



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:28 AM GMT

PDB ID : 3ERR  
Title : Microtubule binding domain from mouse cytoplasmic dynein as a fusion with seryl-tRNA synthetase  
Authors : Carter, A.P.  
Deposited on : 2008-10-03  
Resolution : 2.27 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

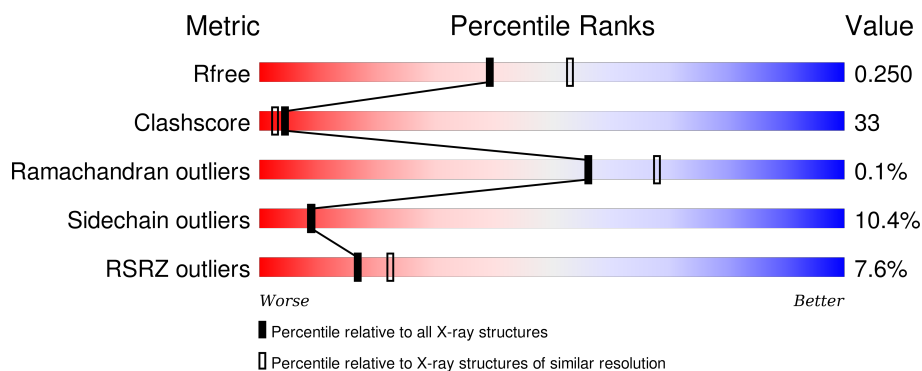
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.27 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))
$R_{free}$	91344	5193 (2.30-2.26)
Clashscore	102246	5929 (2.30-2.26)
Ramachandran outliers	100387	5851 (2.30-2.26)
Sidechain outliers	100360	5850 (2.30-2.26)
RSRZ outliers	91569	5204 (2.30-2.26)

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	536	 4% 65% 28% 5% ...
1	B	536	 10% 54% 38% 5% ...

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8589 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 fusion protein of microtubule binding domain from mouse cytoplasmic dynein and seryl-tRNA synthetase from *Thermus thermophilus*.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	527	Total	C	N	O	S	0	0	0
			4210	2677	741	776	16			
1	B	527	Total	C	N	O	S	0	0	0
			4210	2677	741	776	16			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP Q9JHU4
A	2	VAL	-	EXPRESSION TAG	UNP Q9JHU4
A	3	ASP	-	EXPRESSION TAG	UNP Q9JHU4
A	4	LEU	-	EXPRESSION TAG	UNP Q9JHU4
A	5	LYS	-	EXPRESSION TAG	UNP Q9JHU4
A	6	ARG	-	EXPRESSION TAG	UNP Q9JHU4
A	7	LEU	-	EXPRESSION TAG	UNP Q9JHU4
A	8	ARG	-	EXPRESSION TAG	UNP Q9JHU4
A	9	GLN	-	EXPRESSION TAG	UNP Q9JHU4
A	10	GLU	-	EXPRESSION TAG	UNP Q9JHU4
A	11	PRO	-	EXPRESSION TAG	UNP Q9JHU4
A	12	GLU	-	EXPRESSION TAG	UNP Q9JHU4
A	13	VAL	-	EXPRESSION TAG	UNP Q9JHU4
A	14	PHE	-	EXPRESSION TAG	UNP Q9JHU4
A	15	HIS	-	EXPRESSION TAG	UNP Q9JHU4
A	16	ARG	-	EXPRESSION TAG	UNP Q9JHU4
A	17	ALA	-	EXPRESSION TAG	UNP Q9JHU4
A	18	ILE	-	EXPRESSION TAG	UNP Q9JHU4
A	19	ARG	-	EXPRESSION TAG	UNP Q9JHU4
A	20	GLU	-	EXPRESSION TAG	UNP Q9JHU4
A	21	LYS	-	EXPRESSION TAG	UNP Q9JHU4
A	22	GLY	-	EXPRESSION TAG	UNP Q9JHU4
A	23	VAL	-	EXPRESSION TAG	UNP Q9JHU4
A	24	ALA	-	EXPRESSION TAG	UNP Q9JHU4

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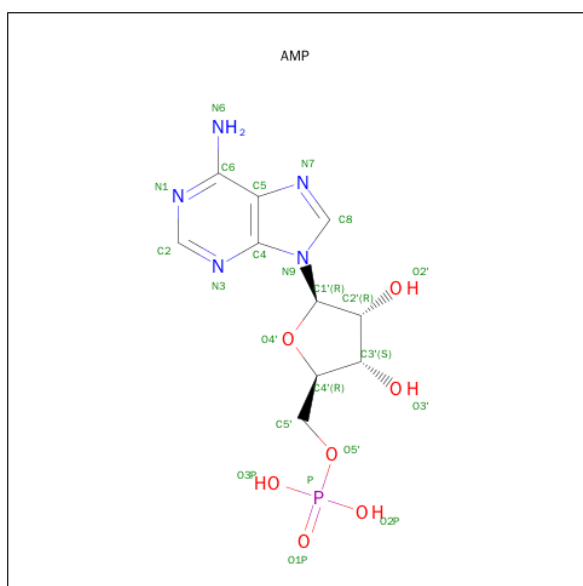
Chain	Residue	Modelled	Actual	Comment	Reference
A	25	LEU	-	EXPRESSION TAG	UNP Q9JHU4
A	26	ASP	-	EXPRESSION TAG	UNP Q9JHU4
A	27	LEU	-	EXPRESSION TAG	UNP Q9JHU4
A	28	GLU	-	EXPRESSION TAG	UNP Q9JHU4
A	29	ALA	-	EXPRESSION TAG	UNP Q9JHU4
A	30	LEU	-	EXPRESSION TAG	UNP Q9JHU4
A	31	LEU	-	EXPRESSION TAG	UNP Q9JHU4
A	32	ALA	-	EXPRESSION TAG	UNP Q9JHU4
A	33	VAL	-	EXPRESSION TAG	UNP Q9JHU4
A	34	ASP	-	EXPRESSION TAG	UNP Q9JHU4
A	3323	ALA	CYS	ENGINEERED	UNP Q9JHU4
A	3387	ALA	CYS	ENGINEERED	UNP Q9JHU4
A	420	GLY	-	EXPRESSION TAG	UNP P34945
A	421	ALA	-	EXPRESSION TAG	UNP P34945
A	422	HIS	-	EXPRESSION TAG	UNP P34945
A	423	HIS	-	EXPRESSION TAG	UNP P34945
A	424	HIS	-	EXPRESSION TAG	UNP P34945
A	425	HIS	-	EXPRESSION TAG	UNP P34945
A	426	HIS	-	EXPRESSION TAG	UNP P34945
A	427	HIS	-	EXPRESSION TAG	UNP P34945
B	1	MET	-	EXPRESSION TAG	UNP Q9JHU4
B	2	VAL	-	EXPRESSION TAG	UNP Q9JHU4
B	3	ASP	-	EXPRESSION TAG	UNP Q9JHU4
B	4	LEU	-	EXPRESSION TAG	UNP Q9JHU4
B	5	LYS	-	EXPRESSION TAG	UNP Q9JHU4
B	6	ARG	-	EXPRESSION TAG	UNP Q9JHU4
B	7	LEU	-	EXPRESSION TAG	UNP Q9JHU4
B	8	ARG	-	EXPRESSION TAG	UNP Q9JHU4
B	9	GLN	-	EXPRESSION TAG	UNP Q9JHU4
B	10	GLU	-	EXPRESSION TAG	UNP Q9JHU4
B	11	PRO	-	EXPRESSION TAG	UNP Q9JHU4
B	12	GLU	-	EXPRESSION TAG	UNP Q9JHU4
B	13	VAL	-	EXPRESSION TAG	UNP Q9JHU4
B	14	PHE	-	EXPRESSION TAG	UNP Q9JHU4
B	15	HIS	-	EXPRESSION TAG	UNP Q9JHU4
B	16	ARG	-	EXPRESSION TAG	UNP Q9JHU4
B	17	ALA	-	EXPRESSION TAG	UNP Q9JHU4
B	18	ILE	-	EXPRESSION TAG	UNP Q9JHU4
B	19	ARG	-	EXPRESSION TAG	UNP Q9JHU4
B	20	GLU	-	EXPRESSION TAG	UNP Q9JHU4
B	21	LYS	-	EXPRESSION TAG	UNP Q9JHU4
B	22	GLY	-	EXPRESSION TAG	UNP Q9JHU4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	23	VAL	-	EXPRESSION TAG	UNP Q9JHU4
B	24	ALA	-	EXPRESSION TAG	UNP Q9JHU4
B	25	LEU	-	EXPRESSION TAG	UNP Q9JHU4
B	26	ASP	-	EXPRESSION TAG	UNP Q9JHU4
B	27	LEU	-	EXPRESSION TAG	UNP Q9JHU4
B	28	GLU	-	EXPRESSION TAG	UNP Q9JHU4
B	29	ALA	-	EXPRESSION TAG	UNP Q9JHU4
B	30	LEU	-	EXPRESSION TAG	UNP Q9JHU4
B	31	LEU	-	EXPRESSION TAG	UNP Q9JHU4
B	32	ALA	-	EXPRESSION TAG	UNP Q9JHU4
B	33	VAL	-	EXPRESSION TAG	UNP Q9JHU4
B	34	ASP	-	EXPRESSION TAG	UNP Q9JHU4
B	3323	ALA	CYS	ENGINEERED	UNP Q9JHU4
B	3387	ALA	CYS	ENGINEERED	UNP Q9JHU4
B	420	GLY	-	EXPRESSION TAG	UNP P34945
B	421	ALA	-	EXPRESSION TAG	UNP P34945
B	422	HIS	-	EXPRESSION TAG	UNP P34945
B	423	HIS	-	EXPRESSION TAG	UNP P34945
B	424	HIS	-	EXPRESSION TAG	UNP P34945
B	425	HIS	-	EXPRESSION TAG	UNP P34945
B	426	HIS	-	EXPRESSION TAG	UNP P34945
B	427	HIS	-	EXPRESSION TAG	UNP P34945

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula:  $C_{10}H_{14}N_5O_7P$ ).

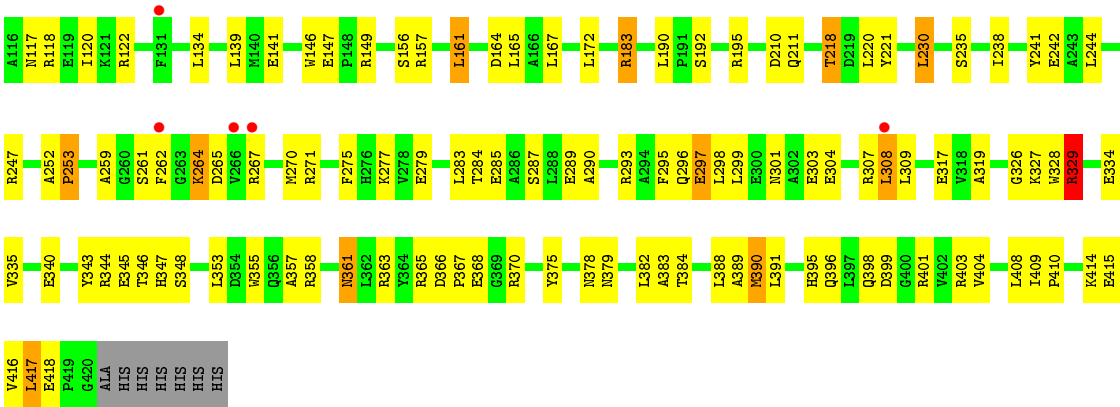


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	71	Total	O	0	0
			71	71		
3	B	52	Total	O	0	0
			52	52		







## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	144.30Å 144.30Å 159.95Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.27 – 2.27 49.24 – 2.27	Depositor EDS
% Data completeness (in resolution range)	99.1 (49.27-2.27) 99.1 (49.24-2.27)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.94 (at 2.27Å)	Xtriage
Refinement program	REFMAC 5.4.0067	Depositor
R, $R_{free}$	0.197 , 0.247 0.217 , 0.250	Depositor DCC
$R_{free}$ test set	2856 reflections (5.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	51.6	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 60.7	EDS
Estimated twinning fraction	0.021 for h,-h-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 57094 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8589	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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

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	0.99	6/4301 (0.1%)	0.99	16/5828 (0.3%)
1	B	0.90	6/4301 (0.1%)	0.93	14/5828 (0.2%)
All	All	0.95	12/8602 (0.1%)	0.96	30/11656 (0.3%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	369	GLY	CA-C	7.26	1.63	1.51
1	A	349	CYS	CB-SG	-6.83	1.70	1.82
1	B	115	GLU	CD-OE2	6.31	1.32	1.25
1	A	115	GLU	CG-CD	6.02	1.60	1.51
1	A	3278	GLU	CB-CG	-5.92	1.40	1.52
1	B	295	PHE	CE2-CZ	5.73	1.48	1.37
1	B	297	GLU	CD-OE2	5.62	1.31	1.25
1	A	169	GLU	CD-OE2	5.61	1.31	1.25
1	B	115	GLU	CD-OE1	5.55	1.31	1.25
1	B	221	TYR	CD1-CE1	5.23	1.47	1.39
1	B	3309	ALA	C-O	5.18	1.33	1.23
1	A	95	GLU	CB-CG	5.15	1.61	1.52

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	329	ARG	NE-CZ-NH1	12.33	126.46	120.30
1	A	344	ARG	NE-CZ-NH1	-12.18	114.21	120.30
1	A	329	ARG	NE-CZ-NH1	11.30	125.95	120.30
1	A	408	LEU	CA-CB-CG	-9.66	93.08	115.30
1	A	344	ARG	NE-CZ-NH2	9.39	124.99	120.30
1	B	329	ARG	NE-CZ-NH2	-8.93	115.83	120.30
1	B	253	PRO	CA-N-CD	-8.88	99.07	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	157	ARG	NE-CZ-NH1	8.75	124.67	120.30
1	B	3380	VAL	CB-CA-C	-8.53	95.19	111.40
1	B	183	ARG	NE-CZ-NH1	8.35	124.48	120.30
1	A	157	ARG	NE-CZ-NH2	-7.98	116.31	120.30
1	A	329	ARG	NE-CZ-NH2	-7.07	116.77	120.30
1	B	408	LEU	CA-CB-CG	-6.91	99.41	115.30
1	B	271	ARG	N-CA-C	-6.86	92.49	111.00
1	A	323	MET	CG-SD-CE	-6.69	89.50	100.20
1	B	122	ARG	NE-CZ-NH2	-6.61	116.99	120.30
1	A	195	ARG	NE-CZ-NH2	-6.47	117.06	120.30
1	A	195	ARG	NE-CZ-NH1	6.00	123.30	120.30
1	A	3331	THR	CB-CA-C	-5.84	95.83	111.60
1	A	299	LEU	CA-CB-CG	5.76	128.55	115.30
1	A	3338	SER	CB-CA-C	-5.68	99.31	110.10
1	A	352	LEU	CB-CA-C	5.66	120.96	110.20
1	B	3332	ASP	N-CA-C	-5.65	95.75	111.00
1	A	386	ARG	NE-CZ-NH2	-5.59	117.51	120.30
1	A	259	ALA	C-N-CA	-5.59	110.57	122.30
1	B	183	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	B	403	ARG	NE-CZ-NH2	-5.14	117.73	120.30
1	B	307	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	B	24	ALA	CB-CA-C	5.08	117.72	110.10
1	B	3369	TYR	CB-CA-C	-5.02	100.35	110.40

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	4210	0	4230	238	0
1	B	4210	0	4230	323	0
2	A	23	0	12	0	0
2	B	23	0	12	0	0
3	A	71	0	0	2	0
3	B	52	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8589	0	8484	558	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 33.

All (558) 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:B:7:LEU:HD12	1:B:14:PHE:CD2	1.52	1.44
1:B:3308:MET:SD	1:B:3311:PRO:HB3	1.58	1.43
1:A:3339:ILE:HD13	1:A:3340:ILE:N	1.33	1.41
1:A:3308:MET:CE	1:A:3312:PRO:HD2	1.55	1.34
1:B:3340:ILE:HA	1:B:3345:PHE:CD1	1.64	1.32
1:B:7:LEU:HD12	1:B:14:PHE:CE2	1.66	1.28
1:B:3332:ASP:O	1:B:3336:ILE:HD12	1.36	1.21
1:B:3376:ASN:O	1:B:3380:VAL:HG22	1.40	1.19
1:A:3407:VAL:CG1	1:A:3411:ARG:HD2	1.70	1.19
1:B:3294:VAL:HG11	1:B:3349:ILE:HD11	1.24	1.17
1:B:3319:LEU:HD12	1:B:3333:TRP:CH2	1.77	1.16
1:B:3337:ARG:HH11	1:B:3337:ARG:HG3	1.00	1.16
1:B:3344:ASN:O	1:B:3348:THR:HG23	1.45	1.13
1:B:183:ARG:HD2	1:B:301:ASN:ND2	1.63	1.13
1:B:3324:LEU:HD12	1:B:3365:MET:HG2	1.30	1.13
1:B:7:LEU:HA	1:B:14:PHE:CE2	1.84	1.12
1:B:10:GLU:HB3	1:B:13:VAL:HG23	1.31	1.12
1:B:3319:LEU:HD12	1:B:3333:TRP:HH2	0.99	1.12
1:B:3355:GLU:OE2	1:B:3404:LEU:HD13	1.46	1.12
1:B:3387:ALA:HA	1:B:3390:MET:CE	1.79	1.12
1:B:183:ARG:HD2	1:B:301:ASN:HD21	0.98	1.12
1:B:8:ARG:O	1:B:11:PRO:HD3	1.50	1.12
1:B:3337:ARG:HH11	1:B:3337:ARG:CG	1.61	1.11
1:A:3316:LYS:HE3	1:A:3320:GLU:OE2	1.51	1.10
1:A:3346:ILE:HD12	1:A:3346:ILE:N	1.59	1.10
1:A:3361:ILE:C	1:A:3361:ILE:HD12	1.72	1.09
1:A:3346:ILE:HD13	1:A:3347:PRO:HD3	1.22	1.09
1:A:3294:VAL:O	1:A:3297:ILE:HG13	1.50	1.09
1:A:3346:ILE:CD1	1:A:3346:ILE:H	1.63	1.08
1:A:3311:PRO:HG3	1:A:3333:TRP:CZ2	1.87	1.07
1:B:7:LEU:CD1	1:B:14:PHE:CD2	2.40	1.04
1:A:3361:ILE:C	1:A:3361:ILE:CD1	2.27	1.04
1:A:3308:MET:HE1	1:A:3312:PRO:HD2	1.06	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3346:ILE:HD12	1:A:3346:ILE:H	0.87	1.03
1:A:3358:SER:OG	1:A:3361:ILE:HG22	1.57	1.03
1:B:3308:MET:SD	1:B:3311:PRO:CB	2.48	1.01
1:B:3340:ILE:HA	1:B:3345:PHE:CE1	1.94	1.01
1:A:3407:VAL:HG12	1:A:3411:ARG:HD2	1.40	1.01
1:B:3387:ALA:HA	1:B:3390:MET:HE2	1.02	1.01
1:B:3332:ASP:HB3	1:B:3335:GLN:HG3	1.42	1.00
1:A:267:ARG:HD3	1:A:267:ARG:H	1.24	1.00
1:B:110:PRO:HG3	1:B:118:ARG:CZ	1.92	0.99
1:B:3337:ARG:HG3	1:B:3337:ARG:NH1	1.72	0.98
1:A:3308:MET:HE1	1:A:3312:PRO:CD	1.92	0.98
1:A:3322:ILE:HD11	1:A:3390:MET:CB	1.91	0.98
1:A:3322:ILE:CD1	1:A:3390:MET:HB3	1.93	0.98
1:B:3301:HIS:HA	1:B:3304:GLU:HG2	1.42	0.98
1:A:3322:ILE:HD11	1:A:3390:MET:HB3	1.00	0.98
1:B:3423:ASP:O	1:B:3427:LYS:HG2	1.64	0.98
1:B:289:GLU:HG2	1:B:293:ARG:HH12	1.29	0.97
1:A:3308:MET:CE	1:A:3312:PRO:CD	2.42	0.97
1:A:3346:ILE:CD1	1:A:3347:PRO:HD3	1.93	0.97
1:B:3324:LEU:CD1	1:B:3365:MET:HG2	1.93	0.97
1:B:10:GLU:HB3	1:B:13:VAL:CG2	1.95	0.97
1:B:218:THR:HG23	1:B:220:LEU:H	1.28	0.97
1:B:3320:GLU:HG2	1:B:3369:TYR:OH	1.63	0.96
1:B:3322:ILE:HD11	1:B:3390:MET:HB3	1.45	0.96
1:A:284:THR:HG22	1:A:375:TYR:HB2	1.45	0.96
1:B:3387:ALA:CA	1:B:3390:MET:HE2	1.95	0.96
1:A:3339:ILE:HD13	1:A:3339:ILE:C	1.81	0.95
1:B:14:PHE:O	1:B:18:ILE:HG13	1.67	0.95
1:A:3332:ASP:OD1	1:A:3335:GLN:HG3	1.67	0.94
1:B:270:MET:CE	1:B:389:ALA:CB	2.45	0.94
1:B:270:MET:CE	1:B:389:ALA:HB3	1.98	0.93
1:B:7:LEU:CD1	1:B:14:PHE:CG	2.51	0.93
1:A:3386:ALA:O	1:A:3390:MET:HE3	1.68	0.93
1:B:11:PRO:O	1:B:15:HIS:HD2	1.50	0.93
1:B:3316:LYS:HE2	3:B:3479:HOH:O	1.69	0.92
1:A:267:ARG:CD	1:A:267:ARG:H	1.82	0.92
1:A:3339:ILE:CD1	1:A:3340:ILE:N	2.30	0.92
1:A:3346:ILE:HD13	1:A:3347:PRO:CD	2.01	0.91
1:A:3361:ILE:O	1:A:3361:ILE:CD1	2.19	0.91
1:B:270:MET:HE1	1:B:389:ALA:HB3	1.49	0.91
1:B:192:SER:OG	1:B:253:PRO:HD2	1.70	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:LEU:CD1	1:B:14:PHE:CE2	2.51	0.91
1:A:3:ASP:OD2	1:A:6:ARG:HG3	1.71	0.91
1:A:3339:ILE:HA	1:A:3342:ARG:HG3	1.53	0.90
1:B:289:GLU:CG	1:B:293:ARG:HH12	1.84	0.90
1:B:7:LEU:HD12	1:B:14:PHE:CG	2.06	0.90
1:A:267:ARG:CD	1:A:267:ARG:N	2.35	0.89
1:A:3425:GLN:O	1:A:95:GLU:HG3	1.72	0.89
1:B:218:THR:CG2	1:B:220:LEU:H	1.84	0.89
1:B:289:GLU:HG2	1:B:293:ARG:NH1	1.87	0.89
1:B:3294:VAL:HG11	1:B:3349:ILE:CD1	2.04	0.88
1:B:7:LEU:HA	1:B:14:PHE:HE2	1.34	0.88
1:B:10:GLU:OE1	1:B:13:VAL:HG21	1.72	0.88
1:A:30:LEU:HD13	1:A:97:LEU:HB3	1.55	0.87
1:B:3408:GLU:HB3	1:B:3409:PRO:HD3	1.57	0.87
1:B:3335:GLN:O	1:B:3339:ILE:HG12	1.74	0.87
1:A:3361:ILE:HD13	1:A:3361:ILE:O	1.74	0.87
1:B:3376:ASN:HB3	1:B:3379:ILE:HB	1.56	0.86
1:A:3331:THR:HG23	1:A:3331:THR:O	1.75	0.86
1:A:3316:LYS:CE	1:A:3320:GLU:OE2	2.22	0.86
1:B:3312:PRO:O	1:B:3315:VAL:HG22	1.74	0.86
1:B:3409:PRO:HG2	1:B:3410:LEU:CD2	2.07	0.85
1:A:3339:ILE:HD13	1:A:3340:ILE:H	1.41	0.85
1:B:192:SER:OG	1:B:253:PRO:CD	2.24	0.85
1:B:346:THR:CG2	1:B:390:MET:HE3	2.05	0.85
1:A:3407:VAL:CG1	1:A:3411:ARG:CD	2.55	0.84
1:B:3301:HIS:CA	1:B:3304:GLU:HG2	2.06	0.84
1:B:3319:LEU:CD1	1:B:3333:TRP:HH2	1.88	0.84
1:B:3340:ILE:HA	1:B:3345:PHE:HD1	1.38	0.84
1:B:3406:ARG:O	1:B:3410:LEU:HD23	1.77	0.84
1:B:3340:ILE:CA	1:B:3345:PHE:CD1	2.57	0.83
1:B:11:PRO:O	1:B:15:HIS:CD2	2.32	0.83
1:A:3308:MET:HE2	1:A:3311:PRO:HA	1.61	0.83
1:A:3324:LEU:HD23	1:A:3324:LEU:C	1.97	0.82
1:A:3388:GLY:O	1:A:3391:VAL:HG12	1.79	0.82
1:A:3425:GLN:HG3	1:A:95:GLU:OE1	1.79	0.82
1:A:3300:GLN:O	1:A:3303:VAL:HG12	1.79	0.82
1:A:3311:PRO:HG3	1:A:3333:TRP:CE2	2.14	0.82
1:A:3407:VAL:HG12	1:A:3411:ARG:CD	2.10	0.82
1:B:8:ARG:HE	1:B:31:LEU:HD22	1.45	0.81
1:A:3322:ILE:O	1:A:3326:LEU:HD22	1.80	0.81
1:B:3311:PRO:HB2	1:B:3315:VAL:HG21	1.60	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:ARG:HH12	1:B:358:ARG:NH2	1.77	0.81
1:A:3:ASP:OD2	1:A:6:ARG:CD	2.29	0.81
1:A:3:ASP:OD2	1:A:6:ARG:CG	2.29	0.81
1:B:3291:GLN:O	1:B:3295:LYS:HE3	1.80	0.81
1:A:134:LEU:H	1:A:396:GLN:HE22	1.26	0.80
1:B:3344:ASN:O	1:B:3348:THR:CG2	2.27	0.80
1:A:382:LEU:HD23	1:A:383:ALA:N	1.97	0.80
1:B:3336:ILE:O	1:B:3340:ILE:CG2	2.30	0.80
1:B:3302:LEU:O	1:B:3306:ARG:HG2	1.81	0.80
1:B:8:ARG:O	1:B:11:PRO:CD	2.31	0.79
1:B:192:SER:OG	1:B:253:PRO:HG2	1.83	0.79
1:B:3298:LYS:HB2	1:B:3301:HIS:CE1	2.17	0.78
1:A:30:LEU:HD13	1:A:97:LEU:CB	2.14	0.77
1:B:3363:GLU:O	1:B:3367:LYS:HG3	1.84	0.77
1:B:3316:LYS:HG2	1:B:3333:TRP:CE3	2.20	0.77
1:A:3358:SER:OG	1:A:3361:ILE:CG2	2.32	0.77
1:A:218:THR:CG2	1:A:220:LEU:H	1.98	0.77
1:B:3328:GLU:O	1:B:3328:GLU:HG3	1.83	0.76
1:B:3322:ILE:CD1	1:B:3390:MET:HB3	2.14	0.76
1:B:3407:VAL:CG1	1:B:3411:ARG:CD	2.62	0.76
1:B:106:TRP:NE1	1:B:329:ARG:HG2	2.01	0.76
1:B:3376:ASN:O	1:B:3380:VAL:CG2	2.29	0.76
1:A:3346:ILE:CD1	1:A:3347:PRO:CD	2.62	0.76
1:B:3410:LEU:N	1:B:3410:LEU:HD22	2.00	0.76
1:B:147:GLU:OE2	1:B:149:ARG:HG3	1.84	0.76
1:B:3301:HIS:HA	1:B:3304:GLU:CG	2.16	0.76
1:B:3311:PRO:HB2	1:B:3315:VAL:CG2	2.14	0.76
1:B:3336:ILE:O	1:B:3340:ILE:HG23	1.85	0.76
1:B:7:LEU:HD13	1:B:14:PHE:CE1	2.21	0.76
1:B:3410:LEU:N	1:B:3410:LEU:CD2	2.48	0.76
1:A:3308:MET:CE	1:A:3311:PRO:HA	2.16	0.75
1:B:284:THR:CG2	1:B:290:ALA:HB1	2.16	0.75
1:B:3407:VAL:HG12	1:B:3411:ARG:HD3	1.68	0.75
1:B:117:ASN:ND2	1:B:319:ALA:H	1.84	0.75
1:B:3406:ARG:O	1:B:3410:LEU:CD2	2.33	0.75
1:B:3355:GLU:OE2	1:B:3404:LEU:CD1	2.31	0.75
1:B:7:LEU:CD1	1:B:14:PHE:CD1	2.70	0.75
1:B:3410:LEU:CD2	1:B:3410:LEU:H	2.00	0.75
1:B:3312:PRO:HG2	1:B:3315:VAL:HG13	1.68	0.74
1:B:3407:VAL:HG12	1:B:3411:ARG:CD	2.18	0.74
1:B:3319:LEU:CD1	1:B:3333:TRP:CH2	2.65	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:ARG:HH11	1:A:372:ARG:HG2	1.53	0.74
1:B:7:LEU:CD1	1:B:14:PHE:CZ	2.71	0.73
1:B:3408:GLU:HB3	1:B:3409:PRO:CD	2.18	0.73
1:B:335:VAL:HG12	1:B:390:MET:HG2	1.69	0.73
1:A:3322:ILE:O	1:A:3326:LEU:CD2	2.38	0.72
1:B:3409:PRO:HG2	1:B:3410:LEU:HD22	1.71	0.72
1:B:317:GLU:OE2	1:B:329:ARG:HD3	1.89	0.72
1:A:11:PRO:HG2	1:A:12:GLU:OE1	1.89	0.72
1:B:3283:VAL:HG11	1:B:3400:TYR:CA	2.18	0.72
1:B:192:SER:OG	1:B:253:PRO:CG	2.38	0.72
1:B:157:ARG:NH1	1:B:265:ASP:O	2.22	0.72
1:B:3316:LYS:HA	1:B:3333:TRP:CZ3	2.25	0.72
1:B:238:ILE:HD11	1:B:363:ARG:NH2	2.05	0.71
1:B:3306:ARG:HB3	1:B:3340:ILE:HD11	1.71	0.71
1:A:3386:ALA:O	1:A:3390:MET:CE	2.38	0.71
1:B:366:ASP:OD2	1:B:370:ARG:HG2	1.90	0.71
1:A:3366:LYS:HE3	1:A:3398:LEU:HD11	1.72	0.71
1:A:3324:LEU:CD2	1:A:3361:ILE:HG12	2.20	0.71
1:B:106:TRP:CD1	1:B:329:ARG:HG2	2.25	0.71
1:B:3407:VAL:CG1	1:B:3411:ARG:HD2	2.19	0.71
1:A:3346:ILE:CD1	1:A:3346:ILE:N	2.35	0.70
1:A:117:ASN:ND2	1:A:319:ALA:H	1.88	0.70
1:A:3311:PRO:CG	1:A:3333:TRP:CE2	2.74	0.69
1:A:12:GLU:HB3	1:A:16:ARG:HH12	1.56	0.69
1:A:372:ARG:NH1	1:A:372:ARG:HG2	2.05	0.69
1:A:12:GLU:HB3	1:A:16:ARG:NH1	2.07	0.69
1:B:218:THR:HG23	1:B:220:LEU:N	2.06	0.69
1:A:267:ARG:N	1:A:267:ARG:HD3	1.93	0.69
1:B:3354:ALA:HA	1:B:3357:ILE:HD12	1.75	0.69
1:B:289:GLU:CG	1:B:293:ARG:NH1	2.50	0.69
1:B:3347:PRO:O	1:B:3351:ASN:ND2	2.26	0.69
1:A:267:ARG:HD2	1:A:267:ARG:N	2.07	0.69
1:B:3295:LYS:HG3	1:B:3350:VAL:HG21	1.75	0.69
1:B:3290:ALA:O	1:B:3294:VAL:HG23	1.92	0.69
1:B:275:PHE:HB2	1:B:384:THR:O	1.94	0.68
1:B:3283:VAL:HG11	1:B:3400:TYR:HA	1.74	0.68
1:B:3294:VAL:CG1	1:B:3349:ILE:HD11	2.15	0.68
1:A:3361:ILE:HD12	1:A:3361:ILE:O	1.88	0.68
1:A:366:ASP:HB2	1:A:367:PRO:CD	2.23	0.68
1:A:3388:GLY:O	1:A:3391:VAL:CG1	2.41	0.68
1:A:3358:SER:HG	1:A:3361:ILE:HG22	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:LEU:O	1:A:375:TYR:HA	1.94	0.68
1:B:3306:ARG:CB	1:B:3340:ILE:HD11	2.24	0.67
1:A:346:THR:HG21	1:A:390:MET:HE3	1.75	0.67
1:B:134:LEU:H	1:B:396:GLN:HE22	1.41	0.67
1:A:354:ASP:O	1:A:358:ARG:HG3	1.94	0.67
1:A:218:THR:HG23	1:A:220:LEU:H	1.59	0.67
1:A:157:ARG:NH2	1:A:271:ARG:HD2	2.10	0.67
1:B:3312:PRO:HD2	1:B:3315:VAL:HG21	1.77	0.67
1:A:3407:VAL:O	1:A:3411:ARG:HG3	1.95	0.67
1:A:335:VAL:HB	1:A:390:MET:HE3	1.77	0.67
1:A:241:TYR:HB2	1:A:365:ARG:O	1.95	0.67
1:A:3342:ARG:HH11	1:A:3342:ARG:CG	2.09	0.66
1:B:253:PRO:HD2	1:B:253:PRO:O	1.94	0.66
1:B:3332:ASP:CB	1:B:3335:GLN:HG3	2.20	0.66
1:B:3407:VAL:HG11	1:B:3411:ARG:HD2	1.78	0.66
1:B:5:LYS:O	1:B:9:GLN:HG3	1.96	0.66
1:B:3324:LEU:HD12	1:B:3365:MET:CG	2.16	0.65
1:A:366:ASP:HB2	1:A:367:PRO:HD2	1.77	0.65
1:A:406:GLN:HA	1:A:409:ILE:HD12	1.78	0.65
1:A:3339:ILE:HD13	1:A:3340:ILE:CA	2.23	0.65
1:B:8:ARG:NE	1:B:31:LEU:HD22	2.12	0.65
1:B:3403:MET:HA	1:B:3406:ARG:HD3	1.79	0.65
1:A:3425:GLN:HE21	1:A:95:GLU:CG	2.10	0.65
1:B:94:LEU:O	1:B:98:LEU:CD2	2.44	0.65
1:B:241:TYR:HB2	1:B:365:ARG:O	1.97	0.64
1:B:3337:ARG:NH1	1:B:3337:ARG:CG	2.34	0.64
1:A:3407:VAL:HG11	1:A:3411:ARG:HD2	1.75	0.64
1:A:3306:ARG:HD3	1:A:3341:MET:SD	2.37	0.64
1:B:3334:LYS:O	1:B:3337:ARG:HB3	1.98	0.64
1:B:10:GLU:CD	1:B:13:VAL:HG21	2.18	0.64
1:B:346:THR:HG21	1:B:390:MET:HE3	1.79	0.64
1:B:7:LEU:CD1	1:B:14:PHE:CE1	2.80	0.64
1:B:3332:ASP:C	1:B:3336:ILE:HD12	2.18	0.63
1:A:3408:GLU:HB3	1:A:3409:PRO:HD3	1.80	0.63
1:B:3328:GLU:OE1	1:B:3339:ILE:HG21	1.99	0.63
1:B:3354:ALA:HB3	1:B:3400:TYR:HD2	1.64	0.63
1:A:183:ARG:HD2	1:A:301:ASN:ND2	2.13	0.63
1:B:3324:LEU:CD1	1:B:3365:MET:CG	2.75	0.63
1:A:382:LEU:C	1:A:382:LEU:HD23	2.19	0.63
1:A:215:ILE:HB	1:A:218:THR:HG21	1.81	0.62
1:A:3376:ASN:OD1	1:A:3378:GLU:N	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3311:PRO:CG	1:A:3333:TRP:CZ2	2.77	0.62
1:B:3283:VAL:HG11	1:B:3400:TYR:N	2.14	0.62
1:B:3336:ILE:O	1:B:3340:ILE:HG22	1.98	0.62
1:B:3406:ARG:O	1:B:3409:PRO:HD2	2.00	0.62
1:A:401:ARG:CG	1:A:419:PRO:HG3	2.30	0.62
1:B:94:LEU:O	1:B:98:LEU:HD22	2.00	0.62
1:B:3316:LYS:CE	3:B:3479:HOH:O	2.37	0.61
1:B:30:LEU:HD12	1:B:94:LEU:HD12	1.82	0.61
1:A:3359:ASP:O	1:A:3363:GLU:HG3	2.01	0.61
1:A:284:THR:HG23	1:A:285:GLU:O	2.00	0.61
1:B:7:LEU:HD11	1:B:14:PHE:CG	2.35	0.61
1:B:8:ARG:NH2	1:B:34:ASP:OD2	2.34	0.61
1:A:3294:VAL:O	1:A:3297:ILE:CG1	2.39	0.61
1:B:3385:LEU:HB2	3:B:3477:HOH:O	2.00	0.61
1:A:266:VAL:HG22	1:A:267:ARG:HH11	1.66	0.61
1:B:347:HIS:HB3	1:B:379:ASN:HD21	1.65	0.61
1:B:3410:LEU:HD23	1:B:3410:LEU:H	1.64	0.60
1:B:7:LEU:HD13	1:B:14:PHE:CZ	2.34	0.60
1:B:3295:LYS:HG3	1:B:3350:VAL:CG2	2.31	0.60
1:A:3340:ILE:HG22	1:A:3341:MET:HG3	1.83	0.60
1:A:7:LEU:HD12	1:A:14:PHE:CE2	2.37	0.60
1:B:3333:TRP:O	1:B:3337:ARG:HB2	2.00	0.60
1:A:282:VAL:CG2	1:A:298:LEU:HD11	2.32	0.60
1:A:335:VAL:HG12	1:A:390:MET:HG2	1.85	0.59
1:B:270:MET:HE1	1:B:389:ALA:CB	2.18	0.59
1:B:30:LEU:CD1	1:B:94:LEU:HD12	2.33	0.58
1:B:3328:GLU:CD	1:B:3339:ILE:HG21	2.23	0.58
1:A:183:ARG:HD2	1:A:301:ASN:HD21	1.68	0.58
1:B:3312:PRO:HG2	1:B:3315:VAL:CG1	2.31	0.58
1:B:3355:GLU:CD	1:B:3404:LEU:HD13	2.22	0.58
1:B:284:THR:HG21	1:B:290:ALA:HB1	1.85	0.58
1:A:419:PRO:O	1:A:420:GLY:C	2.42	0.58
1:A:3308:MET:HE3	1:A:3312:PRO:HD2	1.74	0.58
1:A:3425:GLN:HE21	1:A:95:GLU:CD	2.08	0.57
1:A:3334:LYS:HA	1:A:3337:ARG:HD3	1.86	0.57
1:A:218:THR:HG22	1:A:220:LEU:H	1.69	0.57
1:A:387:ILE:HD12	1:A:390:MET:HE1	1.87	0.57
1:B:6:ARG:NH1	1:B:358:ARG:NH2	2.51	0.57
1:A:3316:LYS:NZ	1:A:3320:GLU:OE2	2.38	0.57
1:B:3299:LYS:HA	1:B:3302:LEU:HD12	1.85	0.57
1:B:3316:LYS:HA	1:B:3333:TRP:HZ3	1.67	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:ILE:HG23	1:A:23:VAL:O	2.04	0.57
1:A:3407:VAL:HG13	1:A:3411:ARG:HG3	1.85	0.57
1:B:8:ARG:HE	1:B:31:LEU:CD2	2.15	0.57
1:B:366:ASP:HB2	1:B:367:PRO:CD	2.34	0.57
1:A:106:TRP:CD1	1:A:329:ARG:HG2	2.39	0.57
1:A:3291:GLN:O	1:A:3295:LYS:HG3	2.05	0.57
1:B:3321:SER:O	1:B:3324:LEU:HB3	2.06	0.56
1:B:3306:ARG:HH11	1:B:3341:MET:HE3	1.69	0.56
1:A:346:THR:CG2	1:A:390:MET:HE3	2.34	0.56
1:A:218:THR:HG23	1:A:220:LEU:N	2.19	0.56
1:B:147:GLU:OE2	1:B:149:ARG:CG	2.52	0.56
1:B:3403:MET:HA	1:B:3406:ARG:CD	2.35	0.56
1:B:183:ARG:HH11	1:B:301:ASN:ND2	2.03	0.56
1:A:3324:LEU:HD21	1:A:3361:ILE:HG12	1.87	0.56
1:B:285:GLU:HG3	1:B:287:SER:HB3	1.87	0.56
1:B:3377:TYR:CE1	1:B:3381:ASN:HB2	2.40	0.56
1:B:3334:LYS:O	1:B:3338:SER:N	2.30	0.56
1:A:3407:VAL:HG13	1:A:3411:ARG:HD2	1.81	0.56
1:A:3344:ASN:C	1:A:3347:PRO:HD2	2.26	0.56
1:A:3342:ARG:HG3	1:A:3342:ARG:NH1	2.21	0.56
1:A:12:GLU:OE1	1:A:12:GLU:N	2.31	0.56
1:B:391:LEU:O	1:B:395:HIS:HB2	2.06	0.56
1:B:353:LEU:O	1:B:375:TYR:HA	2.06	0.55
1:B:7:LEU:CA	1:B:14:PHE:CE2	2.74	0.55
1:B:3283:VAL:O	1:B:3283:VAL:HG12	2.07	0.55
1:A:103:LEU:HD22	1:A:352:LEU:O	2.07	0.55
1:B:190:LEU:HD11	1:B:230:LEU:HD13	1.89	0.55
1:A:346:THR:HG21	1:A:390:MET:CE	2.36	0.55
1:A:3422:LYS:O	1:A:3426:GLN:HG3	2.06	0.55
1:B:3387:ALA:CA	1:B:3390:MET:CE	2.66	0.55
1:A:387:ILE:HD12	1:A:390:MET:CE	2.37	0.55
1:B:164:ASP:OD2	1:B:418:GLU:HB2	2.07	0.55
1:A:3308:MET:HE3	1:A:3312:PRO:CD	2.32	0.54
1:B:3323:ALA:HB1	1:B:3328:GLU:O	2.07	0.54
1:B:3291:GLN:C	1:B:3295:LYS:HE3	2.27	0.54
1:B:382:LEU:HD23	1:B:383:ALA:N	2.22	0.54
1:B:7:LEU:HD12	1:B:14:PHE:CZ	2.25	0.54
1:B:3340:ILE:CA	1:B:3345:PHE:CE1	2.81	0.54
1:B:3332:ASP:O	1:B:3336:ILE:CD1	2.31	0.54
1:A:7:LEU:HD12	1:A:14:PHE:CD2	2.43	0.54
1:A:3322:ILE:HD13	1:A:3390:MET:SD	2.47	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:344:ARG:NH1	3:A:3455:HOH:O	2.39	0.54
1:A:282:VAL:HG23	1:A:298:LEU:HD11	1.90	0.54
1:A:216:ALA:O	1:A:217:GLU:HB2	2.07	0.54
1:B:3280:LEU:O	1:B:3284:GLU:HB2	2.07	0.54
1:B:366:ASP:HB2	1:B:367:PRO:HD2	1.88	0.54
1:A:3336:ILE:O	1:A:3339:ILE:HD12	2.08	0.54
1:B:3366:LYS:NZ	1:B:3402:ASP:OD2	2.41	0.54
1:B:3301:HIS:C	1:B:3304:GLU:HG2	2.28	0.54
1:B:382:LEU:C	1:B:382:LEU:HD23	2.28	0.54
1:B:3336:ILE:HA	1:B:3339:ILE:HG13	1.89	0.54
1:A:3:ASP:OD2	1:A:6:ARG:HD2	2.08	0.54
1:A:3342:ARG:NH1	1:A:3342:ARG:CG	2.68	0.53
1:A:141:GLU:O	1:A:142:LYS:C	2.47	0.53
1:A:275:PHE:HB2	1:A:384:THR:O	2.08	0.53
1:A:3407:VAL:HG13	1:A:3411:ARG:CG	2.38	0.53
1:B:3311:PRO:HB2	1:B:3312:PRO:HD2	1.91	0.53
1:B:264:LYS:O	1:B:265:ASP:C	2.46	0.53
1:A:3340:ILE:CG2	1:A:3341:MET:HG3	2.38	0.53
1:A:3324:LEU:HD21	1:A:3361:ILE:CG1	2.39	0.53
1:B:7:LEU:HD13	1:B:14:PHE:CD1	2.43	0.53
1:A:3359:ASP:HA	1:A:3362:ARG:HH11	1.73	0.53
1:B:120:ILE:HD13	1:B:317:GLU:HG2	1.91	0.53
1:A:157:ARG:HH21	1:A:271:ARG:HB3	1.73	0.53
1:B:404:VAL:CG2	1:B:417:LEU:HD13	2.39	0.53
1:B:7:LEU:HA	1:B:14:PHE:CZ	2.42	0.53
1:A:3316:LYS:O	1:A:3320:GLU:HG3	2.08	0.53
1:B:283:LEU:C	1:B:283:LEU:HD23	2.29	0.53
1:B:414:LYS:NZ	1:B:418:GLU:OE1	2.42	0.53
1:A:3332:ASP:CG	1:A:3335:GLN:HG3	2.29	0.52
1:A:3324:LEU:HD23	1:A:3361:ILE:HG12	1.91	0.52
1:A:3295:LYS:HE2	1:A:3350:VAL:HG22	1.92	0.52
1:B:3366:LYS:HE3	1:B:3398:LEU:HD21	1.90	0.52
1:B:3:ASP:O	1:B:7:LEU:HB2	2.09	0.52
1:A:3359:ASP:HB3	1:A:3362:ARG:NH1	2.24	0.52
1:B:270:MET:HE3	1:B:389:ALA:CB	2.38	0.52
1:B:3265:GLN:O	1:B:3269:ILE:HG13	2.10	0.52
1:A:3376:ASN:OD1	1:A:3376:ASN:C	2.48	0.52
1:B:28:GLU:N	1:B:28:GLU:OE1	2.43	0.52
1:B:10:GLU:N	1:B:11:PRO:HD3	2.24	0.52
1:A:218:THR:CG2	1:A:220:LEU:HB2	2.40	0.52
1:B:3376:ASN:O	1:B:3379:ILE:HG22	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3405:LYS:O	1:B:3408:GLU:HB2	2.10	0.52
1:A:3346:ILE:N	1:A:3347:PRO:CD	2.73	0.52
1:B:3408:GLU:CB	1:B:3409:PRO:CD	2.86	0.52
1:A:309:LEU:HD12	1:A:408:LEU:HD13	1.91	0.52
1:B:3319:LEU:CD2	1:B:3390:MET:HE3	2.40	0.52
1:A:266:VAL:H	1:A:267:ARG:NH1	2.08	0.52
1:B:3403:MET:O	1:B:3406:ARG:HD3	2.10	0.52
1:B:94:LEU:CD1	1:B:98:LEU:HD21	2.40	0.52
1:A:401:ARG:HG3	1:A:419:PRO:HG3	1.92	0.52
1:B:110:PRO:HG3	1:B:118:ARG:NH2	2.25	0.51
1:B:3334:LYS:O	1:B:3337:ARG:CB	2.58	0.51
1:A:106:TRP:NE1	1:A:329:ARG:HG2	2.25	0.51
1:B:3408:GLU:N	1:B:3409:PRO:HD2	2.26	0.51
1:B:3354:ALA:HB3	1:B:3400:TYR:CD2	2.45	0.51
1:A:27:LEU:HD12	1:A:30:LEU:HD23	1.92	0.51
1:A:3324:LEU:CD2	1:A:3324:LEU:C	2.74	0.50
1:B:3291:GLN:O	1:B:3295:LYS:CE	2.56	0.50
1:A:372:ARG:HH11	1:A:372:ARG:CG	2.22	0.50
1:B:3374:SER:O	1:B:3379:ILE:HG21	2.11	0.50
1:B:3380:VAL:HG21	1:B:3391:VAL:HG11	1.94	0.50
1:B:15:HIS:CD2	1:B:27:LEU:HD23	2.46	0.50
1:B:3298:LYS:HD2	1:B:3301:HIS:CE1	2.47	0.50
1:B:3301:HIS:O	1:B:3304:GLU:HG3	2.12	0.50
1:B:195:ARG:HG2	1:B:220:LEU:HD23	1.92	0.50
1:B:277:LYS:NZ	1:B:279:GLU:OE2	2.44	0.50
1:A:3344:ASN:HA	1:A:3347:PRO:HG2	1.93	0.50
1:A:3370:MET:HG3	1:A:3398:LEU:HD21	1.93	0.50
1:B:3377:TYR:CD1	1:B:3381:ASN:HB2	2.46	0.50
1:A:366:ASP:CB	1:A:367:PRO:CD	2.88	0.50
1:B:3:ASP:OD2	1:B:6:ARG:HB2	2.12	0.50
1:B:3400:TYR:O	1:B:3404:LEU:HG	2.12	0.50
1:A:3:ASP:OD2	1:A:6:ARG:NE	2.45	0.50
1:A:3354:ALA:HB2	1:A:3397:GLN:OE1	2.12	0.50
1:B:95:GLU:HA	1:B:98:LEU:HD23	1.93	0.50
1:A:419:PRO:O	1:A:420:GLY:O	2.30	0.50
1:A:131:PHE:HB2	1:A:132:PRO:HD2	1.94	0.49
1:A:215:ILE:O	1:A:218:THR:HG22	2.11	0.49
1:B:30:LEU:HD12	1:B:94:LEU:CD1	2.41	0.49
1:B:3336:ILE:O	1:B:3337:ARG:C	2.47	0.49
1:A:254:ALA:O	1:A:274:GLN:HA	2.12	0.49
1:B:296:GLN:HG2	3:B:3440:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:357:ALA:O	1:B:361:ASN:N	2.47	0.48
1:A:3336:ILE:C	1:A:3338:SER:H	2.16	0.48
1:A:3361:ILE:HD12	1:A:3362:ARG:N	2.26	0.48
1:A:174:ARG:NE	1:A:178:ASP:OD1	2.40	0.48
1:B:3:ASP:OD2	1:B:6:ARG:CB	2.61	0.48
1:B:3407:VAL:HG13	1:B:3411:ARG:HG3	1.94	0.48
1:B:3376:ASN:ND2	1:B:3378:GLU:OE1	2.47	0.48
1:A:3324:LEU:HD23	1:A:3324:LEU:O	2.12	0.48
1:A:3391:VAL:HG13	1:A:3392:LYS:N	2.29	0.48
1:A:3311:PRO:HB2	1:A:3316:LYS:HB2	1.94	0.48
1:A:266:VAL:H	1:A:267:ARG:HH11	1.61	0.48
1:A:3339:ILE:HA	1:A:3342:ARG:NH1	2.28	0.47
1:B:3304:GLU:HG3	1:B:3305:VAL:N	2.29	0.47
1:A:218:THR:HG21	1:A:220:LEU:HB2	1.96	0.47
1:B:3:ASP:HB3	1:B:6:ARG:HB3	1.96	0.47
1:B:94:LEU:O	1:B:98:LEU:HD23	2.14	0.47
1:B:3299:LYS:N	1:B:3299:LYS:HD2	2.30	0.47
1:B:10:GLU:CB	1:B:13:VAL:CG2	2.83	0.47
1:B:192:SER:HG	1:B:253:PRO:HD2	1.76	0.47
1:B:110:PRO:HG3	1:B:118:ARG:NH1	2.27	0.47
1:A:3387:ALA:HA	1:A:3390:MET:HE3	1.97	0.47
1:A:3361:ILE:HD13	1:A:3361:ILE:C	2.17	0.47
1:B:3306:ARG:NH1	1:B:3341:MET:HE3	2.29	0.47
1:A:3324:LEU:HD21	1:A:3361:ILE:CD1	2.45	0.47
1:A:376:THR:C	1:A:377:LEU:HD12	2.34	0.47
1:B:304:GLU:HG3	1:B:308:LEU:HD22	1.97	0.47
1:B:14:PHE:O	1:B:18:ILE:CG1	2.51	0.47
1:B:3406:ARG:O	1:B:3410:LEU:HD21	2.14	0.47
1:B:253:PRO:CD	1:B:253:PRO:O	2.61	0.47
1:B:3335:GLN:O	1:B:3339:ILE:CG1	2.54	0.47
1:B:3405:LYS:O	1:B:3408:GLU:CB	2.63	0.47
1:A:11:PRO:HG2	1:A:12:GLU:CD	2.36	0.47
1:A:106:TRP:CD1	1:A:109:ALA:HB2	2.49	0.47
1:A:377:LEU:HD12	1:A:377:LEU:N	2.30	0.47
1:B:3297:ILE:HG22	1:B:3298:LYS:O	2.15	0.46
1:A:3300:GLN:C	1:A:3303:VAL:HG12	2.35	0.46
1:A:3324:LEU:HD21	1:A:3361:ILE:HD13	1.96	0.46
1:A:335:VAL:HB	1:A:390:MET:CE	2.45	0.46
1:B:270:MET:HE2	1:B:389:ALA:CB	2.40	0.46
1:B:157:ARG:HH21	1:B:262:PHE:HA	1.80	0.46
1:A:117:ASN:HD21	1:A:319:ALA:H	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3346:ILE:N	1:B:3347:PRO:CD	2.79	0.46
1:A:3290:ALA:HB1	1:A:3393:TRP:HA	1.98	0.46
1:B:3333:TRP:O	1:B:3337:ARG:N	2.30	0.46
1:B:3337:ARG:HG2	1:B:3337:ARG:HH11	1.68	0.46
1:B:94:LEU:HD11	1:B:98:LEU:HD21	1.97	0.46
1:B:3362:ARG:NH2	1:B:3405:LYS:HD2	2.31	0.46
1:A:346:THR:CG2	1:A:390:MET:CE	2.94	0.46
1:B:409:ILE:HD13	1:B:415:GLU:HG2	1.98	0.46
1:B:3324:LEU:HA	1:B:3329:SER:HB3	1.98	0.46
1:B:3298:LYS:HB2	1:B:3301:HIS:ND1	2.31	0.45
1:B:3328:GLU:CG	1:B:3328:GLU:O	2.54	0.45
1:A:11:PRO:CG	1:A:12:GLU:OE1	2.63	0.45
1:B:30:LEU:CD1	1:B:94:LEU:CD1	2.95	0.45
1:A:330:GLN:HA	1:A:349:CYS:O	2.16	0.45
1:B:3335:GLN:O	1:B:3338:SER:HB2	2.16	0.45
1:B:3393:TRP:HE1	1:B:3397:GLN:HE21	1.63	0.45
1:B:409:ILE:N	1:B:410:PRO:CD	2.79	0.45
1:B:3407:VAL:O	1:B:3407:VAL:HG12	2.16	0.45
1:B:134:LEU:HB2	1:B:139:LEU:HG	1.98	0.45
1:A:157:ARG:HH21	1:A:271:ARG:HD2	1.82	0.45
1:A:3368:ASN:HB2	1:A:3369:TYR:CD2	2.52	0.45
1:B:3330:THR:HG21	1:B:3335:GLN:OE1	2.16	0.45
1:A:30:LEU:CD1	1:A:97:LEU:CB	2.91	0.45
1:B:3406:ARG:C	1:B:3408:GLU:H	2.20	0.45
1:A:3336:ILE:C	1:A:3338:SER:N	2.68	0.45
1:B:3335:GLN:HA	1:B:3338:SER:HB2	1.99	0.45
1:B:270:MET:CE	1:B:389:ALA:HB1	2.38	0.45
1:A:30:LEU:CD1	1:A:97:LEU:HB2	2.47	0.45
1:A:3376:ASN:OD1	1:A:3377:TYR:N	2.50	0.45
1:A:241:TYR:HA	1:A:244:LEU:HD22	1.99	0.45
1:A:401:ARG:HG2	1:A:419:PRO:HG3	1.97	0.45
1:B:326:GLY:HA3	1:B:355:TRP:CD2	2.52	0.45
1:B:156:SER:O	1:B:157:ARG:HB2	2.17	0.45
1:A:3308:MET:HE2	1:A:3311:PRO:CA	2.38	0.45
1:B:3319:LEU:HD23	1:B:3390:MET:HE3	1.98	0.45
1:A:3359:ASP:HB3	1:A:3362:ARG:HH12	1.82	0.45
1:A:274:GLN:HE22	1:B:253:PRO:CG	2.30	0.45
1:A:3310:ASN:N	1:A:3311:PRO:HD3	2.32	0.44
1:B:3352:PHE:HZ	1:B:3357:ILE:HG13	1.80	0.44
1:A:3346:ILE:HD12	1:A:3347:PRO:CD	2.47	0.44
1:A:3332:ASP:HB3	1:A:3335:GLN:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3:ASP:O	1:B:7:LEU:CB	2.65	0.44
1:B:3290:ALA:HB1	1:B:3393:TRP:HA	1.99	0.44
1:A:160:ALA:HB1	1:B:190:LEU:HD23	2.00	0.44
1:A:3290:ALA:CB	1:A:3393:TRP:HA	2.48	0.44
1:B:3306:ARG:NH1	1:B:3341:MET:HA	2.32	0.44
1:B:3267:GLU:OE1	1:B:3267:GLU:HA	2.16	0.44
1:B:8:ARG:O	1:B:11:PRO:CG	2.66	0.44
1:A:97:LEU:O	1:A:100:GLN:HB2	2.18	0.44
1:B:299:LEU:O	1:B:303:GLU:HG3	2.18	0.44
1:B:211:GLN:OE1	1:B:259:ALA:O	2.34	0.44
1:B:3378:GLU:CD	1:B:3378:GLU:H	2.21	0.44
1:B:3301:HIS:HA	1:B:3304:GLU:CD	2.37	0.44
1:B:3301:HIS:O	1:B:3304:GLU:CG	2.66	0.43
1:A:3311:PRO:HG3	1:A:3333:TRP:CH2	2.46	0.43
1:A:3311:PRO:HG2	1:A:3333:TRP:CD2	2.52	0.43
1:B:284:THR:HG22	1:B:285:GLU:N	2.33	0.43
1:A:309:LEU:CD1	1:A:408:LEU:HD13	2.48	0.43
1:A:3324:LEU:CD2	1:A:3361:ILE:CG1	2.93	0.43
1:B:192:SER:HG	1:B:253:PRO:CD	2.26	0.43
1:B:247:ARG:HH11	1:B:247:ARG:HD2	1.69	0.43
1:B:3308:MET:SD	1:B:3311:PRO:CA	3.06	0.43
1:B:3319:LEU:HD21	1:B:3390:MET:CE	2.49	0.43
1:A:3319:LEU:HA	1:A:3319:LEU:HD13	1.61	0.43
1:A:7:LEU:HG	1:A:27:LEU:HD11	2.01	0.42
1:A:284:THR:CG2	1:A:285:GLU:O	2.66	0.42
1:A:3413:GLU:HA	1:A:3416:LYS:HD2	2.01	0.42
1:B:345:GLU:HG2	1:B:346:THR:N	2.33	0.42
1:A:3358:SER:O	1:A:3362:ARG:HB2	2.19	0.42
1:B:3339:ILE:H	1:B:3339:ILE:HG12	1.49	0.42
1:B:340:GLU:OE1	1:B:344:ARG:HD3	2.18	0.42
1:A:274:GLN:HE22	1:B:253:PRO:HG2	1.85	0.42
1:A:3392:LYS:NZ	3:A:3479:HOH:O	2.52	0.42
1:A:3334:LYS:O	1:A:3337:ARG:HG2	2.19	0.42
1:A:3324:LEU:CD2	1:A:3361:ILE:CD1	2.97	0.42
1:B:238:ILE:CD1	1:B:363:ARG:NH2	2.79	0.42
1:A:7:LEU:HA	1:A:7:LEU:HD12	1.82	0.42
1:B:3407:VAL:CG1	1:B:3407:VAL:O	2.67	0.42
1:B:172:LEU:HD12	1:B:388:LEU:HD21	2.02	0.42
1:A:3322:ILE:O	1:A:3326:LEU:HD23	2.16	0.41
1:B:378:ASN:ND2	3:B:3473:HOH:O	2.52	0.41
1:A:147:GLU:HA	1:A:148:PRO:HD2	1.76	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:190:LEU:CD1	1:B:230:LEU:HD13	2.50	0.41
1:A:3377:TYR:HD1	1:A:3388:GLY:O	2.03	0.41
1:B:30:LEU:HD11	1:B:98:LEU:HD22	2.02	0.41
1:B:261:SER:OG	1:B:261:SER:O	2.12	0.41
1:B:30:LEU:HD13	1:B:97:LEU:HB2	2.03	0.41
1:A:326:GLY:HA3	1:A:355:TRP:CE3	2.56	0.41
1:B:3340:ILE:HB	1:B:3345:PHE:CE1	2.54	0.41
1:A:3346:ILE:N	1:A:3347:PRO:HD2	2.35	0.41
1:A:3262:LEU:HD13	1:A:3424:ASN:HB3	2.03	0.41
1:B:10:GLU:HB3	1:B:13:VAL:HG21	1.94	0.41
1:B:8:ARG:HG2	1:B:31:LEU:HD22	2.01	0.41
1:B:301:ASN:HD22	1:B:301:ASN:HA	1.65	0.41
1:A:3359:ASP:CB	1:A:3362:ARG:NH1	2.84	0.41
1:B:183:ARG:NH1	1:B:301:ASN:HD22	2.18	0.41
1:A:3346:ILE:HD12	1:A:3347:PRO:HD2	2.03	0.41
1:B:3346:ILE:N	1:B:3347:PRO:HD2	2.35	0.41
1:B:161:LEU:HA	1:B:161:LEU:HD12	1.82	0.41
1:B:334:GLU:CB	1:B:343:TYR:HB3	2.51	0.41
1:B:3342:ARG:O	1:B:3343:GLU:C	2.57	0.41
1:A:3359:ASP:OD1	1:A:3362:ARG:NH1	2.54	0.40
1:A:3290:ALA:HB1	1:A:3393:TRP:CA	2.51	0.40
1:A:162:LYS:HB3	1:A:162:LYS:HE2	1.88	0.40
1:A:3297:ILE:H	1:A:3297:ILE:HG13	1.70	0.40
1:B:328:TRP:CE3	1:B:353:LEU:HD11	2.56	0.40
1:B:3328:GLU:OE2	1:B:3339:ILE:HG21	2.21	0.40
1:B:252:ALA:HB1	1:B:253:PRO:CD	2.50	0.40
1:B:106:TRP:CD1	1:B:109:ALA:HB2	2.56	0.40
1:A:241:TYR:O	1:A:244:LEU:HB2	2.22	0.40
1:B:165:LEU:HD12	1:B:165:LEU:HA	1.91	0.40
1:B:3311:PRO:CB	1:B:3312:PRO:HD2	2.51	0.40
1:A:265:ASP:OD2	1:A:344:ARG:NH2	2.54	0.40
1:B:401:ARG:HG3	1:B:416:VAL:HG11	2.02	0.40
1:A:335:VAL:CG1	1:A:390:MET:HG2	2.49	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	525/536 (98%)	512 (98%)	12 (2%)	1 (0%)	52	63
1	B	525/536 (98%)	513 (98%)	12 (2%)	0	100	100
All	All	1050/1072 (98%)	1025 (98%)	24 (2%)	1 (0%)	56	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	PRO

### 5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	443/451 (98%)	400 (90%)	43 (10%)	10	11
1	B	443/451 (98%)	394 (89%)	49 (11%)	8	7
All	All	886/902 (98%)	794 (90%)	92 (10%)	9	9

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	9	GLN
1	A	3296	SER
1	A	3304	GLU
1	A	3307	SER

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Mol	Chain	Res	Type
1	A	3308	MET
1	A	3319	LEU
1	A	3326	LEU
1	A	3329	SER
1	A	3331	THR
1	A	3338	SER
1	A	3339	ILE
1	A	3340	ILE
1	A	3342	ARG
1	A	3346	ILE
1	A	3349	ILE
1	A	3356	GLU
1	A	3361	ILE
1	A	3376	ASN
1	A	3389	PRO
1	A	3407	VAL
1	A	3410	LEU
1	A	3422	LYS
1	A	106	TRP
1	A	114	GLU
1	A	146	TRP
1	A	161	LEU
1	A	167	LEU
1	A	218	THR
1	A	225	THR
1	A	230	LEU
1	A	244	LEU
1	A	267	ARG
1	A	279	GLU
1	A	284	THR
1	A	308	LEU
1	A	309	LEU
1	A	327	LYS
1	A	329	ARG
1	A	342	ARG
1	A	361	ASN
1	A	390	MET
1	A	408	LEU
1	B	3266	GLN
1	B	3274	MET
1	B	3284	GLU
1	B	3294	VAL

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Mol	Chain	Res	Type
1	B	3300	GLN
1	B	3308	MET
1	B	3324	LEU
1	B	3332	ASP
1	B	3334	LYS
1	B	3337	ARG
1	B	3339	ILE
1	B	3340	ILE
1	B	3341	MET
1	B	3348	THR
1	B	3349	ILE
1	B	3353	SER
1	B	3371	SER
1	B	3379	ILE
1	B	3380	VAL
1	B	3385	LEU
1	B	3392	LYS
1	B	3398	LEU
1	B	3406	ARG
1	B	3410	LEU
1	B	141	GLU
1	B	146	TRP
1	B	161	LEU
1	B	167	LEU
1	B	210	ASP
1	B	218	THR
1	B	230	LEU
1	B	235	SER
1	B	242	GLU
1	B	244	LEU
1	B	264	LYS
1	B	267	ARG
1	B	297	GLU
1	B	298	LEU
1	B	308	LEU
1	B	309	LEU
1	B	327	LYS
1	B	329	ARG
1	B	348	SER
1	B	361	ASN
1	B	368	GLU
1	B	390	MET

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Mol	Chain	Res	Type
1	B	398	GLN
1	B	399	ASP
1	B	417	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	3300	GLN
1	A	3425	GLN
1	A	117	ASN
1	A	280	GLN
1	A	301	ASN
1	A	356	GLN
1	A	361	ASN
1	A	379	ASN
1	A	396	GLN
1	B	15	HIS
1	B	3301	HIS
1	B	3376	ASN
1	B	3381	ASN
1	B	117	ASN
1	B	211	GLN
1	B	231	ASN
1	B	301	ASN
1	B	356	GLN
1	B	361	ASN
1	B	378	ASN
1	B	379	ASN
1	B	396	GLN

### 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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

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	$\# Z  > 2$
2	AMP	A	1507	-	20,25,25	1.54	2 (10%)	22,38,38	2.27	7 (31%)
2	AMP	B	1508	-	20,25,25	1.40	3 (15%)	22,38,38	2.16	6 (27%)

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	AMP	A	1507	-	-	0/6/26/26	0/3/3/3
2	AMP	B	1508	-	-	0/6/26/26	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1508	AMP	C2-N3	2.49	1.36	1.32
2	B	1508	AMP	O4'-C1'	3.32	1.45	1.41
2	A	1507	AMP	C5-C4	3.35	1.48	1.40
2	B	1508	AMP	C5-C4	3.68	1.48	1.40
2	A	1507	AMP	O4'-C1'	4.63	1.47	1.41

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1507	AMP	N3-C2-N1	-7.43	123.21	128.89
2	B	1508	AMP	N3-C2-N1	-6.90	123.61	128.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1507	AMP	C4'-O4'-C1'	-2.94	106.49	109.72
2	B	1508	AMP	C4-C5-N7	-2.78	106.92	109.48
2	A	1507	AMP	O3P-P-O5'	-2.58	99.12	106.56
2	B	1508	AMP	C2'-C1'-N9	-2.04	111.18	114.29
2	B	1508	AMP	O3P-P-O5'	-2.04	100.70	106.56
2	A	1507	AMP	O3P-P-O2P	2.01	115.03	107.38
2	A	1507	AMP	N6-C6-N1	2.05	123.60	119.20
2	B	1508	AMP	C2-N1-C6	2.22	122.74	118.77
2	A	1507	AMP	O3P-P-O1P	2.63	119.04	110.58
2	B	1508	AMP	O4'-C1'-N9	3.06	114.50	108.10
2	A	1507	AMP	C2-N1-C6	4.05	126.01	118.77

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 [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	527/536 (98%)	0.24	24 (4%) 36 44	23, 55, 90, 112	0
1	B	527/536 (98%)	0.55	56 (10%) 8 11	7, 68, 118, 162	0
All	All	1054/1072 (98%)	0.39	80 (7%) 17 22	7, 59, 110, 162	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3309	ALA	6.7
1	B	266	VAL	6.5
1	B	3306	ARG	6.1
1	B	3283	VAL	6.0
1	B	3276	VAL	5.8
1	A	3309	ALA	5.7
1	B	3305	VAL	5.7
1	B	12	GLU	5.4
1	B	3277	LYS	5.0
1	B	3375	TYR	4.8
1	A	370	ARG	4.7
1	A	3339	ILE	4.4
1	B	3308	MET	4.3
1	A	3303	VAL	4.3
1	A	3341	MET	4.2
1	A	3305	VAL	4.2
1	B	7	LEU	4.0
1	A	19	ARG	3.9
1	B	3274	MET	3.7
1	B	262	PHE	3.7
1	B	30	LEU	3.7
1	A	3368	ASN	3.7
1	B	3273	GLN	3.6
1	B	3268	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	3287	VAL	3.5
1	B	3380	VAL	3.4
1	B	3315	VAL	3.3
1	B	3410	LEU	3.3
1	B	3311	PRO	3.2
1	B	14	PHE	3.2
1	B	3280	LEU	3.2
1	B	3355	GLU	3.2
1	A	3330	THR	3.2
1	B	3412	ASN	3.2
1	B	3310	ASN	3.1
1	A	3355	GLU	2.9
1	B	3290	ALA	2.8
1	A	3	ASP	2.8
1	B	11	PRO	2.8
1	B	97	LEU	2.7
1	A	371	VAL	2.7
1	A	419	PRO	2.7
1	B	3272	LYS	2.7
1	B	23	VAL	2.6
1	A	3342	ARG	2.6
1	B	3337	ARG	2.6
1	A	3329	SER	2.6
1	B	3407	VAL	2.6
1	B	3269	ILE	2.6
1	B	3423	ASP	2.5
1	B	3278	GLU	2.5
1	B	3333	TRP	2.4
1	B	3417	LEU	2.4
1	B	3422	LYS	2.4
1	B	3367	LYS	2.4
1	B	3307	SER	2.4
1	B	3413	GLU	2.4
1	A	10	GLU	2.3
1	A	3302	LEU	2.3
1	B	3275	SER	2.3
1	B	3267	GLU	2.3
1	B	3284	GLU	2.3
1	B	3409	PRO	2.3
1	B	24	ALA	2.3
1	B	3314	ALA	2.3
1	A	3297	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	3300	GLN	2.2
1	A	3311	PRO	2.2
1	A	3407	VAL	2.2
1	B	3279	ASP	2.2
1	B	308	LEU	2.1
1	B	3295	LYS	2.1
1	A	3307	SER	2.1
1	B	267	ARG	2.1
1	A	3300	GLN	2.1
1	B	3341	MET	2.0
1	A	9	GLN	2.0
1	B	3294	VAL	2.0
1	A	3343	GLU	2.0
1	B	131	PHE	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	AMP	A	1507	23/23	0.96	0.15	-0.97	36,43,66,71	0
2	AMP	B	1508	23/23	0.89	0.12	-2.02	63,72,90,92	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.