269	ASN
1	B	300	HIS
1	B	313	ASN
1	B	323	GLN
1	B	352	HIS
1	B	359	ASN
1	B	363	ASN
1	B	374	HIS
1	B	383	HIS
1	B	397	HIS
1	B	412	GLN
1	C	84	GLN
1	C	86	HIS
1	C	136	ASN
1	C	190	ASN
1	C	247	ASN
1	C	250	GLN
1	C	269	ASN
1	C	300	HIS
1	C	313	ASN
1	C	323	GLN
1	C	352	HIS
1	C	363	ASN
1	C	368	GLN
1	C	397	HIS
1	D	84	GLN

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Mol	Chain	Res	Type
1	D	86	HIS
1	D	136	ASN
1	D	190	ASN
1	D	247	ASN
1	D	250	GLN
1	D	269	ASN
1	D	313	ASN
1	D	323	GLN
1	D	363	ASN
1	D	368	GLN
1	D	374	HIS
1	D	383	HIS
1	D	397	HIS
1	D	412	GLN

### 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](#)

8 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	NAD	A	432	-	41,48,48	2.30	8 (19%)	43,73,73	1.64	8 (18%)
3	ADN	A	433	-	18,21,21	1.29	3 (16%)	17,31,31	2.66	4 (23%)
2	NAD	B	432	-	41,48,48	2.40	8 (19%)	43,73,73	1.57	7 (16%)
3	ADN	B	433	-	18,21,21	1.37	3 (16%)	17,31,31	2.45	4 (23%)
2	NAD	C	432	-	41,48,48	2.33	9 (21%)	43,73,73	1.65	6 (13%)
3	ADN	C	433	-	18,21,21	1.45	3 (16%)	17,31,31	2.66	3 (17%)
2	NAD	D	432	-	41,48,48	2.37	8 (19%)	43,73,73	1.54	8 (18%)
3	ADN	D	433	-	18,21,21	1.26	2 (11%)	17,31,31	2.61	3 (17%)

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	NAD	A	432	-	-	0/22/62/62	0/5/5/5
3	ADN	A	433	-	-	0/2/22/22	0/3/3/3
2	NAD	B	432	-	-	0/22/62/62	0/5/5/5
3	ADN	B	433	-	-	0/2/22/22	0/3/3/3
2	NAD	C	432	-	-	0/22/62/62	0/5/5/5
3	ADN	C	433	-	-	0/2/22/22	0/3/3/3
2	NAD	D	432	-	-	0/22/62/62	0/5/5/5
3	ADN	D	433	-	-	0/2/22/22	0/3/3/3

All (44) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	432	NAD	O4B-C1B	-5.79	1.33	1.41
2	A	432	NAD	O4B-C1B	-3.53	1.36	1.41
2	C	432	NAD	O4B-C1B	-3.09	1.37	1.41
2	D	432	NAD	O4B-C1B	-3.02	1.37	1.41
2	C	432	NAD	C2D-C1D	-2.91	1.49	1.53
3	A	433	ADN	C8-N7	-2.43	1.30	1.34
3	C	433	ADN	C8-N7	-2.35	1.30	1.34
2	A	432	NAD	C2D-C1D	-2.33	1.49	1.53
3	A	433	ADN	C2'-C1'	-2.26	1.50	1.53
3	D	433	ADN	C8-N7	-2.20	1.30	1.34
3	B	433	ADN	C8-N7	-2.17	1.30	1.34
2	D	432	NAD	C2D-C1D	-2.03	1.50	1.53
2	B	432	NAD	C7N-N7N	2.03	1.36	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	432	NAD	C2A-N3A	2.10	1.35	1.32
3	B	433	ADN	C2-N1	2.13	1.37	1.33
2	C	432	NAD	C2A-N3A	2.42	1.36	1.32
2	A	432	NAD	C7N-N7N	2.51	1.37	1.33
2	C	432	NAD	C7N-N7N	2.52	1.37	1.33
2	D	432	NAD	C7N-N7N	2.63	1.38	1.33
3	C	433	ADN	C4-N3	2.66	1.39	1.35
3	A	433	ADN	C2-N3	2.68	1.36	1.32
2	A	432	NAD	C2A-N1A	2.96	1.39	1.33
2	D	432	NAD	C2A-N1A	3.02	1.39	1.33
2	B	432	NAD	C2A-N1A	3.22	1.40	1.33
3	D	433	ADN	C2-N3	3.34	1.37	1.32
2	C	432	NAD	C2A-N1A	3.35	1.40	1.33
3	B	433	ADN	C2-N3	3.45	1.37	1.32
3	C	433	ADN	C2-N3	3.71	1.38	1.32
2	A	432	NAD	C6N-N1N	4.07	1.46	1.35
2	C	432	NAD	C6N-N1N	4.36	1.46	1.35
2	B	432	NAD	C6N-N1N	4.49	1.47	1.35
2	D	432	NAD	C6N-N1N	4.91	1.48	1.35
2	C	432	NAD	C2N-C3N	5.65	1.47	1.39
2	A	432	NAD	C2N-C3N	6.14	1.48	1.39
2	A	432	NAD	C4N-C3N	6.22	1.49	1.39
2	D	432	NAD	C2N-C3N	6.39	1.48	1.39
2	B	432	NAD	C2N-C3N	6.41	1.48	1.39
2	B	432	NAD	C4N-C3N	6.54	1.50	1.39
2	C	432	NAD	C4N-C3N	6.67	1.50	1.39
2	D	432	NAD	C4N-C3N	6.98	1.50	1.39
2	B	432	NAD	C5N-C4N	7.69	1.53	1.38
2	A	432	NAD	C5N-C4N	7.96	1.54	1.38
2	D	432	NAD	C5N-C4N	8.37	1.54	1.38
2	C	432	NAD	C5N-C4N	8.56	1.55	1.38

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	433	ADN	C4'-O4'-C1'	-9.16	100.02	109.77
3	D	433	ADN	C4'-O4'-C1'	-8.86	100.34	109.77
3	A	433	ADN	C4'-O4'-C1'	-8.83	100.37	109.77
3	B	433	ADN	C4'-O4'-C1'	-8.12	101.12	109.77
2	C	432	NAD	O7N-C7N-C3N	-5.03	113.74	119.62
2	A	432	NAD	O7N-C7N-C3N	-4.78	114.04	119.62
2	B	432	NAD	O7N-C7N-C3N	-4.70	114.13	119.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	432	NAD	O7N-C7N-C3N	-4.67	114.16	119.62
2	A	432	NAD	N3A-C2A-N1A	-3.75	125.59	128.86
2	C	432	NAD	N3A-C2A-N1A	-3.38	125.91	128.86
2	C	432	NAD	C5N-C4N-C3N	-3.26	116.51	120.35
3	B	433	ADN	O4'-C4'-C3'	-3.14	98.92	105.17
3	C	433	ADN	O4'-C4'-C3'	-3.14	98.93	105.17
3	A	433	ADN	O4'-C4'-C3'	-3.13	98.94	105.17
2	B	432	NAD	N3A-C2A-N1A	-3.13	126.13	128.86
3	A	433	ADN	N3-C2-N1	-3.08	126.17	128.86
2	A	432	NAD	C5N-C4N-C3N	-3.04	116.77	120.35
3	D	433	ADN	O4'-C4'-C3'	-2.96	99.27	105.17
3	D	433	ADN	N3-C2-N1	-2.92	126.32	128.86
2	D	432	NAD	C5N-C4N-C3N	-2.90	116.94	120.35
2	D	432	NAD	N3A-C2A-N1A	-2.63	126.57	128.86
2	B	432	NAD	C5N-C4N-C3N	-2.55	117.35	120.35
3	C	433	ADN	N3-C2-N1	-2.50	126.68	128.86
3	B	433	ADN	N3-C2-N1	-2.42	126.75	128.86
2	A	432	NAD	O5B-C5B-C4B	-2.41	100.44	109.00
2	B	432	NAD	O2N-PN-O5D	2.01	117.62	108.14
2	D	432	NAD	C5A-C6A-N6A	2.03	124.60	120.47
2	D	432	NAD	C5N-C6N-N1N	2.06	123.57	120.40
2	D	432	NAD	C3N-C2N-N1N	2.12	122.56	120.43
2	A	432	NAD	C3N-C2N-N1N	2.13	122.57	120.43
3	B	433	ADN	C4-C5-N7	2.16	111.49	109.41
3	A	433	ADN	C4-C5-N7	2.21	111.55	109.41
2	A	432	NAD	C5N-C6N-N1N	2.22	123.82	120.40
2	B	432	NAD	C5N-C6N-N1N	2.28	123.90	120.40
2	C	432	NAD	C3N-C2N-N1N	2.60	123.05	120.43
2	D	432	NAD	C4A-C5A-N7A	2.62	111.94	109.41
2	B	432	NAD	C4A-C5A-N7A	2.67	111.99	109.41
2	C	432	NAD	C4A-C5A-N7A	2.80	112.12	109.41
2	A	432	NAD	C4A-C5A-N7A	3.32	112.62	109.41
2	D	432	NAD	C3N-C7N-N7N	4.90	123.37	117.77
2	A	432	NAD	C3N-C7N-N7N	4.97	123.45	117.77
2	B	432	NAD	C3N-C7N-N7N	5.14	123.65	117.77
2	C	432	NAD	C3N-C7N-N7N	5.27	123.80	117.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	432	NAD	4	0
2	B	432	NAD	4	0
2	C	432	NAD	5	0
2	D	432	NAD	5	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	430/431 (99%)	-0.88	1 (0%) 94 94	2, 26, 49, 73	0
1	B	430/431 (99%)	-0.87	0 100 100	4, 26, 51, 73	0
1	C	430/431 (99%)	-0.94	1 (0%) 94 94	3, 28, 50, 73	0
1	D	430/431 (99%)	-0.87	1 (0%) 94 94	3, 28, 51, 75	0
All	All	1720/1724 (99%)	-0.89	3 (0%) 94 94	2, 27, 51, 75	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	2	ASP	3.9
1	A	2	ASP	2.6
1	C	2	ASP	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

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
3	ADN	B	433	19/19	0.96	0.12	0.53	13,18,22,25	0
3	ADN	A	433	19/19	0.96	0.11	0.32	12,17,24,33	0
3	ADN	C	433	19/19	0.97	0.10	-0.27	10,16,27,30	0
2	NAD	B	432	44/44	0.97	0.10	-0.33	2,8,16,24	0
3	ADN	D	433	19/19	0.96	0.10	-0.38	10,18,23,26	0
2	NAD	C	432	44/44	0.97	0.09	-0.62	5,14,22,25	0
2	NAD	A	432	44/44	0.98	0.09	-0.72	2,16,21,23	0
2	NAD	D	432	44/44	0.98	0.10	-0.92	2,17,21,23	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.