



## Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 05:08 pm GMT

PDB ID : 2DU5  
Title : Crystal structure of Archaeoglobus fulgidus O-phosphoseryl-tRNA synthetase E418N/E420N mutant complexed with tRNA<sup>Opal</sup> and O-phosphoserine ("opal complex")  
Authors : Fukunaga, R.  
Deposited on : 2006-07-20  
Resolution : 3.20 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  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

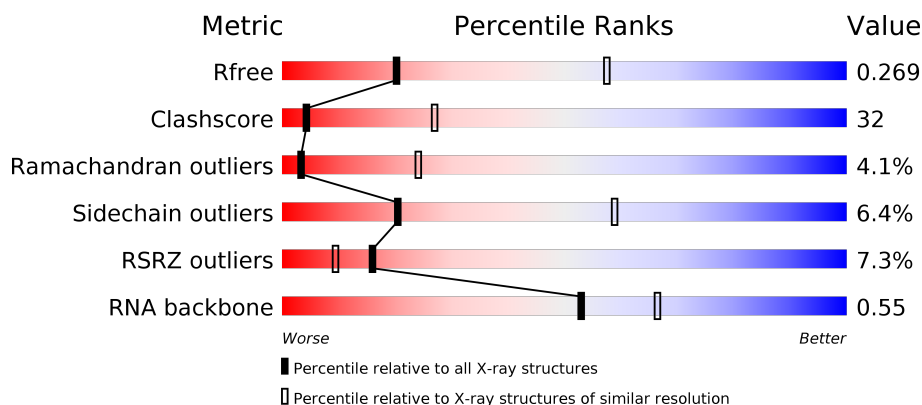
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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))
$R_{free}$	100719	1015 (3.22-3.18)
Clashscore	112137	1009 (3.20-3.20)
Ramachandran outliers	110173	1118 (3.22-3.18)
Sidechain outliers	110143	1117 (3.22-3.18)
RSRZ outliers	101464	1020 (3.22-3.18)
RNA backbone	2435	1045 (3.60-2.80)

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	D	71	<div> <div>48%</div> <div> <div>48%</div> <div>38%</div> <div>14%</div> </div> </div>
2	A	534	<div> <div>7%</div> <div> <div>43%</div> <div>50%</div> <div>6%</div> </div> </div>
2	B	534	<div> <div>0%</div> <div> <div>38%</div> <div>43%</div> <div>5%</div> <div>13%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SEP	A	1001	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9619 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 RNA chain called tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	71	Total	C	N	O	P	0	0	0
			1517	674	269	503	71			

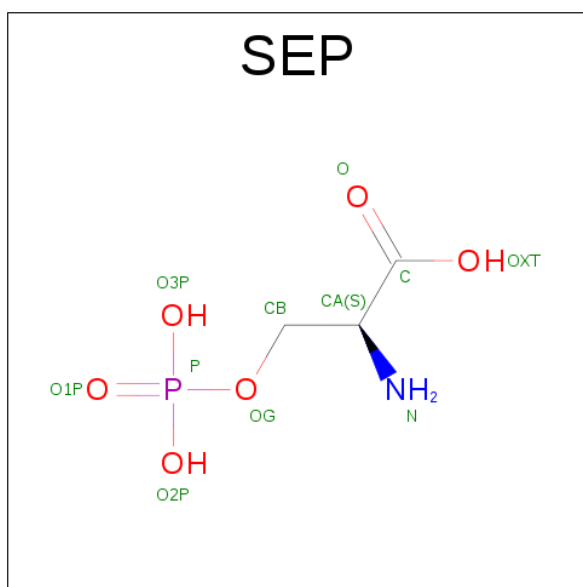
- Molecule 2 is a protein called O-phosphoseryl-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	534	Total	C	N	O	S	0	0	0
			4319	2784	721	801	13			
2	B	465	Total	C	N	O	S	0	0	0
			3761	2427	632	689	13			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	418	ASN	GLU	ENGINEERED	UNP O30126
A	420	ASN	GLU	ENGINEERED	UNP O30126
B	418	ASN	GLU	ENGINEERED	UNP O30126
B	420	ASN	GLU	ENGINEERED	UNP O30126

- Molecule 3 is PHOSPHOSERINE (three-letter code: SEP) (formula: C<sub>3</sub>H<sub>8</sub>NO<sub>6</sub>P).

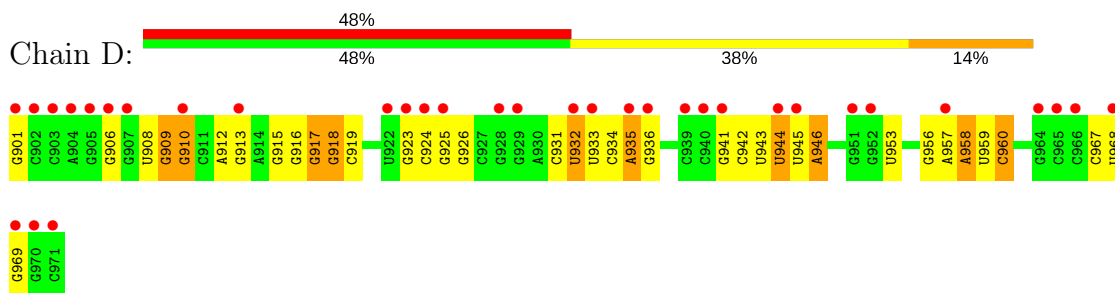


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	2	Total	C	N	O	P	0	0
			22	6	2	12	2		

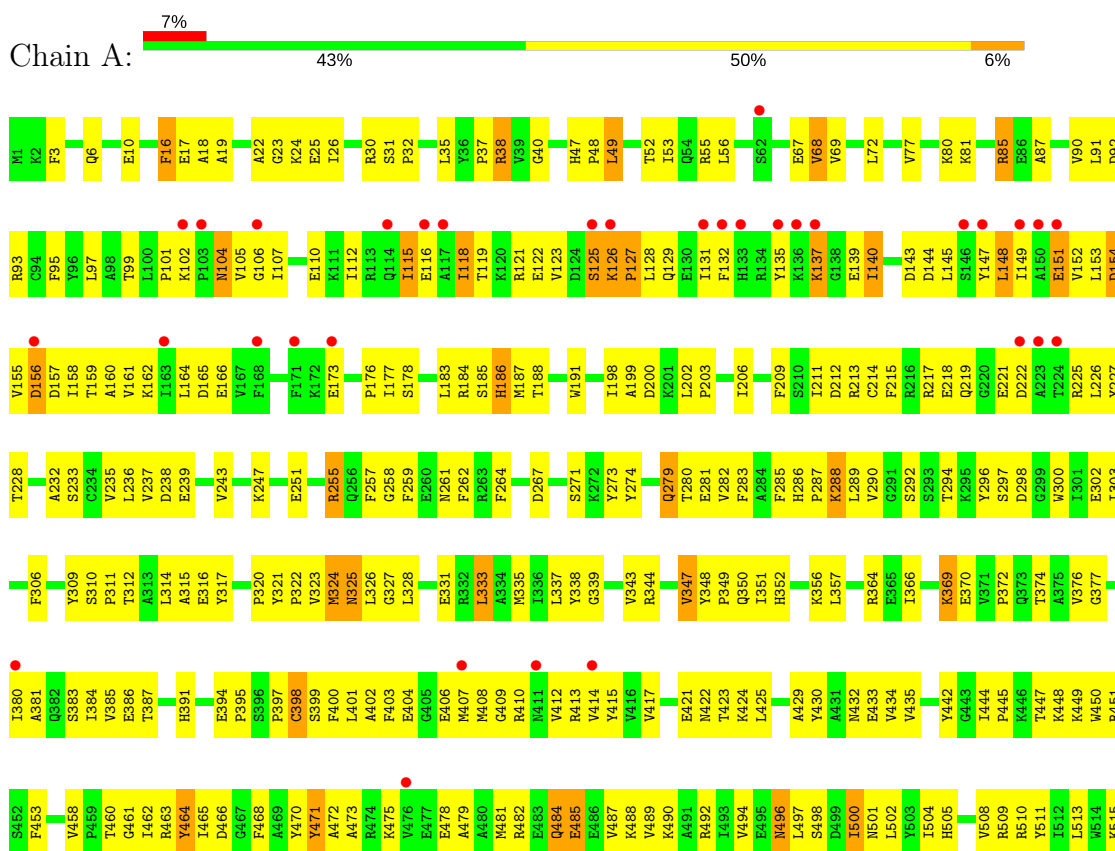
### 3 Residue-property plots

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: tRNA

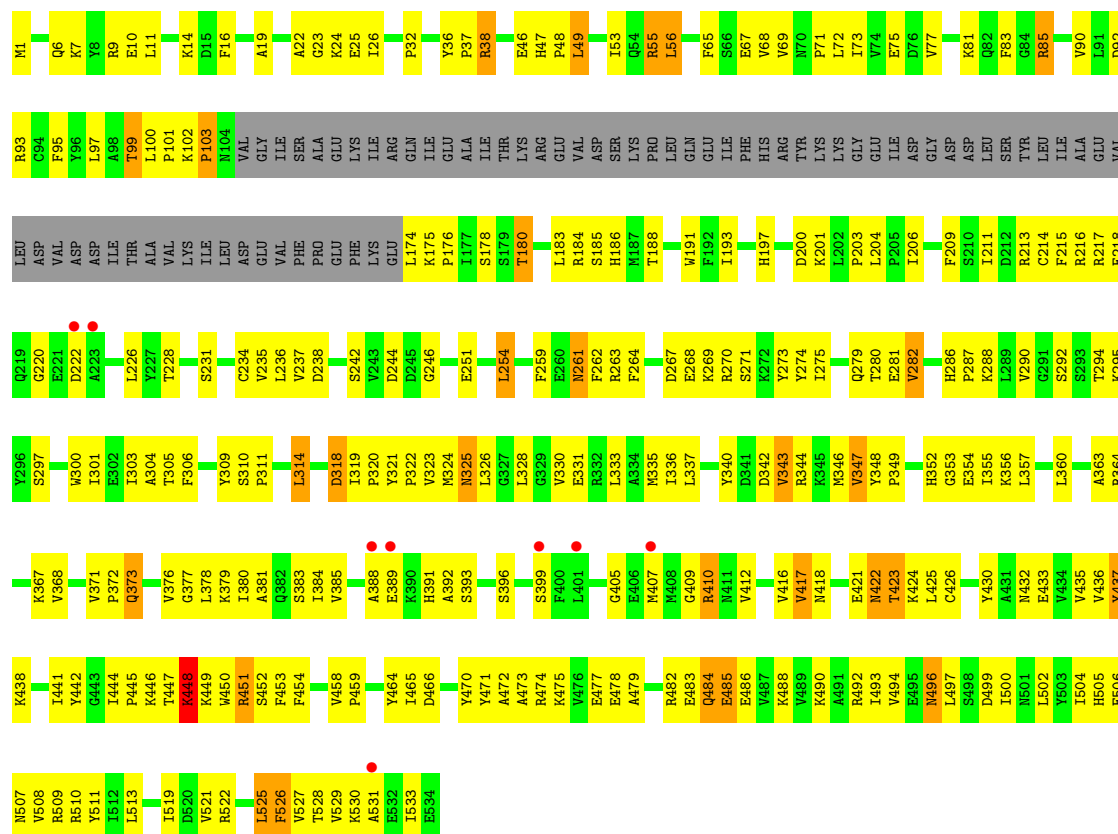


#### • Molecule 2: O-phosphoseryl-tRNA synthetase





● Molecule 2: O-phosphoseryl-tRNA synthetase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	148.04Å 148.04Å 152.48Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.07 – 3.20 49.07 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.07-3.20) 99.9 (49.07-3.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.60 (at 3.19Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.223 , 0.299 0.208 , 0.269	Depositor DCC
$R_{free}$ test set	1603 reflections (4.97%)	DCC
Wilson B-factor (Å <sup>2</sup> )	102.1	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 116.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.038 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	9619	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	113.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.91% 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: SEP

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	D	0.32	1/1693 (0.1%)	0.67	0/2637
2	A	0.31	0/4416	0.55	0/5966
2	B	0.33	0/3849	0.58	0/5200
All	All	0.32	1/9958 (0.0%)	0.59	0/13803

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	901	G	OP3-P	-7.04	1.52	1.61

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	D	1517	0	768	35	0
2	A	4319	0	4339	330	0
2	B	3761	0	3774	249	0
3	A	22	0	10	5	0
All	All	9619	0	8891	593	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 (593) 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)
2:B:464:TYR:HA	2:B:500:ILE:HD11	1.32	1.07
2:B:448:LYS:HD3	2:B:448:LYS:H	1.20	1.05
2:B:55:ARG:HH21	2:B:55:ARG:HG2	1.34	0.92
2:B:47:HIS:HD2	2:B:49:LEU:H	1.13	0.92
2:A:460:THR:HG23	2:A:462:ILE:H	1.36	0.89
1:D:957:A:H1'	1:D:959:U:H5	1.37	0.88
2:A:484:GLN:HG2	2:A:485:GLU:H	1.41	0.86
2:A:200:ASP:HA	2:B:507:ASN:ND2	1.94	0.82
2:A:148:LEU:HG	2:A:160:ALA:HB2	1.63	0.81
1:D:909:G:H5'	1:D:910:G:OP2	1.80	0.80
2:B:385:VAL:HG13	2:B:465:ILE:HD12	1.61	0.80
2:A:106:GLY:HA2	2:A:110:GLU:HB2	1.63	0.80
2:A:380:ILE:O	2:A:384:ILE:HG13	1.82	0.79
2:B:47:HIS:CD2	2:B:49:LEU:H	1.98	0.79
2:B:286:HIS:HD2	2:B:288:LYS:H	1.30	0.79
2:A:227:TYR:HB3	2:B:73:ILE:HD12	1.66	0.78
2:A:434:VAL:O	2:A:460:THR:HG22	1.84	0.77
1:D:957:A:H1'	1:D:959:U:C5	2.18	0.77
2:B:226:LEU:HD21	2:B:344:ARG:HG2	1.64	0.77
2:B:55:ARG:HH21	2:B:55:ARG:CG	1.96	0.77
1:D:942:C:O2'	1:D:943:U:H5'	1.84	0.76
2:A:206:ILE:HB	2:A:237:VAL:HB	1.66	0.76
2:A:465:ILE:HD12	2:A:466:ASP:N	2.01	0.75
2:A:53:ILE:HG23	2:A:211:ILE:HG21	1.67	0.75
2:B:505:HIS:O	2:B:508:VAL:HG22	1.86	0.75
2:A:77:VAL:O	2:A:81:LYS:HG3	1.87	0.75
2:A:434:VAL:HB	2:A:460:THR:HG21	1.67	0.75
2:B:381:ALA:HA	2:B:384:ILE:HD12	1.69	0.75
2:A:374:THR:HG22	2:A:376:VAL:H	1.51	0.74
2:A:505:HIS:O	2:A:508:VAL:HG22	1.88	0.74
2:A:391:HIS:O	2:A:425:LEU:HD23	1.88	0.73
2:A:178:SER:HB3	2:B:176:PRO:HB2	1.71	0.72
2:B:490:LYS:HB3	2:B:528:THR:HG23	1.71	0.72
3:A:1002:SEP:O2P	3:A:1002:SEP:N	2.23	0.72
2:B:376:VAL:HA	2:B:379:LYS:HE2	1.71	0.72
2:B:267:ASP:HB3	2:B:279:GLN:HG2	1.70	0.71
2:B:399:SER:HA	2:B:417:VAL:HG12	1.71	0.71
2:B:504:ILE:HB	2:B:508:VAL:HG21	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:115:ILE:O	2:A:115:ILE:HD13	1.89	0.71
2:A:128:LEU:HD23	2:A:128:LEU:H	1.56	0.71
2:A:37:PRO:O	2:A:364:ARG:HD3	1.90	0.71
1:D:936:G:H21	2:A:522:ARG:H	1.38	0.71
2:B:448:LYS:N	2:B:448:LYS:HD3	2.03	0.71
2:B:381:ALA:HB2	2:B:473:ALA:HB2	1.73	0.71
2:B:504:ILE:HD12	2:B:508:VAL:HG23	1.74	0.70
2:A:97:LEU:HD23	2:B:95:PHE:CE2	2.27	0.69
2:B:263:ARG:HG2	2:B:300:TRP:CZ3	2.27	0.69
2:A:504:ILE:HB	2:A:508:VAL:HG21	1.76	0.68
1:D:934:C:H4'	1:D:935:A:OP2	1.90	0.68
2:A:151:GLU:HG3	2:A:152:VAL:HG13	1.76	0.68
1:D:959:U:H5'	1:D:960:C:OP2	1.93	0.68
2:A:118:ILE:HD12	2:A:118:ILE:H	1.57	0.68
2:A:464:TYR:HD1	2:A:464:TYR:H	1.42	0.67
2:A:326:LEU:HD13	2:A:327:GLY:N	2.09	0.67
2:A:475:LYS:HE2	2:A:475:LYS:HA	1.75	0.67
2:A:97:LEU:HD11	2:A:183:LEU:HG	1.76	0.67
2:B:53:ILE:HG23	2:B:211:ILE:HG21	1.75	0.67
2:A:219:GLN:O	2:A:221:GLU:HG3	1.95	0.67
2:A:434:VAL:HB	2:A:460:THR:CG2	2.25	0.67
2:A:31:SER:O	2:A:35:LEU:HD13	1.95	0.67
2:A:430:TYR:HD2	2:A:465:ILE:HG21	1.60	0.67
2:B:488:LYS:NZ	2:B:530:LYS:HE2	2.10	0.66
2:A:404:GLU:OE2	2:A:413:ARG:HB3	1.95	0.66
2:A:85:ARG:HD2	2:A:85:ARG:N	2.11	0.66
2:B:222:ASP:OD2	2:B:344:ARG:HD3	1.96	0.66
2:B:497:LEU:O	2:B:500:ILE:HG22	1.95	0.66
2:B:325:ASN:HD22	2:B:326:LEU:N	1.94	0.66
2:A:325:ASN:HD22	2:A:326:LEU:N	1.94	0.66
2:A:188:THR:HG23	2:A:309:TYR:OH	1.95	0.66
2:B:55:ARG:NH2	2:B:55:ARG:HG2	2.05	0.66
2:A:22:ALA:O	2:A:25:GLU:HG2	1.96	0.66
2:A:488:LYS:HD3	2:A:530:LYS:HE2	1.77	0.66
2:A:287:PRO:O	2:A:290:VAL:HG22	1.96	0.65
2:A:306:PHE:HB3	2:A:326:LEU:HD22	1.77	0.65
2:A:490:LYS:HD3	2:A:492:ARG:HH12	1.61	0.65
2:B:6:GLN:HG2	2:B:9:ARG:HH11	1.59	0.65
2:B:381:ALA:HB2	2:B:473:ALA:CB	2.27	0.65
1:D:917:G:H4'	1:D:918:G:OP1	1.96	0.65
2:A:85:ARG:HD2	2:A:85:ARG:H	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:385:VAL:HG13	2:A:465:ILE:HD13	1.79	0.65
2:B:263:ARG:HG2	2:B:300:TRP:CH2	2.32	0.65
2:B:465:ILE:HG13	2:B:466:ASP:H	1.62	0.64
2:B:437:TYR:CE2	2:B:438:LYS:HG2	2.32	0.64
2:A:139:GLU:HB3	2:A:143:ASP:OD1	1.97	0.64
2:A:387:THR:HG21	2:A:402:ALA:HA	1.80	0.64
2:B:216:ARG:HG2	2:B:218:GLU:HG2	1.80	0.64
2:A:397:PRO:O	2:A:398:CYS:HB3	1.99	0.63
2:B:360:LEU:HA	2:B:458:VAL:HG21	1.81	0.63
2:A:90:VAL:O	2:A:93:ARG:HG2	1.99	0.63
2:B:47:HIS:HD2	2:B:49:LEU:N	1.93	0.63
2:B:441:ILE:HB	2:B:519:ILE:HG23	1.80	0.63
2:A:414:VAL:HG13	2:A:531:ALA:HB2	1.81	0.63
2:A:137:LYS:HE3	2:A:137:LYS:HA	1.80	0.62
2:A:31:SER:HB2	2:A:32:PRO:HD2	1.81	0.62
2:B:37:PRO:O	2:B:364:ARG:HG3	1.99	0.62
2:A:178:SER:CB	2:B:176:PRO:HB2	2.28	0.62
2:B:485:GLU:HA	2:B:533:ILE:HG12	1.82	0.62
2:B:494:VAL:O	2:B:522:ARG:HA	1.99	0.62
1:D:917:G:H2'	1:D:956:G:N2	2.14	0.62
2:A:148:LEU:HG	2:A:160:ALA:CB	2.29	0.62
2:B:437:TYR:CD2	2:B:438:LYS:HG2	2.35	0.62
2:A:121:ARG:O	2:A:123:VAL:HG13	2.00	0.62
2:B:290:VAL:HA	2:B:297:SER:O	2.00	0.61
2:B:287:PRO:O	2:B:290:VAL:HG22	2.01	0.61
1:D:953:U:H3	1:D:957:A:H62	1.48	0.61
2:A:144:ASP:HA	2:A:147:TYR:CZ	2.36	0.61
2:A:397:PRO:CG	2:A:421:GLU:HG2	2.30	0.61
2:B:67:GLU:HG3	2:B:209:PHE:CZ	2.35	0.60
2:A:485:GLU:HA	2:A:533:ILE:HG13	1.84	0.60
2:A:56:LEU:HD13	2:A:257:PHE:CZ	2.36	0.60
2:A:412:VAL:HG13	2:A:533:ILE:HG22	1.83	0.60
2:B:347:VAL:HG22	2:B:348:TYR:CD2	2.35	0.60
2:B:356:LYS:O	2:B:357:LEU:HD23	2.02	0.59
2:A:395:PRO:HA	2:A:423:THR:O	2.02	0.59
2:A:49:LEU:O	2:A:53:ILE:HG13	2.03	0.59
2:A:144:ASP:HA	2:A:147:TYR:CE1	2.38	0.59
2:B:391:HIS:O	2:B:425:LEU:HD23	2.02	0.59
2:B:372:PRO:HA	2:B:474:ARG:HD3	1.85	0.59
2:A:494:VAL:O	2:A:522:ARG:HA	2.03	0.59
2:B:407:MET:HE1	2:B:477:GLU:HA	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:504:ILE:HD12	2:A:508:VAL:HG23	1.84	0.59
2:B:11:LEU:O	2:B:11:LEU:HD23	2.03	0.58
2:B:432:ASN:HD21	2:B:445:PRO:HD3	1.68	0.58
2:B:451:ARG:O	2:B:454:PHE:N	2.37	0.58
2:B:508:VAL:O	2:B:511:TYR:HB3	2.04	0.58
2:A:213:ARG:HH21	2:A:228:THR:CG2	2.17	0.58
2:A:3:PHE:HD2	2:A:26:ILE:HG21	1.68	0.58
2:A:397:PRO:HD3	2:A:421:GLU:HG2	1.86	0.58
2:A:31:SER:CB	2:A:32:PRO:HD2	2.34	0.58
2:B:471:TYR:O	2:B:475:LYS:HB2	2.04	0.58
2:B:23:GLY:O	2:B:26:ILE:HG12	2.03	0.57
2:A:500:ILE:HG21	2:A:502:LEU:HD22	1.87	0.57
2:B:185:SER:O	2:B:214:CYS:HB3	2.04	0.57
2:A:464:TYR:CB	2:A:500:ILE:HD11	2.34	0.57
2:B:396:SER:OG	2:B:418:ASN:HB3	2.03	0.57
2:B:465:ILE:HG13	2:B:466:ASP:N	2.19	0.57
2:A:285:PHE:HB2	2:A:300:TRP:CE2	2.40	0.57
2:A:222:ASP:OD2	2:A:344:ARG:HG2	2.05	0.57
2:B:301:ILE:HD13	2:B:336:ILE:HD11	1.86	0.57
2:B:346:MET:O	2:B:349:PRO:HD3	2.05	0.57
2:A:314:LEU:HD11	2:A:323:VAL:HG12	1.87	0.57
2:A:397:PRO:HG3	2:A:421:GLU:HG2	1.87	0.56
2:A:213:ARG:HH21	2:A:228:THR:HG22	1.69	0.56
2:B:280:THR:HG22	2:B:281:GLU:N	2.20	0.56
2:A:184:ARG:NH1	2:A:212:ASP:HB3	2.20	0.56
2:A:267:ASP:HB2	2:A:281:GLU:HG3	1.86	0.56
2:A:311:PRO:HA	2:A:314:LEU:HD23	1.88	0.56
2:B:295:LYS:C	2:B:297:SER:H	2.07	0.56
2:B:7:LYS:O	2:B:11:LEU:HB2	2.05	0.56
2:A:115:ILE:HG23	2:A:116:GLU:HG3	1.88	0.56
2:B:325:ASN:C	2:B:325:ASN:ND2	2.59	0.56
2:B:36:TYR:CD1	2:B:37:PRO:HA	2.40	0.56
2:B:388:ALA:O	2:B:392:ALA:HB2	2.05	0.56
2:B:356:LYS:HD2	2:B:357:LEU:H	1.71	0.56
2:B:412:VAL:HG22	2:B:533:ILE:HG22	1.87	0.56
2:A:320:PRO:HG2	2:A:321:TYR:CD1	2.41	0.55
2:A:309:TYR:HD1	2:A:323:VAL:CG1	2.18	0.55
2:A:154:ASP:HA	2:A:158:ILE:HD11	1.87	0.55
2:A:331:GLU:O	2:A:335:MET:HG3	2.06	0.55
2:B:175:LYS:N	2:B:175:LYS:HD2	2.21	0.55
2:B:102:LYS:NZ	2:B:102:LYS:HB3	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:85:ARG:N	2:B:85:ARG:HD2	2.22	0.55
1:D:912:A:H2'	1:D:913:G:O4'	2.06	0.55
2:A:430:TYR:HB2	2:A:465:ILE:CG2	2.37	0.55
2:A:504:ILE:HG13	2:A:504:ILE:O	2.07	0.55
2:B:101:PRO:O	2:B:103:PRO:HD3	2.07	0.55
2:A:510:ARG:HH21	2:B:200:ASP:HB2	1.71	0.55
2:B:335:MET:SD	2:B:343:VAL:HG22	2.46	0.55
2:A:243:VAL:HG12	2:A:247:LYS:HE3	1.88	0.55
2:A:200:ASP:HA	2:B:507:ASN:HD22	1.71	0.55
2:A:492:ARG:HH11	2:A:492:ARG:HG3	1.71	0.55
2:A:160:ALA:O	2:A:164:LEU:HG	2.07	0.55
2:A:458:VAL:HG23	2:A:458:VAL:O	2.07	0.54
2:B:376:VAL:HA	2:B:379:LYS:CE	2.36	0.54
2:A:173:GLU:O	2:A:173:GLU:HG3	2.08	0.54
2:B:432:ASN:ND2	2:B:445:PRO:HD3	2.23	0.54
2:A:202:LEU:HD21	2:B:355:ILE:HB	1.90	0.54
2:A:484:GLN:NE2	2:A:487:VAL:HG22	2.22	0.54
2:A:183:LEU:HD11	2:B:183:LEU:HD11	1.90	0.54
2:B:206:ILE:HB	2:B:237:VAL:HB	1.90	0.54
2:A:258:GLY:HA3	2:A:286:HIS:CE1	2.42	0.54
2:A:344:ARG:HB3	2:A:352:HIS:CE1	2.42	0.54
2:B:376:VAL:O	2:B:380:ILE:HG13	2.07	0.54
2:A:200:ASP:HB2	2:B:510:ARG:HE	1.72	0.54
2:B:306:PHE:HB3	2:B:326:LEU:HD23	1.90	0.54
2:B:488:LYS:HZ2	2:B:530:LYS:HE2	1.72	0.54
2:A:135:TYR:HA	2:A:139:GLU:CG	2.38	0.54
2:A:347:VAL:HG22	2:A:348:TYR:CD2	2.42	0.54
2:A:90:VAL:O	2:A:92:ASP:N	2.41	0.54
2:A:478:GLU:HA	2:A:481:MET:HE3	1.90	0.54
2:B:325:ASN:C	2:B:325:ASN:HD22	2.11	0.54
2:A:236:LEU:HB3	2:A:324:MET:HB3	1.89	0.54
2:A:184:ARG:HH12	2:A:212:ASP:HB3	1.71	0.53
1:D:934:C:H5''	1:D:935:A:O5'	2.08	0.53
2:A:30:ARG:HB2	2:A:35:LEU:HD11	1.90	0.53
2:A:432:ASN:HB2	2:A:464:TYR:CE1	2.43	0.53
2:A:497:LEU:O	2:A:500:ILE:HG22	2.08	0.53
2:A:97:LEU:HD23	2:B:95:PHE:CD2	2.42	0.53
2:B:444:ILE:HG13	2:B:454:PHE:HE1	1.73	0.53
2:A:325:ASN:ND2	2:A:325:ASN:C	2.60	0.53
2:B:437:TYR:CD1	2:B:453:PHE:HA	2.43	0.53
2:B:496:ASN:ND2	2:B:499:ASP:H	2.05	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:451:ARG:HH21	2:B:451:ARG:HG3	1.72	0.53
2:A:414:VAL:HG22	2:A:531:ALA:HB1	1.91	0.53
2:B:75:GLU:OE2	2:B:180:THR:HG23	2.08	0.53
2:B:264:PHE:HB3	2:B:280:THR:HG21	1.90	0.53
2:A:448:LYS:N	2:A:448:LYS:HD3	2.24	0.53
2:B:381:ALA:HA	2:B:384:ILE:CD1	2.38	0.53
2:B:458:VAL:O	2:B:458:VAL:HG23	2.08	0.53
2:A:225:ARG:HG3	2:A:226:LEU:H	1.74	0.53
2:A:442:TYR:CE2	2:A:453:PHE:HE2	2.27	0.53
2:A:259:PHE:CD2	2:A:286:HIS:HB2	2.44	0.52
2:A:464:TYR:HB3	2:A:500:ILE:HD11	1.92	0.52
2:B:197:HIS:O	2:B:201:LYS:HE3	2.08	0.52
2:A:264:PHE:HB3	2:A:280:THR:CG2	2.38	0.52
2:A:444:ILE:HB	2:A:450:TRP:CD1	2.44	0.52
1:D:916:G:H2'	1:D:959:U:O2'	2.09	0.52
1:D:925:G:H2'	1:D:926:G:O4'	2.09	0.52
2:A:30:ARG:HB2	2:A:35:LEU:CD1	2.39	0.52
2:B:448:LYS:CD	2:B:448:LYS:H	2.01	0.52
2:A:218:GLU:HG3	2:A:225:ARG:HG2	1.91	0.52
2:A:188:THR:HG23	2:A:309:TYR:CZ	2.43	0.52
2:A:333:LEU:HD22	2:A:337:LEU:HD11	1.92	0.52
2:A:401:LEU:HD13	2:A:415:TYR:HE1	1.74	0.52
2:B:479:ALA:HB1	2:B:484:GLN:HB2	1.92	0.52
2:B:416:VAL:HG22	2:B:529:VAL:HG22	1.90	0.52
2:A:118:ILE:H	2:A:118:ILE:CD1	2.22	0.52
2:B:320:PRO:HG2	2:B:321:TYR:CD1	2.45	0.52
1:D:925:G:H2'	1:D:926:G:H8	1.75	0.52
2:B:331:GLU:O	2:B:335:MET:HG3	2.10	0.52
2:B:364:ARG:HH21	2:B:364:ARG:HG3	1.74	0.52
2:A:407:MET:HG2	2:A:408:MET:SD	2.50	0.52
2:A:430:TYR:CD2	2:A:465:ILE:HG21	2.42	0.52
2:B:392:ALA:HB1	2:B:426:CYS:HB2	1.91	0.52
2:A:327:GLY:HA3	3:A:1001:SEP:HB2	1.92	0.51
2:B:174:LEU:C	2:B:175:LYS:HD2	2.30	0.51
2:B:363:ALA:HB2	2:B:458:VAL:HG23	1.92	0.51
2:B:53:ILE:HG23	2:B:211:ILE:CG2	2.40	0.51
2:B:482:ARG:O	2:B:483:GLU:HB2	2.11	0.51
2:A:394:GLU:HG3	2:A:400:PHE:CZ	2.46	0.51
2:B:430:TYR:HD2	2:B:465:ILE:HG21	1.74	0.51
2:B:504:ILE:HB	2:B:508:VAL:CG2	2.39	0.51
2:A:156:ASP:CG	2:A:157:ASP:H	2.12	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:396:SER:HB3	2:B:418:ASN:O	2.09	0.51
2:A:185:SER:HA	2:A:215:PHE:O	2.11	0.51
2:A:287:PRO:O	2:A:289:LEU:N	2.43	0.51
2:A:413:ARG:NH1	2:A:532:GLU:HG3	2.24	0.51
2:A:118:ILE:HD12	2:A:118:ILE:N	2.25	0.51
2:A:306:PHE:CD1	2:A:306:PHE:C	2.83	0.51
2:A:432:ASN:ND2	2:A:445:PRO:HD3	2.26	0.51
2:A:479:ALA:C	2:A:481:MET:H	2.14	0.51
2:B:38:ARG:HG2	2:B:367:LYS:HG2	1.91	0.51
1:D:925:G:H2'	1:D:926:G:C8	2.45	0.51
2:B:444:ILE:HG13	2:B:454:PHE:CE1	2.45	0.51
2:A:306:PHE:HB3	2:A:326:LEU:CD2	2.39	0.51
2:A:92:ASP:O	2:A:217:ARG:HD3	2.12	0.51
2:B:412:VAL:CG2	2:B:533:ILE:HG22	2.41	0.50
2:B:484:GLN:O	2:B:533:ILE:HD11	2.11	0.50
2:A:309:TYR:CD1	2:A:323:VAL:HG13	2.47	0.50
2:A:397:PRO:CD	2:A:421:GLU:HG2	2.41	0.50
2:A:238:ASP:O	2:A:322:PRO:HD2	2.12	0.50
2:A:325:ASN:C	2:A:325:ASN:HD22	2.14	0.50
2:B:261:ASN:HD22	2:B:262:PHE:H	1.59	0.50
1:D:916:G:O5'	1:D:916:G:H8	1.95	0.50
2:A:326:LEU:HD13	2:A:326:LEU:C	2.32	0.50
2:A:198:ILE:HD12	2:A:202:LEU:HD12	1.93	0.50
2:A:406:GLU:OE1	2:A:409:GLY:HA2	2.12	0.50
2:B:72:LEU:HA	2:B:184:ARG:NH2	2.26	0.50
2:B:451:ARG:O	2:B:452:SER:C	2.48	0.50
2:B:478:GLU:O	2:B:482:ARG:HB2	2.11	0.50
2:B:83:PHE:CD2	2:B:90:VAL:HG21	2.46	0.50
2:A:158:ILE:HG13	2:A:159:THR:HG23	1.93	0.50
2:A:161:VAL:HG23	2:A:162:LYS:N	2.27	0.50
2:B:213:ARG:HH21	2:B:228:THR:HG22	1.76	0.50
2:A:47:HIS:CD2	2:A:49:LEU:HB2	2.46	0.50
2:A:53:ILE:HG23	2:A:211:ILE:CG2	2.39	0.50
2:B:185:SER:HA	2:B:215:PHE:O	2.11	0.50
2:A:16:PHE:O	2:A:19:ALA:N	2.44	0.50
2:A:478:GLU:HB3	2:A:482:ARG:NH2	2.26	0.50
2:A:347:VAL:O	2:A:349:PRO:HD2	2.12	0.50
2:B:340:TYR:CE2	2:B:346:MET:HA	2.46	0.50
2:A:294:THR:HG23	2:A:296:TYR:H	1.77	0.49
2:A:410:ARG:O	2:A:412:VAL:HG23	2.12	0.49
2:A:23:GLY:O	2:A:25:GLU:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:40:GLY:HA3	2:A:364:ARG:NH2	2.26	0.49
2:B:290:VAL:HG23	2:B:290:VAL:O	2.13	0.49
2:B:218:GLU:C	2:B:220:GLY:H	2.16	0.49
2:B:437:TYR:HD2	2:B:438:LYS:N	2.11	0.49
2:B:47:HIS:CD2	2:B:49:LEU:HB2	2.48	0.49
1:D:915:G:H2'	1:D:916:G:O4'	2.13	0.49
2:A:401:LEU:HA	2:A:415:TYR:HD1	1.77	0.49
2:A:435:VAL:HG21	2:A:444:ILE:HD11	1.95	0.49
1:D:917:G:O2'	1:D:918:G:O5'	2.30	0.49
1:D:923:G:O2'	1:D:924:C:H5'	2.13	0.49
2:A:227:TYR:HB3	2:B:73:ILE:CD1	2.41	0.49
2:A:510:ARG:HE	2:B:200:ASP:HB2	1.78	0.49
2:B:363:ALA:HB2	2:B:458:VAL:CG2	2.42	0.49
2:A:188:THR:HA	2:A:191:TRP:HD1	1.78	0.49
2:A:381:ALA:HB2	2:A:473:ALA:HB2	1.95	0.49
2:B:309:TYR:HB2	2:B:314:LEU:HD21	1.93	0.49
1:D:967:C:H2'	1:D:968:U:O4'	2.13	0.49
2:B:321:TYR:HB3	2:B:322:PRO:HD2	1.95	0.48
2:B:519:ILE:HG22	2:B:521:VAL:HG23	1.95	0.48
2:A:460:THR:HG23	2:A:462:ILE:N	2.17	0.48
2:B:209:PHE:HA	2:B:234:CYS:HA	1.96	0.48
2:B:222:ASP:OD2	2:B:226:LEU:HD23	2.14	0.48
2:A:283:PHE:CE1	2:A:302:GLU:HB2	2.49	0.48
2:A:372:PRO:HG3	2:A:473:ALA:HB3	1.96	0.48
2:A:525:LEU:HD22	2:A:527:VAL:HG12	1.94	0.48
2:B:246:GLY:HA3	2:B:306:PHE:CE1	2.49	0.48
2:A:155:VAL:HG22	2:A:158:ILE:HD13	1.96	0.48
2:A:271:SER:HB3	2:A:273:TYR:CE1	2.48	0.48
2:A:463:ARG:HB2	2:A:466:ASP:OD2	2.13	0.48
2:A:154:ASP:CA	2:A:158:ILE:HD11	2.43	0.48
2:A:68:VAL:HG13	2:A:69:VAL:N	2.27	0.48
2:B:274:TYR:O	2:B:275:ILE:C	2.51	0.48
2:B:376:VAL:HG12	2:B:380:ILE:HD11	1.95	0.48
2:A:285:PHE:HB2	2:A:300:TRP:CD2	2.49	0.48
2:A:351:ILE:HG22	2:A:352:HIS:HD2	1.79	0.48
2:A:478:GLU:HB3	2:A:482:ARG:HH22	1.77	0.48
2:A:264:PHE:HB3	2:A:280:THR:HG21	1.94	0.48
2:A:504:ILE:HB	2:A:508:VAL:CG2	2.42	0.48
2:A:187:MET:HG2	2:A:233:SER:HB3	1.95	0.48
2:B:344:ARG:HB3	2:B:352:HIS:NE2	2.28	0.48
2:B:433:GLU:OE2	2:B:459:PRO:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:267:ASP:HB3	2:A:279:GLN:HG2	1.96	0.47
2:A:148:LEU:HG	2:A:160:ALA:CA	2.44	0.47
2:A:429:ALA:HA	2:A:432:ASN:OD1	2.14	0.47
2:B:19:ALA:O	2:B:22:ALA:HB3	2.14	0.47
2:B:254:LEU:O	2:B:259:PHE:HD1	1.97	0.47
2:A:47:HIS:CD2	2:A:49:LEU:H	2.33	0.47
2:B:102:LYS:HZ3	2:B:102:LYS:HB3	1.80	0.47
2:B:372:PRO:HB2	2:B:378:LEU:HD23	1.95	0.47
3:A:1001:SEP:P	3:A:1001:SEP:H	2.37	0.47
2:A:52:THR:HG23	2:A:337:LEU:HD12	1.97	0.47
2:A:369:LYS:N	2:A:501:ASN:O	2.44	0.47
2:A:380:ILE:HG22	2:A:384:ILE:HD11	1.96	0.47
2:A:97:LEU:HD12	2:A:97:LEU:N	2.29	0.47
2:B:267:ASP:CB	2:B:279:GLN:HG2	2.43	0.47
2:A:309:TYR:HD1	2:A:323:VAL:HG13	1.79	0.47
2:A:464:TYR:N	2:A:464:TYR:CD1	2.81	0.47
2:B:213:ARG:HH21	2:B:228:THR:CG2	2.28	0.47
2:B:237:VAL:HG22	2:B:323:VAL:HG22	1.97	0.47
2:B:490:LYS:HA	2:B:528:THR:HA	1.96	0.47
2:A:93:ARG:O	2:A:217:ARG:HG2	2.15	0.47
2:A:298:ASP:OD2	2:A:298:ASP:N	2.48	0.47
2:B:436:VAL:HG12	2:B:437:TYR:N	2.29	0.47
2:A:149:ILE:HA	2:A:154:ASP:O	2.15	0.47
2:A:489:VAL:O	2:A:528:THR:HG23	2.15	0.47
2:B:275:ILE:HG13	2:B:310:SER:HA	1.95	0.47
2:B:314:LEU:HD12	2:B:319:ILE:HG21	1.96	0.47
2:B:32:PRO:HD2	2:B:371:VAL:HG11	1.96	0.47
2:A:112:ILE:HG13	2:A:112:ILE:O	2.15	0.47
2:A:401:LEU:HD13	2:A:415:TYR:CE1	2.50	0.47
2:A:333:LEU:O	2:A:337:LEU:HG	2.14	0.47
2:A:102:LYS:HD2	2:A:135:TYR:CE1	2.50	0.46
2:B:306:PHE:HB3	2:B:326:LEU:CD2	2.45	0.46
2:B:32:PRO:O	2:B:38:ARG:NH1	2.48	0.46
2:B:385:VAL:O	2:B:389:GLU:HG3	2.15	0.46
2:A:430:TYR:O	2:A:465:ILE:HG23	2.14	0.46
2:A:81:LYS:HE3	2:A:316:GLU:HB3	1.98	0.46
2:B:405:GLY:O	2:B:412:VAL:N	2.49	0.46
2:B:347:VAL:C	2:B:349:PRO:HD2	2.36	0.46
2:A:500:ILE:HG23	2:A:502:LEU:HD13	1.98	0.46
2:B:388:ALA:HB1	2:B:426:CYS:SG	2.56	0.46
2:A:306:PHE:HB2	2:A:325:ASN:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:466:ASP:O	2:A:470:TYR:CD2	2.69	0.46
2:B:318:ASP:O	2:B:320:PRO:HD3	2.15	0.46
2:B:496:ASN:C	2:B:496:ASN:HD22	2.18	0.46
2:A:306:PHE:HB2	2:A:324:MET:CE	2.45	0.46
2:B:410:ARG:N	2:B:410:ARG:HD3	2.30	0.46
2:A:131:ILE:N	2:A:131:ILE:HD12	2.31	0.45
2:A:135:TYR:HA	2:A:139:GLU:HG3	1.98	0.45
2:A:401:LEU:HA	2:A:415:TYR:CD1	2.52	0.45
2:A:533:ILE:HG13	2:A:533:ILE:O	2.16	0.45
2:B:71:PRO:HG2	2:B:193:ILE:HG21	1.98	0.45
2:A:222:ASP:HA	2:A:225:ARG:O	2.16	0.45
2:A:258:GLY:HA3	2:A:286:HIS:HE1	1.79	0.45
2:A:484:GLN:HG2	2:A:485:GLU:N	2.20	0.45
2:B:188:THR:HA	2:B:191:TRP:HD1	1.80	0.45
2:B:450:TRP:O	2:B:451:ARG:C	2.54	0.45
2:A:184:ARG:NH2	2:A:187:MET:SD	2.90	0.45
2:A:349:PRO:HG2	2:A:350:GLN:OE1	2.16	0.45
2:A:414:VAL:HG22	2:A:531:ALA:CB	2.47	0.45
2:B:99:THR:OG1	2:B:100:LEU:N	2.49	0.45
2:A:434:VAL:HG21	2:A:502:LEU:CD2	2.47	0.45
1:D:957:A:HO2'	1:D:958:A:P	2.40	0.45
2:A:95:PHE:CE2	2:B:97:LEU:HD23	2.51	0.45
2:B:391:HIS:C	2:B:393:SER:H	2.20	0.45
1:D:931:C:O2'	1:D:932:U:H5'	2.17	0.45
2:A:145:LEU:HD22	2:A:145:LEU:N	2.32	0.45
2:A:257:PHE:O	2:A:286:HIS:HE1	2.00	0.45
2:A:511:TYR:CZ	2:A:515:LYS:HG3	2.52	0.45
2:B:442:TYR:CE2	2:B:453:PHE:HE2	2.35	0.45
2:A:217:ARG:NH2	2:B:99:THR:OG1	2.49	0.45
1:D:941:G:C2'	1:D:942:C:H5'	2.47	0.45
1:D:957:A:O2'	1:D:958:A:P	2.75	0.45
2:A:399:SER:HA	2:A:417:VAL:HG12	1.99	0.44
2:A:377:GLY:O	2:A:380:ILE:HB	2.17	0.44
2:A:500:ILE:CG2	2:A:502:LEU:HB2	2.47	0.44
2:B:188:THR:HG23	2:B:309:TYR:CZ	2.52	0.44
2:B:275:ILE:HG12	2:B:311:PRO:HD3	1.99	0.44
2:A:434:VAL:HG21	2:A:502:LEU:HD23	1.99	0.44
2:B:75:GLU:HB3	2:B:77:VAL:HG12	1.99	0.44
2:B:16:PHE:O	2:B:19:ALA:HB3	2.17	0.44
2:A:468:PHE:O	2:A:471:TYR:N	2.48	0.44
2:A:496:ASN:C	2:A:496:ASN:HD22	2.20	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:200:ASP:HB2	2:B:510:ARG:HH21	1.83	0.44
2:A:403:PHE:O	2:A:413:ARG:HA	2.17	0.44
2:B:251:GLU:HG3	2:B:262:PHE:CE2	2.51	0.44
2:B:527:VAL:O	2:B:527:VAL:HG13	2.17	0.44
2:B:282:VAL:CG2	2:B:303:ILE:HG22	2.47	0.44
2:A:325:ASN:ND2	2:A:326:LEU:N	2.63	0.44
2:A:176:PRO:HG2	2:B:178:SER:CB	2.48	0.44
2:A:186:HIS:HB2	3:A:1001:SEP:O2P	2.18	0.44
2:A:433:GLU:OE2	2:A:461:GLY:HA2	2.18	0.44
2:A:67:GLU:HG3	2:A:209:PHE:CZ	2.52	0.44
2:A:453:PHE:N	2:A:453:PHE:CD1	2.86	0.43
2:B:377:GLY:O	2:B:380:ILE:HB	2.18	0.43
2:B:485:GLU:HA	2:B:533:ILE:CG1	2.48	0.43
2:B:506:GLU:HB2	2:B:510:ARG:HH12	1.83	0.43
2:A:258:GLY:O	2:A:259:PHE:C	2.57	0.43
2:A:286:HIS:CD2	2:A:288:LYS:HB2	2.53	0.43
2:A:409:GLY:O	2:A:410:ARG:HG3	2.17	0.43
2:A:56:LEU:HB3	2:A:211:ILE:CD1	2.49	0.43
2:B:479:ALA:HA	2:B:482:ARG:HB3	2.00	0.43
2:A:118:ILE:HG22	2:A:119:THR:N	2.34	0.43
2:A:127:PRO:C	2:A:129:GLN:H	2.21	0.43
2:A:215:PHE:CD1	2:A:215:PHE:N	2.86	0.43
2:A:251:GLU:HG3	2:A:262:PHE:CE2	2.53	0.43
2:A:273:TYR:O	2:A:309:TYR:HA	2.19	0.43
2:A:500:ILE:CG2	2:A:502:LEU:HD22	2.47	0.43
2:B:261:ASN:HD22	2:B:262:PHE:N	2.16	0.43
2:B:275:ILE:CG1	2:B:310:SER:HA	2.49	0.43
2:B:472:ALA:O	2:B:475:LYS:N	2.45	0.43
2:B:525:LEU:HD13	2:B:527:VAL:HG12	2.01	0.43
2:A:153:LEU:N	2:A:153:LEU:HD12	2.34	0.43
2:A:162:LYS:O	2:A:166:GLU:HG2	2.19	0.43
2:A:328:LEU:HD11	2:A:333:LEU:HD12	2.00	0.43
2:A:472:ALA:O	2:A:475:LYS:N	2.51	0.43
2:B:340:TYR:CD2	2:B:346:MET:HA	2.53	0.43
2:B:368:VAL:HG11	2:B:371:VAL:HG22	2.01	0.43
2:A:135:TYR:HA	2:A:139:GLU:HG2	2.00	0.43
2:A:286:HIS:HD2	2:A:288:LYS:HB2	1.82	0.43
2:A:303:ILE:HG13	2:A:328:LEU:HD21	1.99	0.43
2:A:351:ILE:HG22	2:A:352:HIS:CD2	2.53	0.43
2:B:292:SER:OG	2:B:294:THR:HG22	2.19	0.43
2:A:157:ASP:HA	2:A:160:ALA:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:187:MET:CB	3:A:1001:SEP:O3P	2.67	0.43
2:A:222:ASP:CG	2:A:344:ARG:HG2	2.39	0.43
2:A:447:THR:C	2:A:449:LYS:H	2.20	0.43
2:A:515:LYS:O	2:A:516:LYS:HB2	2.18	0.43
2:B:294:THR:OG1	2:B:295:LYS:N	2.52	0.43
1:D:957:A:O2'	1:D:958:A:O5'	2.28	0.43
2:A:145:LEU:HD12	2:A:156:ASP:HB2	2.00	0.43
2:A:479:ALA:C	2:A:481:MET:N	2.71	0.43
2:A:315:ALA:C	2:A:317:TYR:N	2.71	0.43
2:A:498:SER:C	2:A:500:ILE:H	2.22	0.43
2:A:52:THR:O	2:A:56:LEU:CD2	2.66	0.43
2:B:282:VAL:HG23	2:B:303:ILE:HG22	2.01	0.43
2:B:421:GLU:O	2:B:423:THR:HG22	2.18	0.43
2:B:451:ARG:NH2	2:B:451:ARG:HG3	2.34	0.43
2:A:155:VAL:HG23	2:A:158:ILE:CG2	2.49	0.43
2:A:213:ARG:NH2	2:A:228:THR:CG2	2.81	0.43
2:A:243:VAL:HG13	2:A:306:PHE:CE1	2.54	0.43
2:B:475:LYS:HD2	2:B:478:GLU:OE2	2.18	0.43
1:D:968:U:H2'	1:D:969:G:C8	2.54	0.43
2:A:251:GLU:HG2	2:A:255:ARG:HG3	2.01	0.42
2:A:468:PHE:O	2:A:471:TYR:HB3	2.18	0.42
2:B:183:LEU:HD13	2:B:215:PHE:CD1	2.54	0.42
1:D:943:U:H2'	1:D:944:U:H5'	2.00	0.42
2:A:153:LEU:O	2:A:154:ASP:HB2	2.19	0.42
2:A:324:MET:HE1	2:A:326:LEU:HB2	2.01	0.42
2:A:370:GLU:O	2:A:501:ASN:ND2	2.45	0.42
2:A:475:LYS:CA	2:A:475:LYS:HE2	2.48	0.42
2:B:421:GLU:O	2:B:422:ASN:C	2.57	0.42
1:D:941:G:O2'	1:D:942:C:H5'	2.19	0.42
2:A:397:PRO:HD3	2:A:421:GLU:CG	2.49	0.42
2:B:286:HIS:CD2	2:B:288:LYS:HB3	2.54	0.42
2:B:486:GLU:HA	2:B:531:ALA:O	2.19	0.42
2:B:90:VAL:O	2:B:93:ARG:HG2	2.19	0.42
2:A:315:ALA:C	2:A:317:TYR:H	2.23	0.42
2:B:328:LEU:C	2:B:328:LEU:HD12	2.40	0.42
1:D:936:G:H2'	2:A:522:ARG:CZ	2.50	0.42
2:A:214:CYS:C	2:A:215:PHE:CD1	2.92	0.42
2:A:464:TYR:HD1	2:A:464:TYR:N	2.13	0.42
2:B:324:MET:C	2:B:324:MET:SD	2.97	0.42
2:B:330:VAL:O	2:B:331:GLU:C	2.57	0.42
2:A:137:LYS:HE3	2:A:137:LYS:CA	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:337:LEU:HB2	2:A:338:TYR:CD1	2.55	0.42
2:A:380:ILE:O	2:A:383:SER:OG	2.27	0.42
2:B:275:ILE:HG13	2:B:309:TYR:O	2.19	0.42
2:B:6:GLN:O	2:B:7:LYS:C	2.56	0.42
2:A:273:TYR:CE2	2:A:274:TYR:CE2	3.07	0.42
2:A:292:SER:OG	2:A:294:THR:HG22	2.19	0.42
2:A:321:TYR:HB3	2:A:322:PRO:HD2	2.02	0.42
2:A:56:LEU:HD13	2:A:257:PHE:HZ	1.84	0.42
2:B:383:SER:O	2:B:384:ILE:C	2.58	0.42
2:B:437:TYR:HE2	2:B:438:LYS:NZ	2.17	0.42
2:A:239:GLU:HG2	2:A:321:TYR:CE2	2.53	0.42
2:A:500:ILE:HG22	2:A:502:LEU:H	1.85	0.42
2:B:23:GLY:O	2:B:25:GLU:N	2.52	0.42
2:B:445:PRO:O	2:B:447:THR:N	2.53	0.42
2:B:496:ASN:HD21	2:B:499:ASP:H	1.67	0.42
2:A:488:LYS:HG2	2:A:530:LYS:HG2	2.01	0.42
2:B:295:LYS:C	2:B:297:SER:N	2.73	0.42
2:B:354:GLU:OE2	2:B:354:GLU:HA	2.20	0.42
2:B:204:LEU:HD23	2:B:238:ASP:HA	2.02	0.42
1:D:909:G:H1'	1:D:946:A:H1'	2.01	0.42
2:B:56:LEU:HB3	2:B:211:ILE:CD1	2.51	0.41
1:D:968:U:H2'	1:D:969:G:H8	1.85	0.41
2:A:155:VAL:HG23	2:A:158:ILE:HG23	2.02	0.41
2:A:394:GLU:HG3	2:A:400:PHE:HZ	1.85	0.41
2:A:511:TYR:CE1	2:A:515:LYS:HG3	2.54	0.41
2:B:282:VAL:HG13	2:B:304:ALA:O	2.19	0.41
2:B:324:MET:SD	2:B:325:ASN:N	2.93	0.41
2:A:331:GLU:CD	2:A:331:GLU:H	2.24	0.41
2:A:448:LYS:N	2:A:448:LYS:CD	2.83	0.41
2:B:271:SER:HB3	2:B:273:TYR:CE1	2.55	0.41
2:B:320:PRO:HG2	2:B:321:TYR:CE1	2.54	0.41
2:A:140:ILE:N	2:A:143:ASP:OD1	2.50	0.41
2:A:445:PRO:O	2:A:450:TRP:HD1	2.04	0.41
2:B:269:LYS:O	2:B:270:ARG:C	2.58	0.41
2:A:285:PHE:C	2:A:285:PHE:CD1	2.93	0.41
2:A:310:SER:C	2:A:312:THR:H	2.24	0.41
2:A:450:TRP:O	2:A:451:ARG:C	2.59	0.41
2:A:484:GLN:HE22	2:A:487:VAL:HG22	1.83	0.41
2:A:56:LEU:HB3	2:A:211:ILE:HD11	2.03	0.41
2:B:281:GLU:HG2	2:B:305:THR:HG22	2.02	0.41
2:B:235:VAL:HA	2:B:324:MET:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:47:HIS:CG	2:B:48:PRO:HD2	2.55	0.41
2:A:310:SER:C	2:A:312:THR:N	2.73	0.41
2:A:366:ILE:HA	2:A:504:ILE:HG22	2.03	0.41
2:A:453:PHE:HD1	2:A:453:PHE:N	2.19	0.41
2:A:6:GLN:O	2:A:10:GLU:HG2	2.21	0.41
2:A:203:PRO:HG3	2:B:508:VAL:HG12	2.02	0.41
1:D:917:G:O2'	1:D:918:G:C5'	2.68	0.41
2:A:463:ARG:O	2:A:464:TYR:C	2.59	0.41
2:A:508:VAL:HG12	2:B:203:PRO:HG3	2.02	0.41
2:B:242:SER:C	2:B:244:ASP:N	2.73	0.41
2:B:288:LYS:NZ	2:B:337:LEU:O	2.50	0.41
2:A:101:PRO:HB3	2:A:177:ILE:CD1	2.51	0.41
2:A:287:PRO:C	2:A:289:LEU:N	2.74	0.41
2:A:294:THR:C	2:A:296:TYR:H	2.22	0.41
2:A:309:TYR:HD1	2:A:323:VAL:HG11	1.82	0.41
2:B:10:GLU:HG3	2:B:11:LEU:N	2.36	0.41
2:B:342:ASP:O	2:B:343:VAL:C	2.59	0.41
2:B:360:LEU:O	2:B:363:ALA:HB3	2.21	0.41
2:B:423:THR:HG23	2:B:424:LYS:N	2.36	0.41
2:A:95:PHE:CD2	2:B:97:LEU:HD23	2.56	0.41
1:D:934:C:O5'	1:D:934:C:H6	2.03	0.41
2:A:38:ARG:NH2	2:A:460:THR:O	2.54	0.41
2:A:520:ASP:OD1	2:A:522:ARG:NH2	2.54	0.41
2:A:72:LEU:HD23	2:A:72:LEU:C	2.41	0.41
2:B:381:ALA:O	2:B:384:ILE:HB	2.19	0.41
2:A:145:LEU:CD1	2:A:156:ASP:HB2	2.51	0.41
2:A:16:PHE:O	2:A:18:ALA:N	2.54	0.41
2:A:211:ILE:HG12	2:A:232:ALA:HA	2.02	0.41
2:A:397:PRO:O	2:A:398:CYS:CB	2.68	0.41
2:B:218:GLU:OE2	2:B:218:GLU:HA	2.21	0.41
2:B:492:ARG:HA	2:B:526:PHE:HD2	1.86	0.41
2:B:77:VAL:HG22	2:B:81:LYS:HD2	2.03	0.41
1:D:918:G:H5''	1:D:958:A:H61	1.85	0.41
2:A:235:VAL:HA	2:A:324:MET:O	2.21	0.41
2:A:383:SER:HA	2:A:386:GLU:HB3	2.03	0.41
2:A:500:ILE:HG23	2:A:500:ILE:O	2.21	0.41
2:B:1:MET:N	2:B:26:ILE:O	2.54	0.41
2:A:259:PHE:CE2	2:A:286:HIS:HB2	2.57	0.40
2:A:314:LEU:HD11	2:A:323:VAL:CG1	2.49	0.40
2:A:67:GLU:HB2	2:B:46:GLU:HA	2.03	0.40
2:B:373:GLN:OE1	2:B:373:GLN:HA	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:32:PRO:HG3	2:B:470:TYR:CZ	2.56	0.40
2:B:513:LEU:HD12	2:B:513:LEU:HA	1.92	0.40
2:A:121:ARG:HH11	2:A:121:ARG:HG3	1.86	0.40
2:A:125:SER:O	2:A:126:LYS:C	2.60	0.40
2:A:356:LYS:O	2:A:357:LEU:HD23	2.20	0.40
2:B:268:GLU:O	2:B:270:ARG:HG3	2.20	0.40
2:B:188:THR:HG23	2:B:309:TYR:OH	2.21	0.40
2:B:65:PHE:N	2:B:65:PHE:CD1	2.89	0.40
2:B:92:ASP:O	2:B:217:ARG:HD3	2.21	0.40
2:A:106:GLY:CA	2:A:110:GLU:HB2	2.43	0.40
2:A:409:GLY:C	2:A:410:ARG:HG3	2.41	0.40
2:A:80:LYS:HA	2:A:87:ALA:CB	2.52	0.40
2:B:211:ILE:HA	2:B:231:SER:O	2.21	0.40
2:A:290:VAL:HA	2:A:297:SER:O	2.22	0.40
2:A:47:HIS:CG	2:A:48:PRO:HD2	2.56	0.40
2:A:85:ARG:CD	2:A:85:ARG:N	2.83	0.40
2:B:271:SER:HB3	2:B:273:TYR:CD1	2.57	0.40
2:B:430:TYR:HB2	2:B:465:ILE:HG23	2.03	0.40
2:B:68:VAL:HG12	2:B:69:VAL:N	2.37	0.40
2:A:423:THR:OG1	2:A:424:LYS:N	2.54	0.40
2:A:504:ILE:O	2:A:505:HIS:C	2.59	0.40
2:B:447:THR:O	2:B:449:LYS:N	2.54	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	
2	A	532/534 (100%)	417 (78%)	88 (16%)	27 (5%)	2	18
2	B	461/534 (86%)	376 (82%)	71 (15%)	14 (3%)	5	32
All	All	993/1068 (93%)	793 (80%)	159 (16%)	41 (4%)	3	24



All (41) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	118	ILE
2	A	398	CYS
2	A	526	PHE
2	B	14	LYS
2	B	484	GLN
2	A	24	LYS
2	A	91	LEU
2	A	107	ILE
2	A	125	SER
2	A	156	ASP
2	A	288	LYS
2	A	484	GLN
2	A	500	ILE
2	B	423	THR
2	A	148	LEU
2	A	151	GLU
2	A	199	ALA
2	B	24	LYS
2	B	448	LYS
2	B	451	ARG
2	B	526	PHE
2	A	16	PHE
2	A	17	GLU
2	A	104	ASN
2	A	122	GLU
2	A	369	LYS
2	B	422	ASN
2	A	154	ASP
2	A	339	GLY
2	A	279	GLN
2	B	353	GLY
2	B	409	GLY
2	B	446	LYS
2	A	140	ILE
2	A	343	VAL
2	B	343	VAL
2	A	105	VAL
2	A	126	LYS
2	A	127	PRO
2	B	103	PRO
2	B	417	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	
2	A	464/464 (100%)	437 (94%)	27 (6%)	23	62
2	B	402/464 (87%)	374 (93%)	28 (7%)	18	54
All	All	866/928 (93%)	811 (94%)	55 (6%)	20	59

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	38	ARG
2	A	49	LEU
2	A	55	ARG
2	A	68	VAL
2	A	85	ARG
2	A	99	THR
2	A	104	ASN
2	A	115	ILE
2	A	132	PHE
2	A	137	LYS
2	A	165	ASP
2	A	186	HIS
2	A	255	ARG
2	A	261	ASN
2	A	282	VAL
2	A	324	MET
2	A	325	ASN
2	A	333	LEU
2	A	347	VAL
2	A	422	ASN
2	A	464	TYR
2	A	471	TYR
2	A	485	GLU
2	A	496	ASN
2	A	509	ARG
2	A	513	LEU
2	A	525	LEU

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Mol	Chain	Res	Type
2	B	38	ARG
2	B	49	LEU
2	B	55	ARG
2	B	56	LEU
2	B	85	ARG
2	B	99	THR
2	B	180	THR
2	B	186	HIS
2	B	236	LEU
2	B	254	LEU
2	B	261	ASN
2	B	282	VAL
2	B	314	LEU
2	B	318	ASP
2	B	325	ASN
2	B	333	LEU
2	B	347	VAL
2	B	373	GLN
2	B	410	ARG
2	B	435	VAL
2	B	437	TYR
2	B	448	LYS
2	B	485	GLU
2	B	493	ILE
2	B	496	ASN
2	B	502	LEU
2	B	509	ARG
2	B	525	LEU

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

Mol	Chain	Res	Type
2	A	47	HIS
2	A	104	ASN
2	A	114	GLN
2	A	261	ASN
2	A	286	HIS
2	A	325	ASN
2	A	352	HIS
2	A	382	GLN
2	A	422	ASN
2	A	484	GLN

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Mol	Chain	Res	Type
2	A	496	ASN
2	B	47	HIS
2	B	261	ASN
2	B	286	HIS
2	B	382	GLN
2	B	420	ASN
2	B	432	ASN
2	B	496	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	D	70/71 (98%)	15 (21%)	0

All (15) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	D	906	G
1	D	908	U
1	D	909	G
1	D	910	G
1	D	917	G
1	D	918	G
1	D	919	C
1	D	932	U
1	D	933	U
1	D	935	A
1	D	944	U
1	D	945	U
1	D	946	A
1	D	958	A
1	D	960	C

There are no RNA pucker outliers to report.

## 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

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	SEP	A	1001	-	6,10,10	1.60	1 (16%)	8,14,14	1.86	2 (25%)
3	SEP	A	1002	-	6,10,10	1.59	1 (16%)	8,14,14	1.97	2 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SEP	A	1001	-	-	0/6/10/10	0/0/0/0
3	SEP	A	1002	-	-	0/6/10/10	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1002	SEP	P-O1P	3.12	1.61	1.50
3	A	1001	SEP	P-O1P	3.14	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1001	SEP	O3P-P-OG	2.20	112.60	106.73
3	A	1002	SEP	O3P-P-OG	2.28	112.80	106.73
3	A	1001	SEP	OG-CB-CA	4.40	111.97	108.07
3	A	1002	SEP	OG-CB-CA	4.69	112.23	108.07

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1001	SEP	4	0
3	A	1002	SEP	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data

### 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	D	71/71 (100%)	2.24	34 (47%) 0 0	104, 195, 200, 200	0
2	A	534/534 (100%)	0.33	36 (6%) 19 10	20, 92, 197, 202	0
2	B	465/534 (87%)	-0.03	8 (1%) 70 57	25, 80, 185, 202	0
All	All	1070/1139 (93%)	0.30	78 (7%) 16 9	20, 91, 198, 202	0

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	223	ALA	9.1
1	D	969	G	7.8
1	D	970	G	7.5
1	D	903	C	5.5
2	A	149	ILE	4.8
1	D	905	G	4.7
2	A	126	LYS	4.6
2	B	223	ALA	4.6
1	D	971	C	4.5
2	A	133	HIS	4.4
2	A	150	ALA	4.4
1	D	944	U	4.4
1	D	933	U	4.3
2	A	407	MET	4.1
1	D	965	C	4.1
2	A	222	ASP	4.1
2	A	168	PHE	4.1
2	A	116	GLU	4.0
1	D	902	C	4.0
1	D	932	U	3.8
1	D	952	G	3.8
2	A	224	THR	3.8
2	A	171	PHE	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	928	G	3.7
1	D	904	A	3.5
2	A	531	ALA	3.5
1	D	925	G	3.5
2	A	132	PHE	3.5
1	D	964	G	3.4
1	D	968	U	3.4
1	D	901	G	3.3
2	B	531	ALA	3.2
1	D	906	G	3.2
2	A	106	GLY	3.2
1	D	907	G	3.1
1	D	910	G	3.1
1	D	924	C	3.1
2	A	147	TYR	3.0
2	B	388	ALA	3.0
2	A	137	LYS	3.0
1	D	940	C	2.9
2	A	151	GLU	2.9
1	D	945	U	2.8
1	D	951	G	2.7
1	D	936	G	2.7
2	A	125	SER	2.7
2	A	117	ALA	2.6
2	A	380	ILE	2.6
2	B	401	LEU	2.6
2	A	533	ILE	2.5
2	B	399	SER	2.5
1	D	966	C	2.4
2	A	102	LYS	2.4
2	A	173	GLU	2.4
1	D	922	U	2.4
2	A	534	GLU	2.4
1	D	913	G	2.3
2	A	163	ILE	2.3
1	D	923	G	2.3
1	D	939	C	2.3
1	D	935	A	2.2
2	A	411	ASN	2.2
2	A	131	ILE	2.2
2	B	222	ASP	2.2
2	A	103	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
2	A	114	GLN	2.2
1	D	929	G	2.1
2	A	146	SER	2.1
2	A	135	TYR	2.1
2	B	389	GLU	2.1
2	A	136	LYS	2.1
1	D	957	A	2.0
2	B	407	MET	2.0
2	A	62	SER	2.0
2	A	156	ASP	2.0
2	A	414	VAL	2.0
2	A	476	VAL	2.0
1	D	941	G	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	SEP	A	1002	11/11	0.95	0.22	0.57	41,77,116,154	0
3	SEP	A	1001	11/11	0.94	0.25	0.11	41,103,137,172	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.