



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 23, 2018 – 10:36 AM EST

PDB ID : 1IQ8  
Title : Crystal Structure of archaeosine tRNA-guanine transglycosylase from *Pyrococcus horikoshii*  
Authors : Ishitani, R.; Nureki, O.; Fukai, S.; Kijimoto, T.; Nameki, N.; Watanabe, M.; Kondo, H.; Sekine, M.; Okada, N.; Nishimura, S.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2001-07-09  
Resolution : 2.20 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
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030736

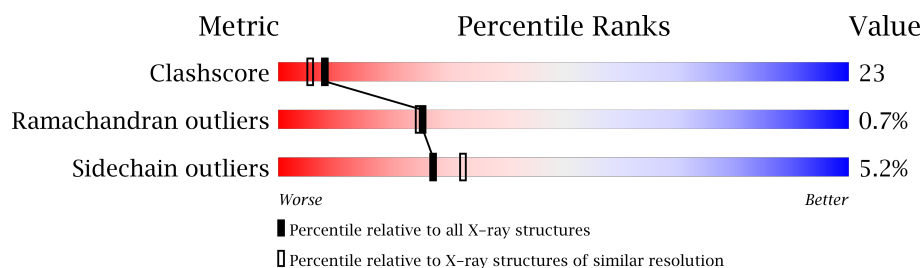
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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))
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	582	
1	B	582	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9599 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 ARCHAEOSINE TRNA-GUANINE TRANSGLYCOSYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	577	Total	C	N	O	S	0	0	0
			4652	2970	815	848	19			
1	B	577	Total	C	N	O	S	0	0	0
			4652	2970	815	848	19			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is water.

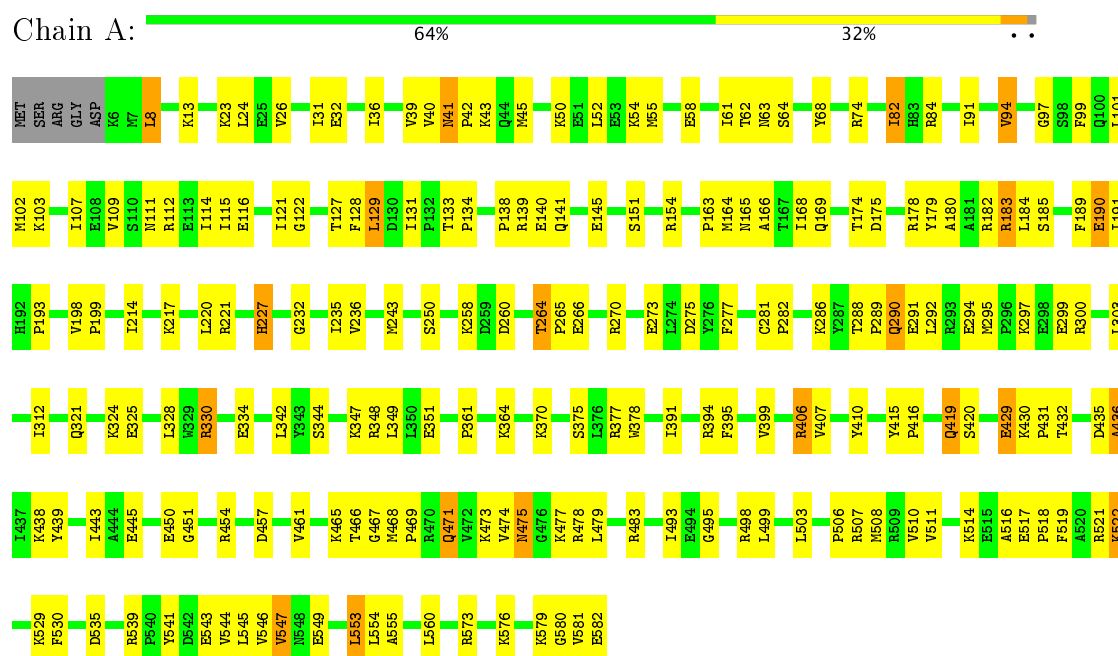
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	175	Total	O	0	0
			175	175		
4	B	116	Total	O	0	0
			116	116		

### 3 Residue-property plots

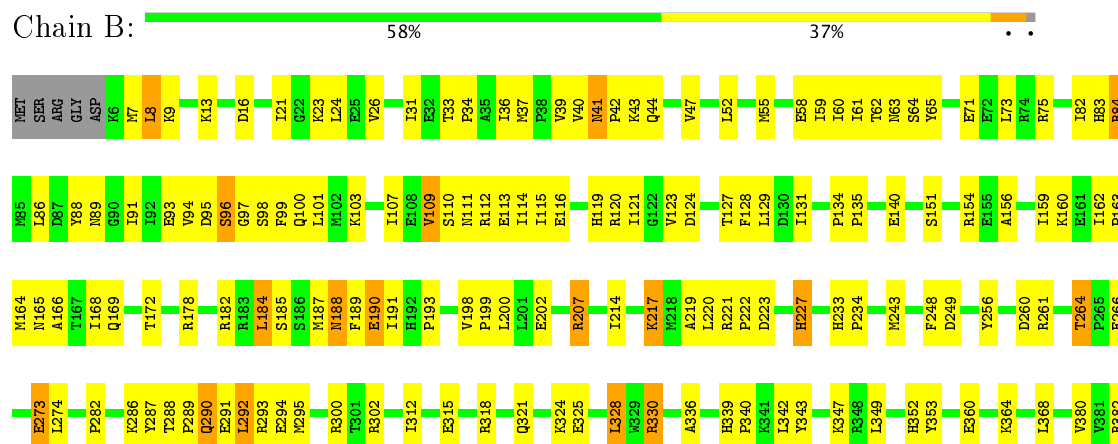
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

Note EDS was not executed.

#### • Molecule 1: ARCHAEOSE TRNA-GUANINE TRANSGLYCOSYLASE



#### • Molecule 1: ARCHAEOSE TRNA-GUANINE TRANSGLYCOSYLASE





## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.28Å 99.28Å 363.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20	Depositor
% Data completeness (in resolution range)	(Not available) (50.00-2.20)	Depositor
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.227 , 0.261	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9599	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	0.36	0/4745	0.61	0/6391
1	B	0.34	0/4745	0.59	0/6391
All	All	0.35	0/9490	0.60	0/12782

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 ⓘ

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	4652	0	4747	206	0
1	B	4652	0	4747	237	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	175	0	0	6	0
4	B	116	0	0	5	0
All	All	9599	0	9494	441	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 23.

All (441) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:477:LYS:HG2	1:A:478:ARG:H	1.03	1.15
1:A:295:MET:HE1	1:A:303:LEU:HD12	1.38	1.03
1:A:264:THR:HG22	1:A:266:GLU:H	1.24	0.97
1:A:13:LYS:HE3	1:A:23:LYS:HB2	1.45	0.97
1:A:514:LYS:H	1:A:514:LYS:HD2	1.28	0.96
1:B:514:LYS:H	1:B:514:LYS:HE3	1.33	0.93
1:B:290:GLN:H	1:B:290:GLN:NE2	1.65	0.93
1:B:514:LYS:N	1:B:514:LYS:HE3	1.85	0.91
1:A:477:LYS:HG2	1:A:478:ARG:N	1.86	0.91
1:B:264:THR:HG22	1:B:266:GLU:H	1.33	0.90
1:B:101:LEU:HD21	1:B:131:ILE:HG12	1.53	0.89
1:A:471:GLN:HG2	1:A:473:LYS:HE3	1.52	0.88
1:A:510:VAL:HG23	1:A:546:VAL:HA	1.55	0.86
1:A:344:SER:HB2	1:B:423:GLU:HG3	1.58	0.86
1:A:477:LYS:CG	1:A:478:ARG:H	1.89	0.84
1:B:510:VAL:HG13	1:B:544:VAL:HG11	1.59	0.83
1:B:84:ARG:HE	1:B:84:ARG:HA	1.43	0.83
1:A:514:LYS:N	1:A:514:LYS:HD2	1.94	0.83
1:A:63:ASN:HD21	1:A:97:GLY:HA2	1.44	0.82
1:B:131:ILE:O	1:B:169:GLN:HG2	1.82	0.80
1:B:168:ILE:HD11	1:B:220:LEU:HD21	1.62	0.80
1:B:290:GLN:H	1:B:290:GLN:HE21	1.29	0.80
1:A:178:ARG:HB3	1:A:182:ARG:HH21	1.44	0.79
1:B:64:SER:HB3	1:B:94:VAL:HG21	1.63	0.79
1:A:131:ILE:O	1:A:169:GLN:HG2	1.82	0.79
1:B:40:VAL:O	1:B:62:THR:HG23	1.82	0.79
1:B:382:ARG:O	1:B:386:GLU:HG3	1.84	0.77
1:A:138:PRO:HD2	1:A:141:GLN:NE2	2.00	0.76
1:B:510:VAL:CG1	1:B:544:VAL:HG11	2.15	0.76
1:A:270:ARG:O	1:A:273:GLU:HG2	1.85	0.76
1:A:138:PRO:HD2	1:A:141:GLN:HE21	1.50	0.76
1:B:525:ASP:HA	1:B:577:VAL:HG23	1.68	0.75
1:B:110:SER:OG	1:B:113:GLU:HG3	1.87	0.74
1:B:406:ARG:N	1:B:406:ARG:HD3	2.01	0.74
1:A:264:THR:HG22	1:A:266:GLU:N	2.02	0.74
1:A:31:ILE:HD12	1:A:91:ILE:HD12	1.70	0.74
1:B:111:ASN:HD21	1:B:128:PHE:HB2	1.52	0.74
1:A:471:GLN:HE21	1:A:478:ARG:HG3	1.53	0.73
1:B:397:GLU:HB3	1:B:409:ARG:HG2	1.70	0.73
1:B:8:LEU:HD22	1:B:26:VAL:HG22	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:SER:HA	1:A:154:ARG:NH1	2.04	0.72
1:B:84:ARG:HH22	1:B:89:ASN:ND2	1.87	0.72
1:A:111:ASN:HD21	1:A:128:PHE:HB2	1.54	0.72
1:B:292:LEU:HA	1:B:295:MET:HE2	1.73	0.71
1:B:41:ASN:HD22	1:B:42:PRO:CD	2.04	0.71
1:A:214:ILE:HD11	1:A:349:LEU:CD1	2.21	0.70
1:B:264:THR:HG22	1:B:266:GLU:N	2.06	0.70
1:B:84:ARG:HH22	1:B:89:ASN:HD21	1.39	0.70
1:A:178:ARG:HB3	1:A:182:ARG:NH2	2.07	0.69
1:B:82:ILE:HD12	1:B:83:HIS:N	2.08	0.69
1:A:288:THR:HG22	1:A:291:GLU:CG	2.23	0.69
1:A:8:LEU:HG	1:A:190:GLU:HB2	1.74	0.69
1:A:445:GLU:OE2	1:A:450:GLU:HA	1.93	0.68
1:B:114:ILE:HD12	1:B:115:ILE:N	2.09	0.68
1:B:519:PHE:HA	1:B:522:LYS:HE3	1.75	0.68
1:A:40:VAL:O	1:A:62:THR:HG23	1.93	0.68
1:A:499:LEU:HB3	1:A:508:MET:CE	2.24	0.68
1:A:288:THR:HG22	1:A:291:GLU:HG3	1.77	0.67
1:A:139:ARG:HG2	1:A:139:ARG:HH11	1.60	0.67
1:B:380:VAL:HG23	4:B:603:HOH:O	1.93	0.67
1:A:168:ILE:HD11	1:A:220:LEU:HD11	1.77	0.67
1:B:82:ILE:HD12	1:B:83:HIS:H	1.60	0.67
1:A:42:PRO:HG3	1:A:62:THR:HG21	1.76	0.67
1:A:36:ILE:HD13	1:A:312:ILE:HG21	1.76	0.67
1:B:207:ARG:HH11	1:B:207:ARG:HB3	1.60	0.67
1:A:474:VAL:HG22	1:A:475:ASN:OD1	1.94	0.66
1:B:214:ILE:HD11	1:B:349:LEU:CD1	2.25	0.66
1:A:514:LYS:H	1:A:514:LYS:CD	2.05	0.66
1:B:330:ARG:HH11	1:B:330:ARG:HB3	1.61	0.66
1:B:290:GLN:HE21	1:B:290:GLN:N	1.94	0.66
1:A:163:PRO:HB3	1:A:190:GLU:HG3	1.79	0.65
1:A:295:MET:HE1	1:A:303:LEU:CD1	2.20	0.65
1:B:493:ILE:HD12	1:B:497:LYS:HE3	1.78	0.65
1:A:503:LEU:HD12	1:A:508:MET:CE	2.27	0.64
1:A:165:ASN:HD22	1:A:191:ILE:HB	1.62	0.64
1:B:31:ILE:HD12	1:B:91:ILE:HD12	1.79	0.64
1:A:499:LEU:HB3	1:A:508:MET:HE3	1.79	0.64
1:A:510:VAL:HG13	1:A:544:VAL:HG21	1.78	0.64
1:B:510:VAL:HG13	1:B:544:VAL:CG1	2.28	0.64
1:A:36:ILE:HD13	1:A:312:ILE:CG2	2.28	0.64
1:B:386:GLU:HA	1:B:389:LYS:NZ	2.12	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:432:THR:H	1:A:435:ASP:HB2	1.61	0.63
1:A:529:LYS:HE3	1:A:530:PHE:CE1	2.34	0.63
1:B:413:LEU:HD23	1:B:428:ILE:CG2	2.28	0.63
1:A:99:PHE:CE2	1:A:103:LYS:HD2	2.35	0.62
1:A:114:ILE:HD12	1:A:115:ILE:N	2.14	0.62
1:A:198:VAL:HB	1:A:199:PRO:HD3	1.80	0.62
1:A:503:LEU:HD12	1:A:508:MET:HE1	1.80	0.62
1:B:264:THR:CG2	1:B:266:GLU:H	2.10	0.62
1:B:41:ASN:HD22	1:B:42:PRO:HD2	1.64	0.62
1:A:275:ASP:OD1	1:B:324:LYS:HG2	1.98	0.62
1:B:185:SER:OG	1:B:221:ARG:HG3	1.98	0.62
1:B:52:LEU:HD23	1:B:55:MET:HE3	1.80	0.62
1:A:510:VAL:CG2	1:A:546:VAL:HA	2.26	0.61
1:B:274:LEU:O	1:B:293:ARG:NH2	2.34	0.61
1:B:330:ARG:NH1	1:B:330:ARG:HB3	2.16	0.61
1:B:41:ASN:HD22	1:B:42:PRO:N	1.98	0.61
1:B:399:VAL:O	1:B:406:ARG:HA	2.01	0.60
1:A:479:LEU:HD22	1:A:498:ARG:HD2	1.84	0.60
1:A:264:THR:CG2	1:A:266:GLU:H	2.08	0.60
1:B:135:PRO:HB3	1:B:200:LEU:HD21	1.82	0.60
1:B:198:VAL:HB	1:B:199:PRO:HD3	1.82	0.60
1:B:13:LYS:HD2	1:B:23:LYS:HB2	1.83	0.60
1:B:286:LYS:HE2	1:B:287:TYR:CE1	2.36	0.60
1:B:395:PHE:HB3	1:B:410:TYR:CD1	2.37	0.60
1:A:185:SER:HB3	1:A:221:ARG:HG3	1.84	0.60
1:A:292:LEU:HD13	1:A:295:MET:HE2	1.83	0.60
1:B:273:GLU:O	1:B:273:GLU:HG2	2.01	0.60
1:B:7:MET:HB3	1:B:163:PRO:HG3	1.83	0.60
1:A:406:ARG:HD3	1:A:406:ARG:H	1.66	0.60
1:A:406:ARG:HD3	1:A:406:ARG:N	2.17	0.59
1:B:286:LYS:HE2	1:B:287:TYR:HE1	1.67	0.59
1:B:493:ILE:HD13	1:B:493:ILE:O	2.02	0.59
1:A:553:LEU:HD22	1:A:581:VAL:CG2	2.32	0.59
1:B:474:VAL:HG11	1:B:498:ARG:HH22	1.67	0.59
1:B:135:PRO:HG2	1:B:199:PRO:HB2	1.84	0.59
1:B:165:ASN:HD22	1:B:191:ILE:HB	1.67	0.59
1:A:165:ASN:ND2	1:A:191:ILE:HB	2.17	0.59
1:A:260:ASP:OD1	1:A:300:ARG:HD2	2.03	0.59
1:B:471:GLN:NE2	1:B:478:ARG:HG3	2.17	0.59
1:B:321:GLN:O	1:B:325:GLU:HG2	2.02	0.58
1:A:112:ARG:O	1:A:116:GLU:HG3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:295:MET:HE3	1:A:299:GLU:HG3	1.84	0.58
1:A:431:PRO:HD2	1:A:467:GLY:O	2.03	0.58
1:B:436:ALA:HB1	1:B:461:VAL:HB	1.85	0.58
1:B:84:ARG:NE	1:B:84:ARG:HA	2.15	0.58
1:B:217:LYS:HD3	1:B:243:MET:O	2.04	0.58
1:B:499:LEU:HG	1:B:508:MET:HE1	1.85	0.58
1:A:174:THR:HG22	1:A:178:ARG:NH2	2.19	0.58
1:B:413:LEU:HD23	1:B:428:ILE:HG21	1.86	0.58
1:B:222:PRO:HD2	1:B:568:VAL:HG21	1.85	0.58
1:A:64:SER:HB3	1:A:94:VAL:HG11	1.86	0.57
1:B:84:ARG:CA	1:B:84:ARG:HE	2.13	0.57
1:A:183:ARG:CB	1:A:183:ARG:HH11	2.17	0.57
1:B:288:THR:HG23	1:B:291:GLU:H	1.68	0.57
1:B:503:LEU:HD12	1:B:508:MET:HE1	1.86	0.57
1:A:63:ASN:ND2	1:A:97:GLY:HA2	2.17	0.56
1:A:270:ARG:H	1:A:273:GLU:CD	2.08	0.56
1:A:553:LEU:HD23	1:A:554:LEU:N	2.20	0.56
1:B:119:HIS:HA	1:B:162:ILE:HD12	1.87	0.56
1:B:112:ARG:HD3	1:B:159:ILE:HD13	1.86	0.56
1:A:415:TYR:HA	1:A:419:GLN:HG2	1.88	0.56
1:A:483:ARG:NH2	1:A:543:GLU:OE2	2.38	0.56
1:B:111:ASN:ND2	1:B:129:LEU:H	2.03	0.56
1:B:114:ILE:HD12	1:B:115:ILE:HG13	1.87	0.56
1:A:560:LEU:HD21	1:A:576:LYS:HE3	1.87	0.56
1:B:184:LEU:HA	1:B:187:MET:HE3	1.88	0.56
1:A:151:SER:HA	1:A:154:ARG:HH11	1.71	0.55
1:A:507:ARG:HD2	4:A:761:HOH:O	2.06	0.55
1:B:286:LYS:HG3	1:B:287:TYR:CD1	2.41	0.55
1:A:183:ARG:HA	1:A:183:ARG:HH11	1.72	0.55
1:A:214:ILE:HD11	1:A:349:LEU:HD13	1.88	0.55
1:B:513:ASN:HD22	1:B:530:PHE:HD2	1.55	0.55
1:A:394:ARG:HD2	1:A:395:PHE:CE1	2.42	0.55
1:A:68:TYR:O	1:A:74:ARG:HD2	2.06	0.55
1:B:439:TYR:O	1:B:443:ILE:HG13	2.07	0.55
1:B:524:LYS:O	1:B:577:VAL:HG21	2.07	0.55
1:B:282:PRO:O	1:B:286:LYS:HG2	2.06	0.54
1:B:71:GLU:O	1:B:75:ARG:HG3	2.08	0.54
1:A:42:PRO:HG3	1:A:62:THR:CG2	2.38	0.54
1:A:84:ARG:HA	1:A:84:ARG:NE	2.23	0.54
1:B:510:VAL:HG23	1:B:510:VAL:O	2.08	0.54
1:B:214:ILE:HD11	1:B:349:LEU:HD12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:395:PHE:HB3	1:B:410:TYR:HD1	1.70	0.54
1:A:31:ILE:HD11	1:A:58:GLU:O	2.08	0.54
1:A:555:ALA:HB2	1:A:580:GLY:HA2	1.89	0.54
1:B:503:LEU:HD12	1:B:508:MET:CE	2.38	0.54
1:B:555:ALA:HB2	1:B:580:GLY:HA2	1.90	0.54
1:B:116:GLU:O	1:B:120:ARG:HG3	2.08	0.54
1:A:471:GLN:HG2	1:A:473:LYS:CE	2.31	0.53
1:B:353:TYR:CE1	1:B:382:ARG:HB2	2.43	0.53
1:B:474:VAL:O	1:B:477:LYS:HG2	2.08	0.53
1:B:477:LYS:HE3	1:B:494:GLU:CD	2.28	0.53
1:B:517:GLU:HG3	1:B:554:LEU:HD11	1.89	0.53
1:A:107:ILE:HG12	1:A:109:VAL:HG12	1.90	0.53
1:B:64:SER:HB3	1:B:94:VAL:CG2	2.33	0.53
1:B:107:ILE:HD11	1:B:129:LEU:HD13	1.89	0.53
1:A:183:ARG:HH11	1:A:183:ARG:HB3	1.74	0.53
1:A:364:LYS:HE3	4:A:728:HOH:O	2.08	0.53
1:B:221:ARG:HB3	1:B:223:ASP:OD1	2.09	0.53
1:A:282:PRO:O	1:A:286:LYS:HG2	2.07	0.53
1:B:41:ASN:ND2	1:B:43:LYS:H	2.06	0.53
1:B:431:PRO:HG2	1:B:469:PRO:CG	2.39	0.53
1:A:183:ARG:CA	1:A:183:ARG:HH11	2.21	0.53
1:A:217:LYS:HD3	1:A:243:MET:O	2.08	0.53
1:A:290:GLN:CD	1:A:290:GLN:H	2.12	0.53
1:B:227:HIS:HE1	1:B:249:ASP:OD2	1.92	0.53
1:B:508:MET:O	1:B:544:VAL:HG13	2.09	0.53
1:A:517:GLU:OE2	1:A:521:ARG:NH1	2.33	0.53
1:B:403:ILE:HD12	1:B:420:SER:OG	2.09	0.53
1:B:31:ILE:HD11	1:B:58:GLU:O	2.09	0.53
1:B:140:GLU:HG3	4:B:618:HOH:O	2.10	0.52
1:A:183:ARG:NH1	1:A:183:ARG:HB3	2.24	0.52
1:A:64:SER:HB3	1:A:94:VAL:CG1	2.38	0.52
1:A:439:TYR:O	1:A:443:ILE:HG13	2.09	0.52
1:B:198:VAL:O	1:B:202:GLU:HG3	2.09	0.52
1:A:127:THR:HG22	1:A:128:PHE:H	1.74	0.52
1:B:360:GLU:HB3	1:B:383:ARG:NH2	2.25	0.52
1:A:519:PHE:HA	1:A:522:LYS:HE3	1.92	0.52
1:B:483:ARG:NH1	1:B:488:LEU:HB2	2.24	0.52
1:A:82:ILE:HD11	1:A:122:GLY:O	2.09	0.52
1:A:8:LEU:CD2	1:A:26:VAL:HG22	2.39	0.52
1:B:413:LEU:HD22	1:B:468:MET:CE	2.40	0.52
1:B:98:SER:O	1:B:101:LEU:HB3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:GLU:HB2	4:A:746:HOH:O	2.10	0.51
1:B:62:THR:HG22	1:B:63:ASN:H	1.75	0.51
1:A:435:ASP:O	1:A:438:LYS:N	2.41	0.51
1:A:82:ILE:HG13	1:A:121:ILE:O	2.10	0.51
1:A:24:LEU:HD21	1:A:26:VAL:CG2	2.39	0.51
1:A:510:VAL:HG23	1:A:510:VAL:O	2.10	0.51
1:B:166:ALA:HB2	1:B:189:PHE:CG	2.46	0.51
1:B:288:THR:HG22	1:B:291:GLU:CG	2.41	0.51
1:A:429:GLU:OE1	1:A:429:GLU:HA	2.11	0.51
1:A:180:ALA:O	1:A:184:LEU:HD23	2.09	0.51
1:A:24:LEU:CD2	1:A:26:VAL:HG23	2.41	0.51
1:A:506:PRO:O	1:A:535:ASP:HB2	2.11	0.51
1:B:493:ILE:CD1	1:B:497:LYS:HE3	2.41	0.51
1:B:163:PRO:HB3	1:B:190:GLU:HG3	1.92	0.50
1:B:387:ARG:O	1:B:391:ILE:HD13	2.10	0.50
1:A:40:VAL:HG22	1:A:62:THR:OG1	2.12	0.50
1:A:41:ASN:O	1:A:45:MET:HG3	2.12	0.50
1:A:514:LYS:HE3	1:A:549:GLU:OE1	2.11	0.50
1:B:431:PRO:HG3	1:B:439:TYR:CE2	2.46	0.50
1:B:386:GLU:HA	1:B:389:LYS:HZ3	1.75	0.50
1:B:493:ILE:HD11	1:B:581:VAL:HG22	1.93	0.50
1:A:109:VAL:CG2	1:A:114:ILE:HG23	2.42	0.50
1:A:395:PHE:HB3	1:A:410:TYR:CD1	2.47	0.50
1:B:165:ASN:ND2	1:B:191:ILE:HB	2.26	0.50
1:B:292:LEU:HD13	1:B:295:MET:CE	2.42	0.50
1:B:343:TYR:CZ	1:B:347:LYS:HD2	2.47	0.50
1:B:498:ARG:O	1:B:502:VAL:HG23	2.11	0.50
1:B:517:GLU:HB3	1:B:518:PRO:HD3	1.93	0.50
1:A:406:ARG:N	1:A:406:ARG:CD	2.75	0.49
1:A:52:LEU:HA	1:A:55:MET:HE3	1.94	0.49
1:B:41:ASN:HB3	1:B:44:GLN:O	2.11	0.49
1:A:435:ASP:O	1:A:438:LYS:HB2	2.11	0.49
1:B:109:VAL:CG2	1:B:114:ILE:HG23	2.41	0.49
1:B:8:LEU:HD13	1:B:9:LYS:N	2.27	0.49
1:A:31:ILE:HG22	1:A:32:GLU:N	2.27	0.49
1:A:510:VAL:HG13	1:A:544:VAL:CG2	2.43	0.49
1:A:529:LYS:HE3	1:A:530:PHE:CZ	2.48	0.49
1:B:95:ASP:C	1:B:97:GLY:H	2.14	0.49
1:A:111:ASN:ND2	1:A:129:LEU:H	2.10	0.49
1:A:174:THR:CG2	1:A:178:ARG:HH22	2.26	0.49
1:B:399:VAL:HG22	1:B:400:GLU:N	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:96:SER:HB2	1:B:129:LEU:HD23	1.95	0.49
1:A:193:PRO:HA	1:A:227:HIS:HB3	1.95	0.49
1:A:174:THR:CG2	1:A:178:ARG:NH2	2.75	0.49
1:A:289:PRO:HD2	1:A:290:GLN:OE1	2.13	0.49
1:A:330:ARG:NH2	1:A:334:GLU:OE2	2.38	0.49
1:B:555:ALA:CB	1:B:580:GLY:HA2	2.43	0.49
1:A:479:LEU:O	1:A:495:GLY:HA3	2.13	0.48
1:B:451:GLY:HA3	1:B:454:ARG:HH21	1.78	0.48
1:B:465:LYS:HG3	1:B:466:THR:N	2.28	0.48
1:A:214:ILE:HD11	1:A:349:LEU:HD12	1.95	0.48
1:B:295:MET:HE3	1:B:300:ARG:HA	1.94	0.48
1:A:227:HIS:HD2	4:A:602:HOH:O	1.96	0.48
1:B:207:ARG:HB3	1:B:207:ARG:NH1	2.27	0.48
1:B:188:ASN:CG	1:B:188:ASN:O	2.51	0.48
1:B:397:GLU:CB	1:B:409:ARG:HG2	2.43	0.48
1:A:133:THR:OG1	1:A:145:GLU:OE2	2.25	0.48
1:A:410:TYR:CE2	1:A:438:LYS:HB3	2.48	0.48
1:A:41:ASN:HD22	1:A:42:PRO:CD	2.27	0.48
1:A:471:GLN:NE2	1:A:478:ARG:HG3	2.24	0.48
1:B:156:ALA:O	1:B:160:LYS:HB2	2.13	0.48
1:B:399:VAL:HG21	1:B:429:GLU:OE2	2.14	0.48
1:B:506:PRO:O	1:B:535:ASP:HB2	2.13	0.48
1:A:264:THR:HG23	1:A:265:PRO:HD2	1.96	0.48
1:B:24:LEU:HD23	1:B:24:LEU:C	2.34	0.48
1:A:41:ASN:ND2	1:A:43:LYS:H	2.10	0.48
1:A:416:PRO:O	1:A:420:SER:HB3	2.14	0.48
1:B:406:ARG:H	1:B:406:ARG:HD3	1.75	0.48
1:B:47:VAL:HG21	1:B:52:LEU:HD21	1.96	0.48
1:B:162:ILE:HG23	1:B:163:PRO:HD2	1.96	0.48
1:B:182:ARG:HG2	1:B:219:ALA:HB1	1.94	0.48
1:B:525:ASP:HA	1:B:577:VAL:CG2	2.42	0.48
1:A:465:LYS:HG3	1:A:466:THR:N	2.29	0.47
1:A:573:ARG:NH1	1:A:576:LYS:HE2	2.30	0.47
1:B:190:GLU:N	1:B:190:GLU:CD	2.68	0.47
1:A:499:LEU:HB3	1:A:508:MET:HE1	1.95	0.47
1:A:445:GLU:OE2	1:A:451:GLY:N	2.48	0.47
1:B:112:ARG:HD3	1:B:159:ILE:CD1	2.44	0.47
1:B:8:LEU:CD2	1:B:26:VAL:HG22	2.41	0.47
1:B:465:LYS:HG3	1:B:466:THR:HG23	1.96	0.47
1:B:47:VAL:HG22	4:B:707:HOH:O	2.15	0.47
1:B:493:ILE:O	1:B:497:LYS:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:510:VAL:CG2	1:B:546:VAL:HA	2.45	0.47
1:A:436:ALA:HB1	1:A:461:VAL:HB	1.95	0.47
1:B:459:ALA:HA	1:B:474:VAL:HG22	1.95	0.47
1:B:497:LYS:HG2	1:B:553:LEU:HD23	1.97	0.47
1:A:24:LEU:HD21	1:A:26:VAL:HG23	1.96	0.47
1:B:31:ILE:CD1	1:B:91:ILE:HD12	2.43	0.47
1:A:139:ARG:HG2	1:A:139:ARG:NH1	2.27	0.47
1:B:114:ILE:CD1	1:B:115:ILE:HG13	2.45	0.47
1:B:490:THR:HG23	1:B:578:ARG:CZ	2.45	0.47
1:A:573:ARG:HH11	1:A:576:LYS:HE2	1.80	0.46
1:B:65:TYR:HB2	1:B:97:GLY:HA3	1.96	0.46
1:B:343:TYR:CE1	1:B:347:LYS:HD2	2.50	0.46
1:B:499:LEU:HG	1:B:508:MET:CE	2.45	0.46
1:A:102:MET:HE2	1:A:134:PRO:HG3	1.98	0.46
1:B:491:LEU:HD11	1:B:499:LEU:HD23	1.97	0.46
1:A:511:VAL:HA	1:A:547:VAL:O	2.16	0.46
1:B:399:VAL:HG12	1:B:407:VAL:O	2.16	0.46
1:B:162:ILE:HG22	1:B:163:PRO:O	2.16	0.46
1:B:52:LEU:HD23	1:B:55:MET:CE	2.46	0.46
1:A:166:ALA:HB2	1:A:189:PHE:CG	2.50	0.46
1:A:474:VAL:O	1:A:475:ASN:C	2.54	0.46
1:B:151:SER:HA	1:B:154:ARG:HE	1.81	0.46
1:B:33:THR:HA	1:B:34:PRO:C	2.36	0.46
1:B:554:LEU:C	1:B:581:VAL:HG23	2.37	0.46
1:A:555:ALA:CB	1:A:580:GLY:HA2	2.45	0.46
1:B:178:ARG:HD3	1:B:182:ARG:HH22	1.81	0.46
1:B:31:ILE:CD1	1:B:59:ILE:HB	2.46	0.46
1:A:292:LEU:HD13	1:A:295:MET:CE	2.45	0.45
1:A:24:LEU:HD23	1:A:24:LEU:C	2.37	0.45
1:A:288:THR:CG2	1:A:291:GLU:HG3	2.44	0.45
1:A:361:PRO:HB3	1:A:541:TYR:HD1	1.81	0.45
1:B:288:THR:OG1	1:B:289:PRO:HD2	2.16	0.45
1:B:95:ASP:O	1:B:97:GLY:N	2.49	0.45
1:A:258:LYS:O	1:A:297:LYS:NZ	2.50	0.45
1:A:128:PHE:HD2	1:A:164:MET:HE2	1.82	0.45
1:A:299:GLU:HA	1:A:299:GLU:OE1	2.16	0.45
1:B:233:HIS:ND1	1:B:234:PRO:HD2	2.31	0.45
1:A:391:ILE:CD1	1:A:445:GLU:HB3	2.46	0.45
1:B:468:MET:HA	1:B:469:PRO:HD3	1.88	0.45
1:B:557:GLY:HA2	1:B:578:ARG:HG3	1.99	0.45
1:A:31:ILE:CD1	1:A:91:ILE:HD12	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:443:ILE:O	1:B:447:GLN:N	2.43	0.45
1:B:416:PRO:O	1:B:420:SER:HB2	2.17	0.44
1:A:101:LEU:O	1:A:101:LEU:HD12	2.18	0.44
1:A:347:LYS:HG2	1:A:377:ARG:HH22	1.81	0.44
1:A:431:PRO:HG2	1:A:469:PRO:HG3	1.99	0.44
1:B:474:VAL:HG12	1:B:475:ASN:ND2	2.33	0.44
1:A:399:VAL:HG12	1:A:407:VAL:O	2.17	0.44
1:B:260:ASP:OD1	1:B:300:ARG:HD2	2.17	0.44
1:A:235:ILE:HG23	1:A:236:VAL:HG13	1.98	0.44
1:A:41:ASN:HD22	1:A:42:PRO:HD2	1.83	0.44
1:A:554:LEU:C	1:A:581:VAL:HG23	2.38	0.44
1:B:510:VAL:HG23	1:B:546:VAL:HA	2.00	0.44
1:B:39:VAL:HG22	1:B:61:ILE:CG2	2.48	0.44
1:B:234:PRO:HG3	1:B:312:ILE:HG12	2.00	0.44
1:B:291:GLU:O	1:B:295:MET:HG3	2.18	0.44
1:B:519:PHE:HA	1:B:522:LYS:CE	2.44	0.44
1:B:273:GLU:O	1:B:273:GLU:CG	2.66	0.44
1:A:264:THR:CG2	1:A:266:GLU:OE1	2.66	0.44
1:B:119:HIS:HD2	1:B:162:ILE:HD12	1.83	0.44
1:B:193:PRO:HA	1:B:227:HIS:O	2.18	0.44
1:B:286:LYS:HD3	4:B:699:HOH:O	2.17	0.44
1:B:36:ILE:HD12	1:B:248:PHE:C	2.37	0.44
1:B:497:LYS:O	1:B:501:ARG:HG2	2.18	0.44
1:B:547:VAL:HG23	1:B:552:GLU:C	2.38	0.44
1:B:60:ILE:HG12	1:B:88:TYR:CE2	2.53	0.44
1:B:461:VAL:HG11	1:B:469:PRO:HB3	2.00	0.43
1:B:84:ARG:NH2	1:B:89:ASN:OD1	2.51	0.43
1:B:166:ALA:HB1	1:B:184:LEU:HG	2.00	0.43
1:B:391:ILE:HD12	1:B:391:ILE:N	2.33	0.43
1:A:31:ILE:CG2	1:A:32:GLU:N	2.81	0.43
1:B:214:ILE:HD12	1:B:352:HIS:CD2	2.53	0.43
1:A:516:ALA:HB2	1:A:530:PHE:CG	2.53	0.43
1:B:97:GLY:O	1:B:100:GLN:OE1	2.37	0.43
1:B:62:THR:HG22	1:B:63:ASN:N	2.34	0.43
1:B:499:LEU:HA	1:B:499:LEU:HD12	1.87	0.43
1:B:95:ASP:C	1:B:97:GLY:N	2.72	0.43
1:A:82:ILE:HD11	1:A:122:GLY:C	2.39	0.43
1:A:168:ILE:CD1	1:A:220:LEU:HD11	2.47	0.43
1:A:277:PHE:CD1	1:A:289:PRO:HG3	2.53	0.43
1:A:468:MET:HA	1:A:469:PRO:HD3	1.84	0.43
1:B:109:VAL:HG21	1:B:114:ILE:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:435:ASP:O	1:B:439:TYR:HD1	2.01	0.43
1:B:544:VAL:CG1	1:B:545:LEU:N	2.82	0.43
1:A:553:LEU:O	1:A:581:VAL:HG21	2.19	0.43
1:B:16:ASP:OD1	1:B:364:LYS:HE2	2.19	0.43
1:B:16:ASP:OD2	1:B:328:LEU:HB2	2.19	0.43
1:B:339:HIS:ND1	1:B:340:PRO:HD2	2.33	0.43
1:B:544:VAL:HG12	1:B:545:LEU:N	2.33	0.43
1:A:179:TYR:O	1:A:183:ARG:HG2	2.19	0.42
1:A:139:ARG:NH2	1:A:175:ASP:OD2	2.52	0.42
1:A:521:ARG:HD3	1:A:582:GLU:CD	2.39	0.42
1:A:361:PRO:HB3	1:A:541:TYR:CD1	2.55	0.42
1:B:99:PHE:O	1:B:103:LYS:HG3	2.19	0.42
1:B:430:LYS:NZ	1:B:466:THR:HB	2.33	0.42
1:A:348:ARG:NH1	1:A:351:GLU:OE1	2.52	0.42
1:A:62:THR:HG22	1:A:63:ASN:H	1.83	0.42
1:B:227:HIS:CE1	1:B:249:ASP:OD2	2.70	0.42
1:A:466:THR:C	1:A:468:MET:H	2.23	0.42
1:A:517:GLU:HB3	1:A:518:PRO:HD3	2.02	0.42
1:B:82:ILE:HG23	1:B:121:ILE:HD12	2.02	0.42
1:B:135:PRO:O	1:B:172:THR:HG23	2.19	0.42
1:A:50:LYS:O	1:A:54:LYS:HG3	2.18	0.42
1:B:290:GLN:NE2	1:B:290:GLN:N	2.47	0.42
1:A:190:GLU:N	1:A:190:GLU:CD	2.72	0.42
1:A:419:GLN:HG2	1:A:419:GLN:H	1.58	0.42
1:B:292:LEU:CA	1:B:295:MET:HE2	2.47	0.42
1:A:454:ARG:HA	1:A:457:ASP:OD2	2.20	0.41
1:A:375:SER:HA	1:A:378:TRP:CE2	2.55	0.41
1:A:8:LEU:HD22	1:A:26:VAL:HG22	2.02	0.41
1:B:227:HIS:HD2	4:B:602:HOH:O	2.04	0.41
1:B:526:VAL:HB	1:B:575:VAL:HB	2.02	0.41
1:A:430:LYS:NZ	1:A:466:THR:HG23	2.36	0.41
1:A:103:LYS:HE2	1:A:103:LYS:HB3	1.87	0.41
1:A:391:ILE:HD12	1:A:445:GLU:HB3	2.00	0.41
1:A:281:CYS:HB2	1:A:282:PRO:HD2	2.01	0.41
1:B:21:ILE:HA	1:B:33:THR:O	2.21	0.41
1:B:37:MET:HG2	1:B:248:PHE:O	2.21	0.41
1:B:41:ASN:HD22	1:B:41:ASN:C	2.20	0.41
1:A:62:THR:HG22	1:A:63:ASN:N	2.36	0.41
1:B:8:LEU:HG	1:B:190:GLU:HB2	2.03	0.41
1:A:295:MET:HE3	1:A:299:GLU:CG	2.51	0.41
1:A:41:ASN:HD22	1:A:41:ASN:C	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:576:LYS:HE3	1:A:576:LYS:HB2	1.83	0.41
1:B:134:PRO:HA	1:B:135:PRO:HD3	1.89	0.41
1:B:160:LYS:HD2	1:B:164:MET:HB2	2.01	0.41
1:B:547:VAL:CG2	1:B:551:ASP:HA	2.51	0.41
1:A:321:GLN:O	1:A:325:GLU:HG2	2.20	0.41
1:B:40:VAL:HG23	1:B:40:VAL:O	2.21	0.41
1:B:61:ILE:HA	1:B:93:GLU:O	2.21	0.41
1:A:471:GLN:HB2	4:A:720:HOH:O	2.21	0.41
1:A:510:VAL:HG22	1:A:545:LEU:O	2.20	0.41
1:B:127:THR:HG22	1:B:128:PHE:N	2.36	0.41
1:B:290:GLN:HA	1:B:293:ARG:NH1	2.36	0.41
1:A:39:VAL:HG22	1:A:61:ILE:HG23	2.03	0.41
1:A:82:ILE:H	1:A:82:ILE:HG13	1.53	0.41
1:B:315:GLU:OE2	1:B:318:ARG:NH1	2.50	0.41
1:B:471:GLN:HG3	1:B:478:ARG:HD3	2.02	0.41
1:A:13:LYS:NZ	4:A:747:HOH:O	2.54	0.40
1:B:83:HIS:CE1	1:B:124:ASP:OD2	2.74	0.40
1:B:415:TYR:HB2	1:B:419:GLN:HE22	1.85	0.40
1:A:232:GLY:CA	1:A:250:SER:HB2	2.51	0.40
1:A:430:LYS:NZ	1:A:466:THR:CG2	2.84	0.40
1:A:579:LYS:HB2	1:A:579:LYS:HE3	1.75	0.40
1:B:336:ALA:HB1	1:B:343:TYR:HA	2.03	0.40
1:A:399:VAL:O	1:A:406:ARG:HA	2.21	0.40
1:B:256:TYR:HB3	1:B:261:ARG:HB2	2.03	0.40
1:B:41:ASN:ND2	1:B:42:PRO:HD2	2.34	0.40
1:A:131:ILE:O	1:A:169:GLN:CG	2.60	0.40
1:A:41:ASN:ND2	1:A:41:ASN:C	2.74	0.40
1:A:431:PRO:HG2	1:A:469:PRO:CG	2.51	0.40
1:B:41:ASN:ND2	1:B:41:ASN:C	2.74	0.40
1:B:42:PRO:HB2	1:B:73:LEU:HD21	2.04	0.40
1:B:582:GLU:HG2	1:B:582:GLU:O	2.22	0.40
1:B:86:LEU:N	1:B:86:LEU:HD12	2.36	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	575/582 (99%)	554 (96%)	18 (3%)	3 (0%)	32	34
1	B	575/582 (99%)	540 (94%)	30 (5%)	5 (1%)	20	18
All	All	1150/1164 (99%)	1094 (95%)	48 (4%)	8 (1%)	25	24

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	475	ASN
1	A	436	ALA
1	B	96	SER
1	B	418	ALA
1	B	464	SER
1	B	466	THR
1	A	129	LEU
1	B	109	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	499/503 (99%)	475 (95%)	24 (5%)	30	36
1	B	499/503 (99%)	471 (94%)	28 (6%)	25	29
All	All	998/1006 (99%)	946 (95%)	52 (5%)	27	32

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LEU
1	A	41	ASN
1	A	82	ILE
1	A	94	VAL

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Mol	Chain	Res	Type
1	A	183	ARG
1	A	190	GLU
1	A	227	HIS
1	A	264	THR
1	A	290	GLN
1	A	294	GLU
1	A	324	LYS
1	A	328	LEU
1	A	330	ARG
1	A	342	LEU
1	A	370	LYS
1	A	406	ARG
1	A	419	GLN
1	A	429	GLU
1	A	471	GLN
1	A	493	ILE
1	A	522	LYS
1	A	539	ARG
1	A	547	VAL
1	A	553	LEU
1	B	8	LEU
1	B	41	ASN
1	B	84	ARG
1	B	123	VAL
1	B	184	LEU
1	B	188	ASN
1	B	190	GLU
1	B	207	ARG
1	B	217	LYS
1	B	227	HIS
1	B	264	THR
1	B	273	GLU
1	B	290	GLN
1	B	292	LEU
1	B	294	GLU
1	B	302	ARG
1	B	328	LEU
1	B	330	ARG
1	B	342	LEU
1	B	368	LEU
1	B	406	ARG
1	B	429	GLU

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Mol	Chain	Res	Type
1	B	477	LYS
1	B	493	ILE
1	B	499	LEU
1	B	506	PRO
1	B	514	LYS
1	B	522	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	83	HIS
1	A	111	ASN
1	A	141	GLN
1	A	165	ASN
1	A	227	HIS
1	A	352	HIS
1	A	419	GLN
1	A	471	GLN
1	B	41	ASN
1	B	83	HIS
1	B	111	ASN
1	B	141	GLN
1	B	165	ASN
1	B	227	HIS
1	B	290	GLN
1	B	471	GLN
1	B	475	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.