



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:03 PM GMT

PDB ID : 3VYW
Title : Crystal structure of MNMC2 from Aquifex Aeolicus
Authors : Shibata, R.; Bessho, Y.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2012-10-03
Resolution : 2.49 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

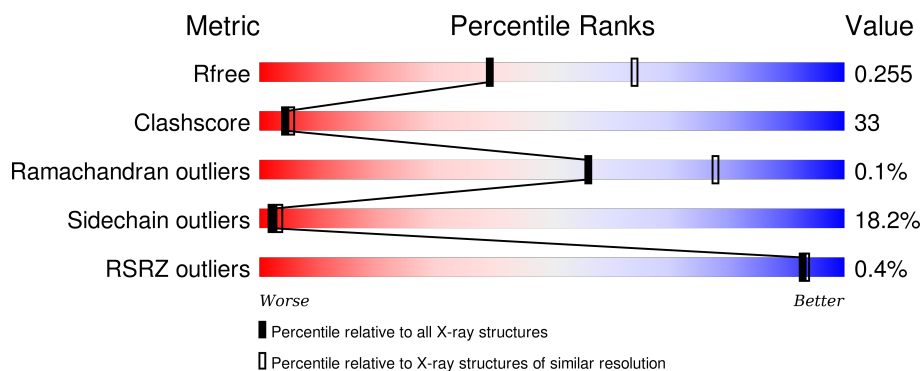
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION





The reported resolution of this entry is 2.49 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 ≥ 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	308	 63% 25% 9% ..
1	B	308	 51% 37% 11% .
1	C	308	 53% 34% 12% .
1	D	308	 50% 35% 14% ..

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	BEN	B	402	-	-	-	X
3	BEN	C	402	-	-	-	X

2 Entry composition [i](#)

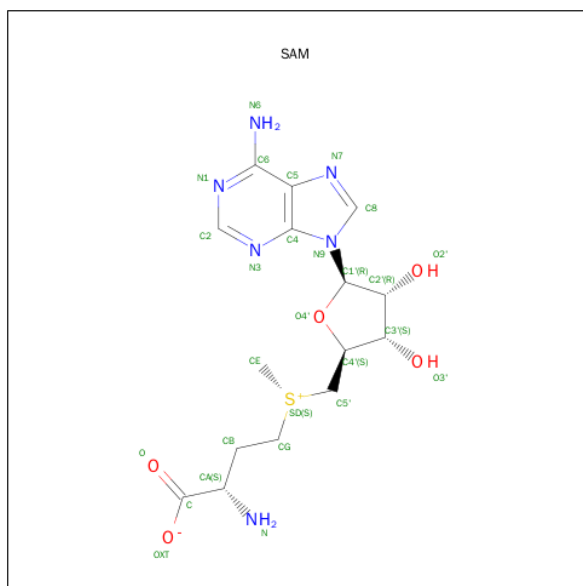
There are 4 unique types of molecules in this entry. The entry contains 10340 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 MNMC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	Se	0	0	0
			2502	1623	419	458	2			
1	B	305	Total	C	N	O	Se	0	0	0
			2520	1634	425	459	2			
1	C	305	Total	C	N	O	Se	0	0	0
			2520	1634	425	459	2			
1	D	306	Total	C	N	O	Se	0	0	0
			2526	1637	426	461	2			

- Molecule 2 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



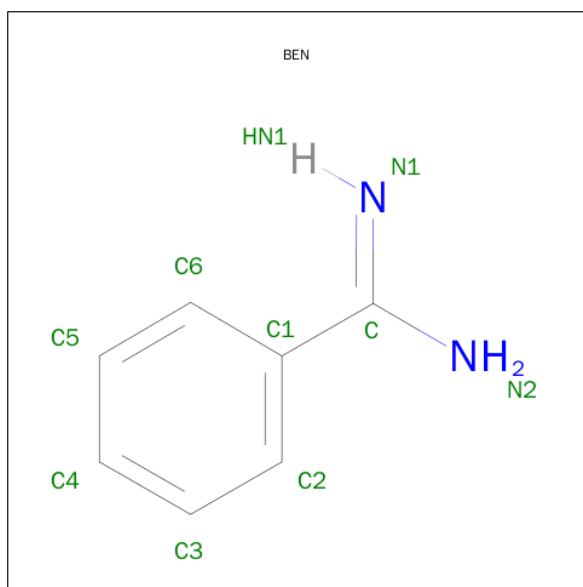
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	B	1	Total	C	N	O	S	0	0
			27	15	6	5	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	D	1	Total	C	N	O	S	0	0
			27	15	6	5	1		

- Molecule 3 is BENZAMIDINE (three-letter code: BEN) (formula: C₇H₈N₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	N	0	0
			9	7	2		
3	C	1	Total	C	N	0	0
			9	7	2		

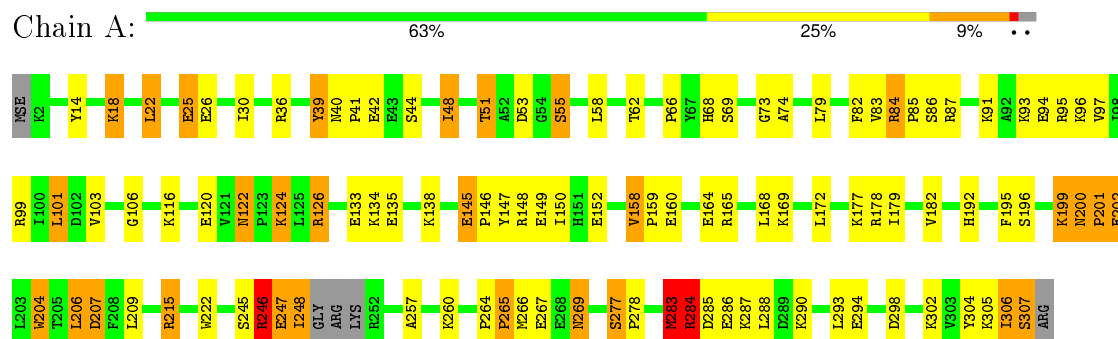
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	42	Total	O	0	0
			42	42		
4	B	32	Total	O	0	0
			32	32		
4	C	34	Total	O	0	0
			34	34		
4	D	38	Total	O	0	0
			38	38		

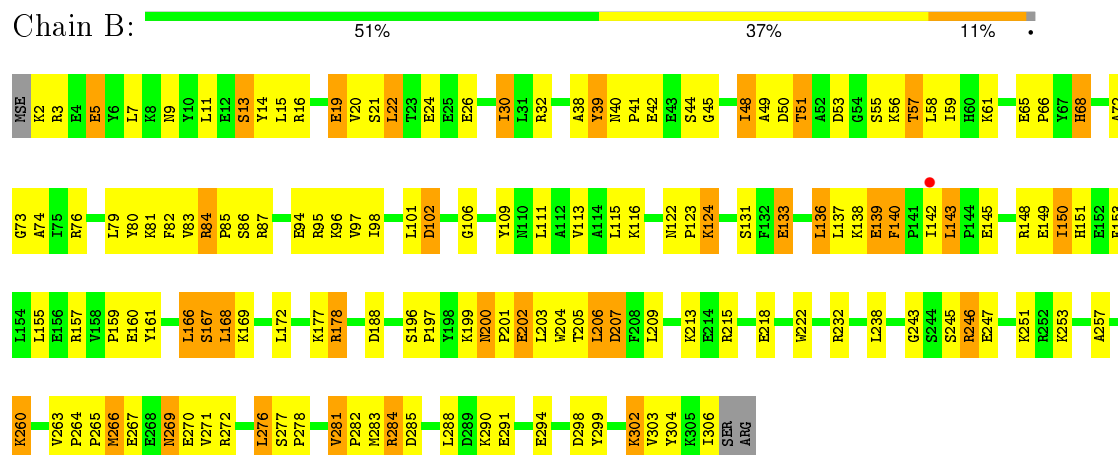
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

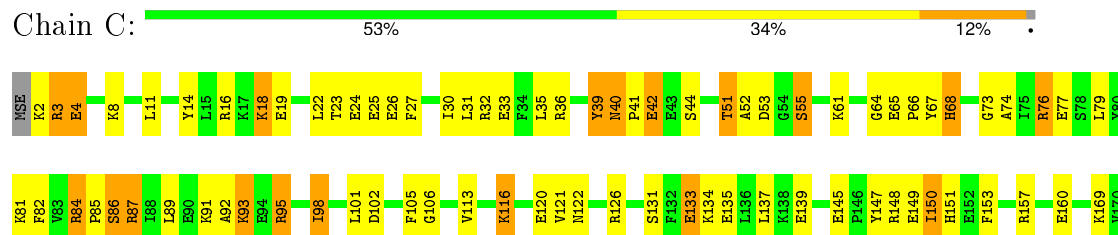
• Molecule 1: MNMC2

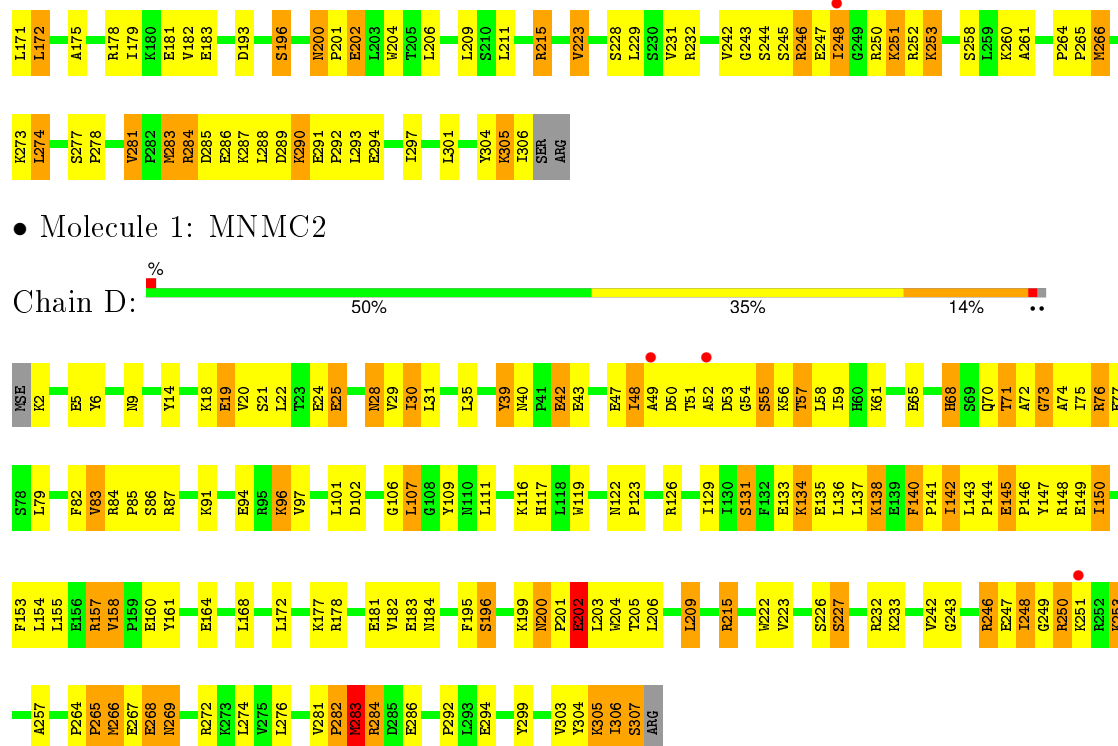


• Molecule 1: MNMC2



• Molecule 1: MNMC2





• Molecule 1: MNMC2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.49Å 107.58Å 117.71Å 90.00° 102.44° 90.00°	Depositor
Resolution (Å)	45.39 – 2.49 45.39 – 2.49	Depositor EDS
% Data completeness (in resolution range)	96.8 (45.39-2.49) 96.9 (45.39-2.49)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.53 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.191 , 0.255 0.191 , 0.255	Depositor DCC
R_{free} test set	2345 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	47.9	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.8	EDS
Estimated twinning fraction	0.025 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 45916 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10340	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: BEN, SAM

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	1.48	2/2554 (0.1%)	0.96	12/3437 (0.3%)
1	B	1.41	5/2573 (0.2%)	0.92	9/3462 (0.3%)
1	C	1.38	1/2573 (0.0%)	0.94	7/3462 (0.2%)
1	D	1.42	5/2579 (0.2%)	0.97	7/3470 (0.2%)
All	All	1.42	13/10279 (0.1%)	0.95	35/13831 (0.3%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	159	PRO	CA-C	-5.97	1.41	1.52
1	B	140	PHE	C-N	5.86	1.45	1.34
1	D	202	GLU	CD-OE1	-5.85	1.19	1.25
1	C	283	MSE	CB-CG	-5.85	1.34	1.52
1	A	202	GLU	CD-OE1	-5.81	1.19	1.25
1	D	265	PRO	CA-C	-5.77	1.41	1.52
1	B	284	ARG	N-CA	-5.68	1.34	1.46
1	B	82	PHE	C-O	-5.60	1.12	1.23
1	D	282	PRO	CA-C	-5.43	1.42	1.52
1	A	204	TRP	NE1-CE2	-5.37	1.30	1.37
1	D	83	VAL	N-CA	-5.18	1.35	1.46
1	D	161	TYR	CE1-CZ	-5.04	1.31	1.38
1	B	283	MSE	N-CA	-5.04	1.36	1.46

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	283	MSE	O-C-N	-15.57	97.79	122.70
1	C	283	MSE	O-C-N	-14.59	99.36	122.70
1	D	283	MSE	CA-C-N	13.82	147.61	117.20
1	A	266	MSE	O-C-N	13.23	143.87	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	266	MSE	CA-C-N	-11.49	91.93	117.20
1	C	266	MSE	O-C-N	10.59	139.65	122.70
1	B	266	MSE	C-N-CA	10.08	146.91	121.70
1	C	283	MSE	CA-C-N	10.00	139.21	117.20
1	A	266	MSE	C-N-CA	-9.64	97.60	121.70
1	B	283	MSE	C-N-CA	-9.51	97.92	121.70
1	C	266	MSE	CA-C-N	-9.06	97.26	117.20
1	A	283	MSE	C-N-CA	8.29	142.43	121.70
1	C	283	MSE	C-N-CA	7.90	141.46	121.70
1	D	266	MSE	O-C-N	-6.51	112.28	122.70
1	D	265	PRO	CA-C-O	5.87	134.29	120.20
1	A	82	PHE	N-CA-C	5.86	126.81	111.00
1	A	206	LEU	CA-CB-CG	5.73	128.47	115.30
1	D	73	GLY	N-CA-C	-5.69	98.88	113.10
1	A	246	ARG	C-N-CA	-5.66	107.56	121.70
1	C	266	MSE	N-CA-CB	-5.61	100.50	110.60
1	D	82	PHE	CA-C-O	-5.46	108.64	120.10
1	B	266	MSE	CB-CA-C	5.44	121.28	110.40
1	B	159	PRO	CA-C-N	5.44	129.16	117.20
1	B	266	MSE	N-CA-CB	5.42	120.35	110.60
1	C	281	VAL	O-C-N	-5.27	111.08	121.10
1	A	283	MSE	O-C-N	5.26	131.12	122.70
1	A	158	VAL	C-N-CD	-5.21	109.13	120.60
1	D	266	MSE	CB-CA-C	5.17	120.75	110.40
1	A	284	ARG	N-CA-C	5.14	124.87	111.00
1	A	267	GLU	CB-CA-C	-5.12	100.16	110.40
1	B	206	LEU	CA-CB-CG	5.11	127.06	115.30
1	B	83	VAL	N-CA-C	-5.11	97.20	111.00
1	B	266	MSE	CG-SE-CE	5.08	110.08	98.90
1	B	276	LEU	N-CA-C	5.03	124.58	111.00
1	A	267	GLU	N-CA-C	-5.01	97.47	111.00

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	2502	0	2566	118	0
1	B	2520	0	2590	205	0
1	C	2520	0	2589	145	0
1	D	2526	0	2596	220	0
2	A	27	0	22	7	0
2	B	27	0	22	3	0
2	C	27	0	22	4	0
2	D	27	0	22	6	0
3	B	9	0	7	1	0
3	C	9	0	7	2	0
4	A	42	0	0	2	0
4	B	32	0	0	5	0
4	C	34	0	0	6	0
4	D	38	0	0	6	0
All	All	10340	0	10443	679	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 (679) 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:D:51:THR:CG2	1:D:73:GLY:HA2	1.31	1.55
1:B:143:LEU:HD11	1:B:151:HIS:CG	1.59	1.36
1:B:172:LEU:CD1	1:D:54:GLY:HA3	1.63	1.27
1:D:50:ASP:CB	1:D:56:LYS:HE2	1.65	1.23
1:C:44:SER:O	1:C:61:LYS:HE2	1.38	1.21
1:D:51:THR:CG2	1:D:73:GLY:CA	2.21	1.18
1:D:246:ARG:HH11	1:D:246:ARG:CG	1.56	1.17
1:B:19:GLU:O	1:B:19:GLU:HG2	1.42	1.16
1:B:143:LEU:CD1	1:B:151:HIS:CG	2.30	1.15
1:C:251:LYS:NZ	1:C:251:LYS:HB3	1.47	1.14
1:D:142:ILE:HD13	1:D:142:ILE:N	1.59	1.12
1:B:246:ARG:CB	1:B:246:ARG:HH11	1.63	1.12
1:B:150:ILE:N	1:B:150:ILE:HD12	1.62	1.12
1:B:22:LEU:N	1:B:22:LEU:HD12	1.51	1.11
1:B:150:ILE:H	1:B:150:ILE:CD1	1.61	1.11
1:B:246:ARG:CG	1:B:246:ARG:HH11	1.61	1.11
1:B:143:LEU:CD1	1:B:151:HIS:HB2	1.79	1.10
1:D:150:ILE:HD12	1:D:150:ILE:O	1.49	1.10
1:A:51:THR:HG23	1:A:73:GLY:HA2	1.24	1.10
1:D:247:GLU:OE1	1:D:250:ARG:HB2	1.49	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:LEU:CD1	1:B:151:HIS:CB	2.30	1.09
1:A:246:ARG:H	1:A:246:ARG:CZ	1.65	1.09
1:D:248:ILE:N	1:D:248:ILE:HD12	1.59	1.09
1:A:51:THR:CG2	1:A:73:GLY:HA2	1.82	1.08
1:D:248:ILE:H	1:D:248:ILE:HD12	0.96	1.08
1:D:42:GLU:OE1	1:D:42:GLU:HA	1.50	1.08
1:B:51:THR:HG23	1:B:73:GLY:HA2	1.33	1.08
1:B:139:GLU:HA	1:B:139:GLU:OE1	1.53	1.08
1:B:22:LEU:HD12	1:B:22:LEU:H	0.95	1.07
1:D:25:GLU:OE2	1:D:25:GLU:HA	1.50	1.07
1:D:48:ILE:HD12	1:D:48:ILE:N	1.59	1.07
1:B:157:ARG:HH11	1:B:157:ARG:HG2	1.19	1.07
1:D:51:THR:HG21	1:D:73:GLY:HA2	1.37	1.06
1:D:246:ARG:HH11	1:D:246:ARG:HG3	1.11	1.06
1:B:51:THR:HB	1:B:55:SER:O	1.55	1.06
1:A:22:LEU:H	1:A:22:LEU:HD23	1.20	1.06
1:D:50:ASP:CA	1:D:56:LYS:HE2	1.86	1.05
1:B:246:ARG:NH1	1:B:246:ARG:HB2	1.71	1.05
1:B:150:ILE:H	1:B:150:ILE:HD12	1.11	1.04
1:B:172:LEU:HD13	1:D:54:GLY:CA	1.86	1.03
1:D:51:THR:HG22	1:D:73:GLY:CA	1.86	1.03
1:C:248:ILE:HD12	1:C:248:ILE:O	1.58	1.02
1:A:246:ARG:H	1:A:246:ARG:NE	1.56	1.02
1:C:251:LYS:HZ1	1:C:251:LYS:HB3	1.23	1.01
1:B:246:ARG:HH11	1:B:246:ARG:HB2	1.22	1.01
1:D:248:ILE:H	1:D:248:ILE:CD1	1.57	1.01
1:B:178:ARG:HG3	1:B:178:ARG:HH11	1.24	1.01
1:D:48:ILE:H	1:D:48:ILE:CD1	1.75	1.00
1:B:153:PHE:CD1	1:B:157:ARG:NH2	2.30	1.00
1:A:22:LEU:N	1:A:22:LEU:HD23	1.73	0.99
1:A:126:ARG:HH11	1:A:126:ARG:HG3	1.23	0.99
1:B:153:PHE:CE1	1:B:157:ARG:NH2	2.30	0.99
1:C:14:TYR:CE1	1:C:294:GLU:HG2	1.98	0.99
1:D:48:ILE:HD12	1:D:48:ILE:H	1.19	0.98
1:C:2:LYS:HG3	4:C:526:HOH:O	1.62	0.98
1:D:50:ASP:HB3	1:D:56:LYS:HE2	1.44	0.98
1:D:50:ASP:HA	1:D:56:LYS:HE2	1.43	0.98
1:B:145:GLU:HG2	1:B:148:ARG:NH2	1.79	0.98
1:B:136:LEU:HD22	1:B:172:LEU:CD2	1.93	0.98
1:D:57:THR:HG23	1:D:58:LEU:N	1.78	0.97
1:C:51:THR:HB	1:C:55:SER:O	1.63	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:41:PRO:HD2	1:B:42:GLU:OE1	1.66	0.96
1:A:106:GLY:HA3	2:A:501:SAM:HA	1.47	0.96
1:B:143:LEU:CD1	1:B:151:HIS:ND1	2.29	0.96
1:C:51:THR:HG23	1:C:73:GLY:HA2	1.47	0.96
1:B:269:ASN:ND2	1:B:269:ASN:H	1.64	0.95
1:A:306:ILE:CD1	1:A:306:ILE:N	2.30	0.95
1:B:136:LEU:HD22	1:B:172:LEU:HD22	1.47	0.95
1:B:246:ARG:HG3	1:B:246:ARG:HH11	1.30	0.94
1:B:22:LEU:N	1:B:22:LEU:CD1	2.30	0.94
1:D:141:PRO:C	1:D:142:ILE:HD13	1.86	0.94
1:B:145:GLU:CG	1:B:148:ARG:NH2	2.30	0.94
1:B:246:ARG:CB	1:B:246:ARG:NH1	2.30	0.94
1:B:56:LYS:HD3	4:B:517:HOH:O	1.67	0.94
1:A:145:GLU:HA	1:A:145:GLU:OE1	1.67	0.93
1:B:168:LEU:CD2	1:B:169:LYS:N	2.32	0.93
1:D:51:THR:HG22	1:D:73:GLY:HA2	0.93	0.92
1:C:42:GLU:HA	1:C:42:GLU:OE1	1.65	0.92
1:B:266:MSE:HE2	1:B:270:GLU:HB3	1.49	0.92
1:A:247:GLU:O	1:A:247:GLU:HG2	1.65	0.92
1:B:172:LEU:HD13	1:D:54:GLY:HA3	0.92	0.92
1:D:142:ILE:CD1	1:D:142:ILE:N	2.30	0.91
1:A:22:LEU:CD2	1:A:22:LEU:N	2.33	0.91
1:B:232:ARG:NH1	1:B:266:MSE:CE	2.34	0.91
1:B:157:ARG:HD3	1:B:161:TYR:CD1	2.05	0.91
1:C:22:LEU:C	1:C:22:LEU:HD12	1.91	0.91
1:C:251:LYS:NZ	1:C:251:LYS:CB	2.30	0.90
1:C:291:GLU:HB2	1:C:294:GLU:OE1	1.70	0.90
1:B:143:LEU:HD11	1:B:151:HIS:ND1	1.87	0.89
1:C:24:GLU:OE1	3:C:402:BEN:H6	1.72	0.89
1:B:143:LEU:HD12	1:B:151:HIS:CB	2.00	0.89
1:A:116:LYS:O	1:A:120:GLU:HG3	1.73	0.88
1:D:286:GLU:HG3	4:D:529:HOH:O	1.72	0.88
1:B:269:ASN:HD22	1:B:269:ASN:H	1.21	0.87
1:B:137:LEU:O	1:B:140:PHE:CE1	2.28	0.87
1:C:251:LYS:HZ2	1:C:251:LYS:HB3	1.35	0.86
1:B:168:LEU:HD22	1:B:169:LYS:N	1.90	0.86
1:B:51:THR:CG2	1:B:73:GLY:HA2	2.04	0.86
1:A:306:ILE:N	1:A:306:ILE:HD12	1.89	0.86
1:D:52:ALA:HB2	1:D:71:THR:O	1.76	0.85
1:C:22:LEU:HD13	1:C:23:THR:O	1.77	0.85
1:D:136:LEU:HD21	1:D:158:VAL:CG1	2.06	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:49:ALA:O	1:D:56:LYS:HD3	1.77	0.84
1:B:291:GLU:HB2	1:B:294:GLU:OE1	1.77	0.84
1:B:22:LEU:H	1:B:22:LEU:CD1	1.86	0.84
1:A:79:LEU:O	1:A:84:ARG:HG2	1.77	0.84
1:B:218:GLU:CD	1:B:260:LYS:HZ3	1.81	0.84
1:B:44:SER:HB2	1:D:249:GLY:O	1.77	0.84
1:D:50:ASP:HA	1:D:56:LYS:CE	2.08	0.83
1:B:266:MSE:HG3	1:B:271:VAL:HG22	1.59	0.83
1:B:168:LEU:C	1:B:168:LEU:CD2	2.46	0.83
1:D:145:GLU:CD	1:D:148:ARG:CZ	2.46	0.83
1:D:246:ARG:HG3	1:D:246:ARG:NH1	1.83	0.83
1:B:232:ARG:NH1	1:B:266:MSE:HE1	1.93	0.83
1:B:136:LEU:CD2	1:B:172:LEU:HD21	2.09	0.83
1:D:138:LYS:HD2	1:D:138:LYS:N	1.93	0.82
1:A:246:ARG:N	1:A:246:ARG:NE	2.28	0.82
1:A:126:ARG:HH11	1:A:126:ARG:CG	1.92	0.82
1:D:51:THR:HB	1:D:55:SER:O	1.79	0.82
1:B:178:ARG:NH1	1:B:178:ARG:HG3	1.83	0.82
1:B:168:LEU:HD22	1:B:168:LEU:C	2.00	0.82
1:C:41:PRO:HD2	4:C:512:HOH:O	1.79	0.81
1:D:52:ALA:CB	1:D:71:THR:O	2.27	0.81
1:B:157:ARG:HD3	1:B:161:TYR:CE1	2.15	0.81
1:D:140:PHE:O	1:D:142:ILE:CD1	2.29	0.81
1:B:145:GLU:CG	1:B:148:ARG:HH22	1.90	0.80
1:D:145:GLU:N	1:D:146:PRO:CD	2.44	0.80
1:D:75:ILE:HD11	1:D:144:PRO:HG2	1.62	0.80
1:A:172:LEU:HD23	1:A:172:LEU:N	1.97	0.80
1:B:168:LEU:HD23	1:B:169:LYS:N	1.96	0.80
1:D:51:THR:HG21	1:D:73:GLY:CA	2.02	0.80
1:D:145:GLU:CD	1:D:148:ARG:NH2	2.36	0.80
1:D:49:ALA:O	1:D:56:LYS:CD	2.30	0.80
1:B:218:GLU:CD	1:B:260:LYS:NZ	2.36	0.80
1:B:232:ARG:HH11	1:B:266:MSE:HE1	1.45	0.79
1:B:143:LEU:HD11	1:B:151:HIS:CB	2.01	0.79
1:C:22:LEU:CD1	1:C:23:THR:O	2.29	0.79
1:D:140:PHE:O	1:D:142:ILE:HD11	1.83	0.79
1:B:139:GLU:OE1	1:B:139:GLU:CA	2.30	0.79
1:C:42:GLU:OE1	1:C:42:GLU:CA	2.30	0.79
1:C:23:THR:OG1	1:C:26:GLU:HG3	1.81	0.79
1:A:51:THR:HG21	1:A:74:ALA:H	1.48	0.79
1:C:153:PHE:CE1	1:C:157:ARG:CZ	2.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:153:PHE:CE1	1:D:157:ARG:NH1	2.51	0.79
1:D:75:ILE:CD1	1:D:144:PRO:HG2	2.14	0.78
1:C:248:ILE:CD1	1:C:248:ILE:O	2.30	0.78
1:D:247:GLU:OE1	1:D:250:ARG:CB	2.30	0.78
1:D:42:GLU:OE1	1:D:42:GLU:CA	2.30	0.78
1:C:247:GLU:OE1	1:C:250:ARG:HD2	1.84	0.77
1:B:106:GLY:HA3	2:B:401:SAM:HA	1.66	0.77
1:B:136:LEU:CD2	1:B:172:LEU:CD2	2.63	0.77
1:D:57:THR:HG23	1:D:58:LEU:O	1.85	0.76
1:D:50:ASP:HB3	1:D:56:LYS:CE	2.16	0.76
1:B:157:ARG:HG2	1:B:157:ARG:NH1	1.92	0.76
1:D:153:PHE:HE1	1:D:157:ARG:HH11	1.30	0.76
1:A:25:GLU:HA	1:A:25:GLU:OE1	1.85	0.76
1:A:246:ARG:N	1:A:246:ARG:CZ	2.48	0.75
1:C:172:LEU:N	1:C:172:LEU:HD23	2.01	0.75
1:D:79:LEU:O	1:D:84:ARG:CG	2.34	0.75
1:A:304:TYR:O	1:A:306:ILE:CD1	2.34	0.75
1:D:153:PHE:HE1	1:D:157:ARG:NH1	1.85	0.75
1:D:306:ILE:CD1	1:D:306:ILE:N	2.49	0.75
1:A:306:ILE:HD13	1:A:306:ILE:H	1.52	0.75
1:B:157:ARG:CD	1:B:161:TYR:CD1	2.69	0.75
1:D:136:LEU:HD21	1:D:158:VAL:HG11	1.67	0.75
1:B:172:LEU:CD1	1:D:54:GLY:CA	2.52	0.75
1:D:150:ILE:O	1:D:150:ILE:CD1	2.33	0.75
1:A:179:ILE:O	1:A:215:ARG:NH1	2.20	0.75
1:B:207:ASP:OD1	1:B:284:ARG:NH1	2.20	0.75
1:C:153:PHE:CE1	1:C:157:ARG:NE	2.55	0.74
1:D:96:LYS:HD2	1:D:126:ARG:HH12	1.51	0.74
1:D:49:ALA:HA	4:D:525:HOH:O	1.88	0.74
1:B:178:ARG:CG	1:B:178:ARG:HH11	1.97	0.73
1:D:246:ARG:HH11	1:D:246:ARG:HG2	1.49	0.73
1:C:247:GLU:CD	1:C:250:ARG:HD3	2.09	0.73
1:B:157:ARG:NH1	1:B:157:ARG:CG	2.49	0.73
1:C:247:GLU:OE1	1:C:250:ARG:CD	2.37	0.73
1:A:306:ILE:HG22	1:A:306:ILE:O	1.89	0.73
1:C:287:LYS:O	1:C:288:LEU:HB2	1.87	0.73
1:D:150:ILE:HD12	1:D:150:ILE:C	2.02	0.73
1:D:50:ASP:CG	1:D:56:LYS:HE2	2.09	0.72
1:B:153:PHE:HE1	1:B:157:ARG:HH21	1.29	0.72
1:D:144:PRO:C	1:D:146:PRO:HD2	2.10	0.72
1:D:79:LEU:O	1:D:84:ARG:HG3	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:248:ILE:CD1	1:D:248:ILE:N	2.30	0.72
1:A:306:ILE:CD1	1:A:306:ILE:H	1.99	0.71
1:C:51:THR:CG2	1:C:73:GLY:HA2	2.20	0.71
1:D:18:LYS:HB3	1:D:20:VAL:HG23	1.73	0.71
1:B:44:SER:CB	1:D:249:GLY:O	2.39	0.71
1:C:193:ASP:OD2	2:C:401:SAM:N	2.24	0.71
1:C:175:ALA:O	1:C:179:ILE:HG22	1.91	0.71
1:D:246:ARG:NH1	1:D:246:ARG:CG	2.30	0.70
1:D:305:LYS:C	1:D:307:SER:H	1.93	0.70
1:B:166:LEU:HD23	1:B:167:SER:N	2.07	0.70
1:C:76:ARG:NH2	1:C:247:GLU:OE1	2.24	0.70
1:D:138:LYS:H	1:D:138:LYS:HD2	1.54	0.70
1:B:143:LEU:HD13	1:B:151:HIS:HB2	1.72	0.70
1:D:135:GLU:O	1:D:135:GLU:HG2	1.92	0.70
1:D:49:ALA:HB3	1:D:57:THR:HG22	1.73	0.69
1:C:51:THR:CG2	1:C:53:ASP:OD1	2.41	0.69
1:B:272:ARG:HG2	1:B:276:LEU:HD12	1.75	0.69
1:A:122:ASN:OD1	1:A:122:ASN:C	2.29	0.69
1:D:28:ASN:HD22	1:D:28:ASN:N	1.90	0.69
1:A:164:GLU:HG3	1:A:165:ARG:H	1.57	0.69
1:B:272:ARG:HD2	4:B:521:HOH:O	1.92	0.69
1:D:141:PRO:C	1:D:142:ILE:CD1	2.60	0.69
1:A:207:ASP:OD1	1:A:284:ARG:NH1	2.25	0.68
1:D:135:GLU:O	1:D:135:GLU:CG	2.41	0.68
1:D:117:HIS:NE2	1:D:147:TYR:OH	2.21	0.68
1:B:2:LYS:HB2	1:B:5:GLU:CG	2.23	0.68
1:A:14:TYR:CE1	1:A:294:GLU:HG2	2.27	0.68
1:B:81:LYS:HE3	4:B:503:HOH:O	1.93	0.68
1:A:207:ASP:OD2	1:A:284:ARG:NH1	2.26	0.68
1:D:122:ASN:OD1	1:D:122:ASN:C	2.31	0.68
1:B:49:ALA:HB2	1:B:59:ILE:CD1	2.23	0.68
1:A:304:TYR:O	1:A:306:ILE:HD12	1.94	0.68
1:D:96:LYS:CD	1:D:126:ARG:NH1	2.57	0.68
1:D:134:LYS:HD3	2:D:401:SAM:C5	2.24	0.68
1:D:50:ASP:CB	1:D:56:LYS:CE	2.58	0.68
1:D:53:ASP:OD1	1:D:53:ASP:C	2.30	0.67
1:C:122:ASN:OD1	1:C:122:ASN:C	2.30	0.67
1:D:42:GLU:HB2	4:D:523:HOH:O	1.93	0.67
1:A:304:TYR:C	1:A:306:ILE:CD1	2.63	0.67
1:D:91:LYS:HE3	4:D:514:HOH:O	1.94	0.67
1:B:168:LEU:HD23	1:B:169:LYS:H	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:246:ARG:HG3	1:B:246:ARG:NH1	1.98	0.67
1:A:269:ASN:H	1:A:269:ASN:HD22	1.42	0.67
1:D:145:GLU:CD	1:D:148:ARG:NH1	2.47	0.66
1:B:218:GLU:OE1	1:B:260:LYS:NZ	2.27	0.66
1:B:24:GLU:OE1	3:B:402:BEN:H2	1.95	0.66
1:D:306:ILE:HG22	1:D:306:ILE:O	1.96	0.65
1:D:24:GLU:O	1:D:28:ASN:ND2	2.29	0.65
1:C:251:LYS:HZ1	1:C:251:LYS:CB	2.01	0.65
1:D:145:GLU:OE2	1:D:148:ARG:NH1	2.30	0.65
1:D:306:ILE:HD12	1:D:306:ILE:N	2.11	0.65
1:A:91:LYS:O	1:A:95:ARG:HG3	1.97	0.65
1:D:145:GLU:OE1	1:D:148:ARG:NH1	2.30	0.65
1:D:145:GLU:OE2	1:D:148:ARG:NH2	2.30	0.65
1:B:290:LYS:NZ	1:B:298:ASP:OD2	2.30	0.65
1:C:51:THR:HG21	1:C:53:ASP:OD1	1.97	0.65
1:A:66:PRO:HB2	1:A:68:HIS:O	1.95	0.65
1:B:213:LYS:NZ	1:B:238:LEU:O	2.27	0.65
1:C:248:ILE:C	1:C:248:ILE:HD12	2.16	0.65
1:C:2:LYS:CG	4:C:526:HOH:O	2.32	0.65
1:D:149:GLU:HA	1:D:149:GLU:OE2	1.96	0.65
1:C:145:GLU:OE1	1:C:148:ARG:NE	2.30	0.65
1:B:172:LEU:O	1:B:178:ARG:NH1	2.30	0.64
1:B:232:ARG:NH1	1:B:266:MSE:HE3	2.12	0.64
1:B:2:LYS:HB2	1:B:5:GLU:HG3	1.79	0.64
1:D:145:GLU:OE1	1:D:145:GLU:HA	1.97	0.64
1:A:51:THR:HB	1:A:55:SER:O	1.98	0.64
1:B:281:VAL:HG11	1:B:302:LYS:HG2	1.79	0.64
1:C:232:ARG:HG2	1:C:242:VAL:HG11	1.80	0.64
1:B:143:LEU:HD12	1:B:151:HIS:CG	2.26	0.64
1:D:79:LEU:O	1:D:84:ARG:HG2	1.97	0.64
1:A:41:PRO:HD2	1:A:42:GLU:OE2	1.98	0.64
1:B:200:ASN:ND2	1:B:202:GLU:OE1	2.30	0.64
1:A:246:ARG:N	1:A:246:ARG:CD	2.61	0.64
1:C:64:GLY:C	1:C:65:GLU:HG2	2.18	0.64
1:B:157:ARG:CD	1:B:161:TYR:CE1	2.81	0.64
1:A:122:ASN:OD1	1:A:124:LYS:N	2.30	0.64
1:D:232:ARG:HH11	1:D:266:MSE:SE	2.30	0.64
1:C:126:ARG:HH11	1:C:126:ARG:HG3	1.62	0.63
1:D:305:LYS:C	1:D:307:SER:N	2.51	0.63
1:D:145:GLU:N	1:D:146:PRO:HD3	2.11	0.63
1:C:22:LEU:HD12	1:C:22:LEU:O	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:246:ARG:HB3	1:C:253:LYS:HE3	1.80	0.63
1:C:89:LEU:O	1:C:93:LYS:HE3	1.99	0.63
1:A:84:ARG:HB2	1:A:85:PRO:HD3	1.80	0.62
1:C:148:ARG:NH2	1:C:149:GLU:HG3	2.14	0.62
1:B:149:GLU:HB2	1:B:150:ILE:HD12	1.81	0.62
1:D:25:GLU:O	1:D:29:VAL:HG23	1.99	0.62
1:C:76:ARG:NH1	1:C:247:GLU:OE1	2.31	0.62
1:B:200:ASN:N	1:B:201:PRO:HD3	2.14	0.62
1:A:207:ASP:CG	1:A:284:ARG:NH1	2.53	0.62
1:A:246:ARG:H	1:A:246:ARG:CD	2.11	0.62
1:D:182:VAL:O	1:D:215:ARG:NH2	2.33	0.62
1:C:24:GLU:OE1	3:C:402:BEN:N1	2.33	0.61
1:D:253:LYS:HE3	1:D:267:GLU:OE1	2.00	0.61
1:B:123:PRO:HB2	1:B:124:LYS:HE2	1.82	0.61
1:D:96:LYS:HD2	1:D:126:ARG:NH1	2.14	0.61
1:B:79:LEU:O	1:B:84:ARG:HG2	1.99	0.61
1:A:195:PHE:CE1	2:A:501:SAM:H5'1	2.35	0.61
1:B:218:GLU:OE2	1:B:260:LYS:NZ	2.33	0.61
1:A:247:GLU:CG	1:A:247:GLU:O	2.43	0.61
1:A:172:LEU:O	1:A:178:ARG:NH1	2.34	0.61
1:B:269:ASN:HD22	1:B:269:ASN:N	1.97	0.61
1:D:14:TYR:CE1	1:D:294:GLU:HG2	2.36	0.61
1:C:82:PHE:O	1:C:86:SER:HB3	2.01	0.61
1:D:145:GLU:OE1	1:D:148:ARG:CZ	2.49	0.61
1:A:79:LEU:O	1:A:84:ARG:CG	2.49	0.61
1:B:45:GLY:O	1:B:61:LYS:HB2	2.01	0.61
1:D:137:LEU:O	1:D:140:PHE:CZ	2.53	0.60
1:D:138:LYS:H	1:D:138:LYS:CD	2.04	0.60
1:B:49:ALA:HB2	1:B:59:ILE:HD12	1.82	0.60
1:B:218:GLU:HB2	1:B:260:LYS:HD3	1.82	0.60
1:D:199:LYS:C	1:D:201:PRO:HD3	2.22	0.60
1:A:246:ARG:O	1:A:246:ARG:NE	2.29	0.60
1:C:66:PRO:HB2	1:C:68:HIS:O	2.01	0.60
1:D:140:PHE:CD1	1:D:155:LEU:HD13	2.37	0.60
1:B:266:MSE:HE2	1:B:270:GLU:CB	2.27	0.60
1:B:143:LEU:HD12	1:B:151:HIS:ND1	2.15	0.59
1:D:96:LYS:CD	1:D:126:ARG:HH12	2.15	0.59
1:A:86:SER:O	1:A:87:ARG:HB2	2.01	0.59
1:C:182:VAL:O	1:C:215:ARG:NH1	2.35	0.59
1:A:126:ARG:NH1	1:A:126:ARG:HG3	2.05	0.59
1:A:304:TYR:C	1:A:306:ILE:HD13	2.23	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:82:PHE:HA	1:C:223:VAL:HG11	1.84	0.59
1:D:182:VAL:HB	1:D:215:ARG:HH21	1.68	0.58
1:B:166:LEU:CD2	1:B:168:LEU:HB2	2.32	0.58
1:C:248:ILE:CD1	1:C:248:ILE:C	2.71	0.58
1:B:153:PHE:CE1	1:B:157:ARG:CZ	2.87	0.58
1:B:166:LEU:HD21	1:B:168:LEU:HB2	1.84	0.58
1:D:227:SER:HB3	1:D:232:ARG:HH21	1.68	0.58
1:B:76:ARG:NH2	1:B:247:GLU:CD	2.57	0.58
1:B:19:GLU:O	1:B:19:GLU:CG	2.30	0.58
1:A:164:GLU:HG3	1:A:165:ARG:N	2.18	0.58
1:D:306:ILE:H	1:D:306:ILE:HD13	1.68	0.58
1:C:22:LEU:CD1	1:C:22:LEU:C	2.67	0.58
1:D:49:ALA:HB1	1:D:70:GLN:NE2	2.19	0.58
1:C:39:TYR:CD2	1:C:39:TYR:C	2.76	0.58
1:D:200:ASN:N	1:D:201:PRO:HD3	2.18	0.58
1:A:126:ARG:NH1	1:A:126:ARG:CG	2.56	0.58
1:B:84:ARG:N	1:B:85:PRO:HD2	2.19	0.57
1:A:287:LYS:O	1:A:288:LEU:HB2	2.02	0.57
1:C:33:GLU:OE1	1:C:304:TYR:OH	2.22	0.57
1:B:3:ARG:HG2	1:B:7:LEU:HD12	1.86	0.57
1:C:84:ARG:N	1:C:85:PRO:HD2	2.18	0.57
1:C:82:PHE:HA	1:C:223:VAL:CG1	2.34	0.57
1:B:42:GLU:N	1:B:42:GLU:OE1	2.30	0.57
1:D:243:GLY:HA2	1:D:266:MSE:HG3	1.84	0.57
1:B:243:GLY:HA3	1:B:264:PRO:O	2.04	0.57
1:D:30:ILE:HG22	1:D:31:LEU:N	2.18	0.57
1:D:138:LYS:CD	1:D:138:LYS:N	2.57	0.57
1:C:11:LEU:HD23	1:C:31:LEU:HD13	1.87	0.57
1:B:22:LEU:CB	1:B:26:GLU:OE1	2.53	0.57
1:D:76:ARG:NH2	1:D:247:GLU:OE2	2.37	0.57
1:B:50:ASP:OD1	1:B:56:LYS:CE	2.52	0.56
1:D:155:LEU:N	1:D:155:LEU:HD23	2.19	0.56
1:D:106:GLY:HA3	2:D:401:SAM:HA	1.87	0.56
1:B:133:GLU:OE2	2:B:401:SAM:O3'	2.23	0.56
1:D:227:SER:HB3	1:D:232:ARG:NH2	2.20	0.56
1:D:76:ARG:NH1	1:D:247:GLU:OE2	2.39	0.56
1:A:245:SER:HA	1:A:246:ARG:NH1	2.21	0.56
1:A:246:ARG:CA	1:A:246:ARG:NE	2.69	0.56
1:D:74:ALA:HB1	1:D:109:TYR:CD2	2.40	0.56
1:A:269:ASN:H	1:A:269:ASN:ND2	2.02	0.56
1:C:64:GLY:O	1:C:65:GLU:HG2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:102:ASP:OD1	1:B:131:SER:OG	2.22	0.56
1:B:222:TRP:HB3	1:B:257:ALA:HB3	1.88	0.56
1:B:95:ARG:NH2	1:B:188:ASP:OD1	2.37	0.55
1:D:222:TRP:HB3	1:D:257:ALA:HB3	1.89	0.55
1:B:51:THR:CG2	1:B:53:ASP:H	2.20	0.55
1:C:42:GLU:HB2	4:C:512:HOH:O	2.06	0.55
1:B:267:GLU:O	1:B:271:VAL:HG23	2.07	0.55
1:D:51:THR:CB	1:D:55:SER:O	2.54	0.55
1:D:140:PHE:CD1	1:D:140:PHE:N	2.75	0.55
1:C:22:LEU:HD11	1:C:27:PHE:HB2	1.89	0.55
1:D:306:ILE:CD1	1:D:306:ILE:H	2.19	0.55
1:B:2:LYS:HB2	1:B:5:GLU:OE2	2.06	0.55
1:D:144:PRO:C	1:D:146:PRO:CD	2.74	0.55
1:D:144:PRO:O	1:D:146:PRO:HD2	2.07	0.54
1:D:76:ARG:NH1	1:D:76:ARG:HB3	2.22	0.54
1:B:153:PHE:CE1	1:B:157:ARG:NE	2.75	0.54
1:C:4:GLU:HB2	4:C:526:HOH:O	2.07	0.54
1:B:41:PRO:CD	1:B:42:GLU:OE1	2.47	0.54
1:D:227:SER:CB	1:D:232:ARG:HH21	2.20	0.54
1:C:286:GLU:H	1:C:286:GLU:CD	2.07	0.54
1:B:86:SER:O	1:B:87:ARG:HB2	2.07	0.54
1:D:306:ILE:O	1:D:307:SER:CB	2.52	0.54
1:D:18:LYS:HB3	1:D:20:VAL:CG2	2.37	0.54
1:D:111:LEU:HD22	1:D:129:ILE:HD13	1.89	0.54
1:C:229:LEU:HD22	1:C:274:LEU:HD13	1.87	0.54
1:B:266:MSE:HG3	1:B:271:VAL:CG2	2.32	0.54
1:D:304:TYR:C	1:D:305:LYS:CG	2.76	0.54
1:B:145:GLU:CD	1:B:148:ARG:HH22	2.10	0.54
1:C:147:TYR:O	1:C:150:ILE:HG22	2.07	0.54
1:D:22:LEU:N	1:D:22:LEU:HD23	2.22	0.54
1:D:51:THR:HG21	1:D:74:ALA:N	2.22	0.54
1:A:304:TYR:HB3	1:A:306:ILE:HD11	1.90	0.54
1:A:84:ARG:CZ	4:A:603:HOH:O	2.55	0.54
1:D:133:GLU:OE2	2:D:401:SAM:O3'	2.23	0.54
1:B:76:ARG:CZ	1:B:247:GLU:OE1	2.55	0.54
1:C:51:THR:HG23	1:C:52:ALA:N	2.23	0.54
1:C:51:THR:CG2	1:C:52:ALA:N	2.70	0.54
1:D:51:THR:HG21	1:D:73:GLY:C	2.28	0.54
1:C:14:TYR:CD1	1:C:294:GLU:HG2	2.43	0.54
1:C:51:THR:HG22	1:C:53:ASP:H	1.73	0.53
1:B:109:TYR:O	1:B:113:VAL:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:227:SER:HA	1:D:232:ARG:HH21	1.74	0.53
1:D:204:TRP:HB2	1:D:283:MSE:CE	2.39	0.53
2:D:401:SAM:N	4:D:504:HOH:O	2.34	0.53
1:B:59:ILE:HA	1:B:66:PRO:HA	1.89	0.53
1:A:199:LYS:HD3	1:A:199:LYS:N	2.16	0.53
1:A:99:ARG:HG3	1:A:99:ARG:HH11	1.73	0.53
1:D:195:PHE:CE1	2:D:401:SAM:H5'1	2.44	0.53
1:D:74:ALA:HB1	1:D:109:TYR:HD2	1.73	0.53
1:A:207:ASP:OD1	1:A:286:GLU:HA	2.08	0.53
1:D:5:GLU:O	1:D:9:ASN:ND2	2.41	0.53
1:D:51:THR:HG22	1:D:52:ALA:N	2.24	0.53
1:C:14:TYR:CZ	1:C:294:GLU:HG2	2.41	0.53
1:C:68:HIS:HD2	1:C:77:GLU:OE1	1.91	0.53
1:C:153:PHE:CE1	1:C:157:ARG:NH2	2.77	0.52
1:A:199:LYS:NZ	4:A:616:HOH:O	2.42	0.52
1:C:243:GLY:HA3	1:C:264:PRO:O	2.09	0.52
1:C:92:ALA:HB3	1:C:121:VAL:HG11	1.91	0.52
1:B:178:ARG:NH2	1:D:145:GLU:HB2	2.24	0.52
1:D:134:LYS:HD3	2:D:401:SAM:C6	2.39	0.52
1:A:134:LYS:HD3	2:A:501:SAM:C5	2.40	0.52
1:B:2:LYS:CB	1:B:5:GLU:HG3	2.39	0.52
1:B:11:LEU:HD11	1:B:15:LEU:HD11	1.90	0.52
1:C:150:ILE:HD12	1:C:150:ILE:O	2.09	0.52
1:A:158:VAL:HG12	1:A:159:PRO:HD3	1.90	0.52
1:D:76:ARG:CZ	1:D:247:GLU:OE2	2.58	0.52
1:C:211:LEU:HD11	1:C:288:LEU:HD11	1.90	0.52
1:B:51:THR:HG21	1:B:74:ALA:H	1.75	0.52
1:C:304:TYR:C	1:C:305:LYS:HG2	2.29	0.52
1:B:48:ILE:HG22	1:B:48:ILE:O	2.08	0.52
1:D:2:LYS:HE2	1:D:6:TYR:HB2	1.91	0.52
1:C:51:THR:CG2	1:C:53:ASP:H	2.23	0.52
1:A:68:HIS:HE1	2:A:501:SAM:C	2.23	0.52
1:D:49:ALA:C	1:D:50:ASP:OD1	2.48	0.51
1:C:150:ILE:CD1	1:C:150:ILE:O	2.58	0.51
1:B:57:THR:OG1	1:B:58:LEU:N	2.41	0.51
1:D:267:GLU:O	1:D:269:ASN:N	2.44	0.51
1:C:150:ILE:CG2	1:C:151:HIS:N	2.73	0.51
1:A:103:VAL:HB	1:A:192:HIS:HA	1.91	0.51
1:D:49:ALA:O	1:D:56:LYS:HD2	2.08	0.51
1:C:133:GLU:OE2	2:C:401:SAM:O3'	2.22	0.51
1:C:3:ARG:NH2	1:C:35:LEU:O	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:ASP:OD1	1:B:56:LYS:HE3	2.10	0.51
1:B:199:LYS:C	1:B:201:PRO:HD3	2.30	0.51
1:D:75:ILE:HD11	1:D:144:PRO:CG	2.35	0.51
1:B:143:LEU:HD12	1:B:151:HIS:HB3	1.89	0.51
1:B:145:GLU:CD	1:B:148:ARG:NH2	2.64	0.51
1:C:105:PHE:HB3	1:C:133:GLU:HG2	1.93	0.51
1:C:287:LYS:CB	1:C:289:ASP:OD2	2.59	0.51
1:D:267:GLU:O	1:D:268:GLU:C	2.46	0.51
1:D:153:PHE:CE1	1:D:157:ARG:HD3	2.46	0.50
1:B:166:LEU:CD2	1:B:166:LEU:C	2.79	0.50
1:D:84:ARG:NH1	4:D:528:HOH:O	2.38	0.50
1:C:8:LYS:HG3	1:C:31:LEU:HD21	1.94	0.50
1:A:204:TRP:HB2	1:A:283:MSE:CE	2.40	0.50
1:C:53:ASP:OD1	1:C:55:SER:OG	2.30	0.50
1:B:39:TYR:HB3	1:B:199:LYS:HD2	1.92	0.50
1:B:9:ASN:O	1:B:13:SER:OG	2.29	0.50
1:D:50:ASP:CG	1:D:56:LYS:CE	2.78	0.50
1:D:57:THR:HG23	1:D:58:LEU:C	2.31	0.50
1:A:53:ASP:OD1	1:A:55:SER:OG	2.29	0.50
1:C:26:GLU:HB3	1:C:306:ILE:CD1	2.42	0.50
1:B:272:ARG:CD	4:B:521:HOH:O	2.54	0.50
1:A:305:LYS:C	1:A:307:SER:H	2.15	0.50
1:D:133:GLU:O	1:D:172:LEU:HA	2.12	0.49
1:D:50:ASP:HA	1:D:56:LYS:CD	2.42	0.49
1:B:22:LEU:HB3	1:B:26:GLU:OE1	2.12	0.49
1:A:172:LEU:CD2	1:A:172:LEU:N	2.65	0.49
1:B:50:ASP:OD1	1:B:56:LYS:HE2	2.13	0.49
1:D:28:ASN:ND2	1:D:28:ASN:N	2.60	0.49
1:B:157:ARG:HD2	1:B:161:TYR:CD1	2.47	0.49
1:C:122:ASN:O	1:C:122:ASN:OD1	2.30	0.49
1:B:50:ASP:HA	1:B:56:LYS:HD2	1.94	0.49
1:A:122:ASN:OD1	1:A:122:ASN:O	2.30	0.49
1:A:51:THR:HG21	1:A:74:ALA:N	2.23	0.49
1:B:157:ARG:HB3	1:B:161:TYR:HB2	1.94	0.49
1:C:204:TRP:HB2	1:C:283:MSE:HE3	1.94	0.49
1:B:96:LYS:HG2	1:B:97:VAL:HG23	1.95	0.49
1:A:26:GLU:O	1:A:30:ILE:HG12	2.13	0.49
1:B:66:PRO:HB2	1:B:68:HIS:O	2.12	0.49
1:C:169:LYS:HD3	1:C:171:LEU:HD21	1.94	0.49
1:B:145:GLU:HG3	1:B:148:ARG:HH22	1.74	0.49
1:A:91:LYS:O	1:A:95:ARG:CG	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:VAL:O	1:A:86:SER:OG	2.29	0.49
1:D:68:HIS:HD2	1:D:77:GLU:HB3	1.77	0.49
1:C:51:THR:HG22	1:C:53:ASP:OD1	2.11	0.49
1:A:200:ASN:N	1:A:201:PRO:CD	2.75	0.49
1:C:293:LEU:O	1:C:297:ILE:HG13	2.13	0.49
1:C:84:ARG:HB2	1:C:85:PRO:HD3	1.94	0.48
1:A:158:VAL:HG13	1:A:159:PRO:HA	1.95	0.48
1:A:133:GLU:O	1:A:172:LEU:HA	2.13	0.48
1:C:41:PRO:HD2	1:C:42:GLU:H	1.79	0.48
1:D:140:PHE:CG	1:D:155:LEU:HD13	2.48	0.48
1:D:84:ARG:N	1:D:85:PRO:CD	2.76	0.48
1:C:84:ARG:HB2	1:C:85:PRO:CD	2.44	0.48
1:D:204:TRP:HB2	1:D:283:MSE:HE1	1.95	0.48
1:C:153:PHE:HE1	1:C:157:ARG:NH2	2.11	0.48
1:C:26:GLU:HB3	1:C:306:ILE:HD13	1.95	0.48
1:D:202:GLU:CG	1:D:292:PRO:HG3	2.43	0.48
1:B:3:ARG:NH2	1:B:38:ALA:O	2.46	0.48
1:A:84:ARG:N	1:A:85:PRO:CD	2.77	0.48
1:C:153:PHE:CD1	1:C:157:ARG:CZ	2.97	0.48
1:B:87:ARG:HA	4:B:516:HOH:O	2.14	0.48
1:D:83:VAL:O	1:D:86:SER:OG	2.30	0.48
1:C:229:LEU:CD2	1:C:274:LEU:HD13	2.44	0.48
1:C:284:ARG:HD2	1:C:284:ARG:HA	1.47	0.48
1:D:52:ALA:HB2	1:D:71:THR:C	2.32	0.48
1:B:109:TYR:CD1	1:B:143:LEU:HD21	2.48	0.48
1:D:50:ASP:OD1	1:D:56:LYS:CE	2.62	0.48
1:D:149:GLU:CA	1:D:149:GLU:OE2	2.62	0.48
1:D:75:ILE:CD1	1:D:144:PRO:CG	2.89	0.48
1:A:145:GLU:OE1	1:A:148:ARG:N	2.42	0.48
1:C:102:ASP:OD1	1:C:131:SER:OG	2.21	0.48
1:B:218:GLU:CD	1:B:260:LYS:HZ2	2.17	0.47
1:D:53:ASP:OD1	1:D:55:SER:OG	2.29	0.47
1:A:182:VAL:O	1:A:215:ARG:NH1	2.47	0.47
1:B:72:ALA:O	1:B:76:ARG:NE	2.39	0.47
1:C:285:ASP:OD1	1:C:290:LYS:HB2	2.14	0.47
1:C:200:ASN:ND2	1:C:202:GLU:OE1	2.47	0.47
1:B:106:GLY:N	1:B:133:GLU:OE2	2.34	0.47
1:B:49:ALA:CB	1:B:59:ILE:CD1	2.91	0.47
1:B:14:TYR:CD1	1:B:294:GLU:HG2	2.50	0.47
1:A:277:SER:HA	1:A:278:PRO:HD3	1.77	0.47
1:D:205:THR:O	1:D:209:LEU:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:51:THR:CG2	1:D:52:ALA:N	2.78	0.47
1:B:51:THR:HG23	1:B:53:ASP:H	1.79	0.47
1:C:39:TYR:HD2	1:C:39:TYR:C	2.17	0.47
1:A:147:TYR:O	1:A:150:ILE:HG22	2.15	0.47
1:C:76:ARG:CZ	1:C:247:GLU:OE1	2.63	0.47
1:C:81:LYS:O	1:C:223:VAL:HG13	2.15	0.47
1:A:126:ARG:HA	1:A:165:ARG:O	2.14	0.47
1:C:258:SER:OG	1:C:261:ALA:HB3	2.15	0.47
1:C:278:PRO:O	1:C:281:VAL:HG23	2.15	0.47
1:B:136:LEU:HD21	1:B:172:LEU:HD21	1.94	0.46
1:C:65:GLU:OE1	1:C:196:SER:HB3	2.16	0.46
1:A:204:TRP:HB2	1:A:283:MSE:HE1	1.97	0.46
1:B:51:THR:CG2	1:B:53:ASP:OD1	2.64	0.46
1:B:272:ARG:O	1:B:276:LEU:HB2	2.15	0.46
1:B:65:GLU:OE2	1:B:196:SER:OG	2.32	0.46
1:D:102:ASP:OD1	1:D:131:SER:OG	2.32	0.46
1:D:28:ASN:H	1:D:28:ASN:HD22	1.58	0.46
1:D:68:HIS:CD2	1:D:77:GLU:OE1	2.68	0.46
1:A:18:LYS:HD2	1:A:18:LYS:HA	1.48	0.46
1:A:51:THR:CG2	1:A:73:GLY:CA	2.75	0.46
1:D:47:GLU:C	1:D:48:ILE:HD12	2.27	0.46
1:B:137:LEU:O	1:B:140:PHE:CZ	2.66	0.46
1:D:272:ARG:HG2	1:D:276:LEU:HD12	1.97	0.46
1:B:178:ARG:HA	1:B:178:ARG:HD2	1.64	0.46
1:D:58:LEU:HD12	1:D:107:LEU:HD21	1.97	0.46
1:B:76:ARG:NH2	1:B:247:GLU:OE1	2.49	0.46
1:B:102:ASP:OD1	1:B:102:ASP:C	2.54	0.46
1:D:233:LYS:HG2	1:D:282:PRO:HD3	1.96	0.46
1:D:145:GLU:OE2	1:D:148:ARG:CZ	2.57	0.46
1:C:116:LYS:HE3	1:C:120:GLU:OE2	2.16	0.46
1:D:18:LYS:C	1:D:19:GLU:HG2	2.36	0.46
1:B:153:PHE:HE2	1:B:166:LEU:HD12	1.81	0.45
1:A:133:GLU:OE2	2:A:501:SAM:O3'	2.26	0.45
1:C:273:LYS:O	1:C:277:SER:HB3	2.16	0.45
1:A:152:GLU:CD	1:B:80:TYR:HH	2.19	0.45
1:A:222:TRP:HB3	1:A:257:ALA:HB3	1.98	0.45
1:C:247:GLU:CD	1:C:250:ARG:CD	2.78	0.45
1:C:228:SER:HB3	1:C:231:VAL:HB	1.99	0.45
1:B:143:LEU:CG	1:B:151:HIS:ND1	2.79	0.45
1:A:304:TYR:CB	1:A:306:ILE:HD11	2.47	0.45
1:D:249:GLY:O	1:D:250:ARG:HD3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:76:ARG:NH1	1:C:250:ARG:CZ	2.80	0.45
1:D:203:LEU:HD23	1:D:203:LEU:HA	1.63	0.45
1:C:178:ARG:HD2	1:C:178:ARG:HA	1.78	0.45
1:D:14:TYR:CD1	1:D:294:GLU:HG2	2.52	0.45
1:D:65:GLU:OE1	1:D:196:SER:HB3	2.16	0.45
1:D:299:TYR:O	1:D:303:VAL:HG23	2.16	0.45
1:A:106:GLY:HA3	2:A:501:SAM:HG2	1.99	0.45
1:D:304:TYR:O	1:D:306:ILE:CD1	2.65	0.45
1:C:287:LYS:HB3	1:C:289:ASP:OD2	2.17	0.45
1:A:39:TYR:C	1:A:39:TYR:CD2	2.89	0.45
1:D:39:TYR:CD2	1:D:39:TYR:C	2.89	0.45
1:B:40:ASN:HB3	1:B:42:GLU:OE2	2.17	0.44
1:C:40:ASN:HA	1:C:41:PRO:HD3	1.70	0.44
1:A:25:GLU:OE1	1:A:25:GLU:CA	2.60	0.44
1:B:39:TYR:CD2	1:B:39:TYR:C	2.89	0.44
1:D:243:GLY:HA3	1:D:264:PRO:O	2.17	0.44
1:C:202:GLU:HG2	1:C:292:PRO:HG3	1.97	0.44
1:D:76:ARG:CZ	1:D:76:ARG:HB3	2.48	0.44
1:B:267:GLU:HG2	1:B:269:ASN:HD21	1.83	0.44
1:D:227:SER:CB	1:D:232:ARG:NH2	2.80	0.44
1:C:86:SER:O	1:C:87:ARG:HB2	2.17	0.44
1:B:203:LEU:HD11	2:B:401:SAM:C5	2.47	0.44
1:A:306:ILE:CG2	1:A:306:ILE:O	2.60	0.44
1:D:150:ILE:HD13	1:D:150:ILE:HA	1.60	0.44
1:B:277:SER:HA	1:B:278:PRO:HD3	1.79	0.44
1:A:290:LYS:HE2	1:A:298:ASP:OD2	2.18	0.44
1:B:53:ASP:OD1	1:B:55:SER:OG	2.30	0.44
1:C:79:LEU:HA	1:C:79:LEU:HD12	1.83	0.44
1:D:50:ASP:HA	1:D:56:LYS:HD3	2.00	0.44
1:D:50:ASP:OD1	1:D:56:LYS:HE2	2.17	0.44
1:B:166:LEU:HD23	1:B:166:LEU:C	2.37	0.44
1:C:76:ARG:NH1	1:C:250:ARG:NH1	2.65	0.44
1:B:264:PRO:HA	1:B:265:PRO:HD2	1.69	0.44
1:D:242:VAL:HG12	1:D:266:MSE:HE2	1.98	0.44
1:B:84:ARG:HB2	1:B:85:PRO:HD3	2.00	0.44
1:C:287:LYS:HB2	1:C:289:ASP:OD2	2.18	0.44
1:D:306:ILE:O	1:D:306:ILE:CG2	2.64	0.43
1:A:96:LYS:C	1:A:97:VAL:HG23	2.38	0.43
1:B:281:VAL:CG1	1:B:302:LYS:HG2	2.48	0.43
1:B:304:TYR:O	1:B:306:ILE:HG13	2.18	0.43
1:C:91:LYS:O	1:C:95:ARG:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:116:LYS:CE	1:C:120:GLU:OE2	2.67	0.43
1:C:211:LEU:HD11	1:C:288:LEU:CD1	2.48	0.43
1:A:39:TYR:O	1:A:41:PRO:HD3	2.17	0.43
1:D:183:GLU:O	1:D:184:ASN:HB2	2.18	0.43
1:D:57:THR:HG23	1:D:58:LEU:CA	2.48	0.43
1:C:30:ILE:HD12	1:C:301:LEU:HD23	1.99	0.43
1:D:145:GLU:CA	1:D:145:GLU:OE1	2.66	0.43
1:A:248:ILE:H	1:A:248:ILE:HG12	1.30	0.43
1:A:96:LYS:O	1:A:97:VAL:CG2	2.67	0.43
1:A:48:ILE:HG12	1:A:58:LEU:CD2	2.48	0.43
1:A:101:LEU:HD23	1:A:101:LEU:HA	1.81	0.43
1:D:56:LYS:HA	1:D:56:LYS:HD3	1.84	0.43
1:B:166:LEU:CD2	1:B:167:SER:N	2.79	0.43
1:C:91:LYS:O	1:C:95:ARG:CG	2.67	0.43
1:D:178:ARG:O	1:D:181:GLU:HG3	2.19	0.43
1:C:51:THR:HG21	1:C:74:ALA:H	1.83	0.43
1:A:44:SER:HA	1:A:62:THR:OG1	2.19	0.43
1:D:49:ALA:O	1:D:50:ASP:OD1	2.37	0.42
1:A:145:GLU:OE1	1:A:146:PRO:C	2.56	0.42
1:D:102:ASP:O	1:D:131:SER:HA	2.19	0.42
1:B:285:ASP:OD2	1:B:288:LEU:HA	2.19	0.42
1:B:150:ILE:H	1:B:150:ILE:HD13	1.70	0.42
1:D:274:LEU:HD12	1:D:274:LEU:HA	1.80	0.42
1:C:135:GLU:O	1:C:135:GLU:HG2	2.19	0.42
1:C:98:ILE:O	1:C:98:ILE:HG22	2.18	0.42
1:D:246:ARG:HG2	1:D:246:ARG:NH1	2.18	0.42
1:B:102:ASP:O	1:B:102:ASP:OD1	2.38	0.42
1:B:111:LEU:HA	1:B:111:LEU:HD23	1.75	0.42
1:B:122:ASN:OD1	1:B:122:ASN:C	2.58	0.42
1:C:76:ARG:CZ	1:C:76:ARG:HB3	2.50	0.42
1:B:49:ALA:CB	1:B:59:ILE:HD12	2.46	0.42
1:C:121:VAL:HG12	1:C:122:ASN:N	2.30	0.42
1:B:11:LEU:CD1	1:B:15:LEU:HD11	2.49	0.42
1:A:152:GLU:CD	1:B:80:TYR:OH	2.58	0.42
1:C:264:PRO:HA	1:C:265:PRO:HD3	1.79	0.42
1:D:202:GLU:HG2	1:D:292:PRO:HG3	2.02	0.42
1:B:115:LEU:HD23	1:B:115:LEU:HA	1.84	0.42
1:D:119:TRP:O	1:D:123:PRO:HD3	2.19	0.42
1:B:44:SER:HB3	1:D:249:GLY:C	2.40	0.42
1:C:106:GLY:HA3	2:C:401:SAM:HG2	2.02	0.42
1:A:135:GLU:HG2	1:A:135:GLU:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:VAL:HG12	1:B:282:PRO:O	2.20	0.41
1:A:285:ASP:OD2	1:A:288:LEU:HA	2.20	0.41
1:B:243:GLY:HA3	1:B:263:VAL:HG13	2.02	0.41
1:D:200:ASN:ND2	1:D:202:GLU:OE1	2.53	0.41
1:C:18:LYS:HD2	1:C:18:LYS:HA	1.70	0.41
1:A:164:GLU:CG	1:A:165:ARG:H	2.30	0.41
1:B:267:GLU:CB	1:B:270:GLU:OE1	2.69	0.41
1:D:31:LEU:O	1:D:35:LEU:HG	2.21	0.41
1:A:264:PRO:HA	1:A:265:PRO:HD3	1.71	0.41
1:C:153:PHE:CZ	1:C:157:ARG:NE	2.89	0.41
1:C:150:ILE:C	1:C:150:ILE:CD1	2.89	0.41
1:C:200:ASN:N	1:C:201:PRO:HD3	2.34	0.41
1:A:200:ASN:N	1:A:201:PRO:HD3	2.35	0.41
1:D:153:PHE:CD1	1:D:157:ARG:NH1	2.86	0.41
1:A:84:ARG:HG2	1:A:84:ARG:H	1.62	0.41
1:D:96:LYS:HG3	1:D:97:VAL:HG23	2.03	0.41
1:A:14:TYR:CD1	1:A:294:GLU:HG2	2.54	0.41
1:D:264:PRO:HA	1:D:265:PRO:HD3	1.80	0.41
1:B:76:ARG:HH22	1:B:247:GLU:CD	2.25	0.41
1:C:39:TYR:HD2	1:C:39:TYR:O	2.03	0.41
1:C:150:ILE:HD13	1:C:150:ILE:HA	1.82	0.41
1:C:30:ILE:CD1	1:C:301:LEU:HD23	2.51	0.41
1:B:197:PRO:HA	1:B:204:TRP:CD1	2.56	0.41
1:D:143:LEU:HD22	1:D:144:PRO:HD2	2.03	0.41
1:A:51:THR:HG21	1:A:73:GLY:HA2	1.89	0.41
1:B:157:ARG:HD2	1:B:161:TYR:CG	2.56	0.41
1:B:84:ARG:N	1:B:85:PRO:CD	2.84	0.41
1:B:30:ILE:CD1	1:B:306:ILE:HD12	2.50	0.41
1:B:205:THR:HG21	1:B:285:ASP:HB2	2.03	0.41
1:D:253:LYS:CE	1:D:267:GLU:OE1	2.69	0.40
1:B:155:LEU:HA	1:B:155:LEU:HD23	1.74	0.40
1:C:32:ARG:HH11	1:C:32:ARG:HD3	1.72	0.40
1:A:134:LYS:HD3	2:A:501:SAM:C6	2.51	0.40
1:B:2:LYS:HB2	1:B:5:GLU:CD	2.41	0.40
1:C:84:ARG:NH2	4:C:529:HOH:O	2.54	0.40
1:D:284:ARG:HD2	1:D:284:ARG:HA	1.61	0.40
1:A:247:GLU:O	1:A:248:ILE:C	2.60	0.40
1:C:67:TYR:HA	2:C:401:SAM:HE1	2.04	0.40
1:D:87:ARG:O	1:D:91:LYS:HG3	2.21	0.40
1:A:53:ASP:C	1:A:53:ASP:OD1	2.59	0.40
1:D:72:ALA:O	1:D:76:ARG:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:299:TYR:O	1:B:303:VAL:HG23	2.21	0.40
1:A:293:LEU:HA	1:A:293:LEU:HD23	1.88	0.40
1:C:79:LEU:HD13	1:C:113:VAL:HG11	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	299/308 (97%)	291 (97%)	7 (2%)	1 (0%)	46	68
1	B	303/308 (98%)	298 (98%)	5 (2%)	0	100	100
1	C	303/308 (98%)	297 (98%)	6 (2%)	0	100	100
1	D	304/308 (99%)	298 (98%)	6 (2%)	0	100	100
All	All	1209/1232 (98%)	1184 (98%)	24 (2%)	1 (0%)	56	78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	265	PRO

5.3.2 Protein sidechains [i](#)

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	275/276 (100%)	231 (84%)	44 (16%)	3	5
1	B	276/276 (100%)	228 (83%)	48 (17%)	2	4
1	C	276/276 (100%)	225 (82%)	51 (18%)	2	3
1	D	277/276 (100%)	219 (79%)	58 (21%)	1	2
All	All	1104/1104 (100%)	903 (82%)	201 (18%)	2	3

All (201) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	LYS
1	A	22	LEU
1	A	25	GLU
1	A	36	ARG
1	A	39	TYR
1	A	40	ASN
1	A	48	ILE
1	A	51	THR
1	A	55	SER
1	A	69	SER
1	A	84	ARG
1	A	93	LYS
1	A	94	GLU
1	A	101	LEU
1	A	122	ASN
1	A	124	LYS
1	A	126	ARG
1	A	138	LYS
1	A	145	GLU
1	A	149	GLU
1	A	160	GLU
1	A	168	LEU
1	A	169	LYS
1	A	177	LYS
1	A	196	SER
1	A	199	LYS
1	A	200	ASN
1	A	201	PRO
1	A	202	GLU
1	A	206	LEU
1	A	207	ASP
1	A	209	LEU
1	A	215	ARG

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Mol	Chain	Res	Type
1	A	246	ARG
1	A	247	GLU
1	A	248	ILE
1	A	260	LYS
1	A	269	ASN
1	A	277	SER
1	A	283	MSE
1	A	284	ARG
1	A	302	LYS
1	A	306	ILE
1	A	307	SER
1	B	5	GLU
1	B	13	SER
1	B	16	ARG
1	B	19	GLU
1	B	20	VAL
1	B	21	SER
1	B	22	LEU
1	B	30	ILE
1	B	32	ARG
1	B	39	TYR
1	B	48	ILE
1	B	51	THR
1	B	57	THR
1	B	68	HIS
1	B	84	ARG
1	B	94	GLU
1	B	98	ILE
1	B	101	LEU
1	B	102	ASP
1	B	116	LYS
1	B	124	LYS
1	B	133	GLU
1	B	136	LEU
1	B	138	LYS
1	B	139	GLU
1	B	142	ILE
1	B	143	LEU
1	B	150	ILE
1	B	160	GLU
1	B	166	LEU
1	B	167	SER

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Mol	Chain	Res	Type
1	B	168	LEU
1	B	177	LYS
1	B	178	ARG
1	B	200	ASN
1	B	202	GLU
1	B	206	LEU
1	B	207	ASP
1	B	209	LEU
1	B	215	ARG
1	B	245	SER
1	B	246	ARG
1	B	251	LYS
1	B	253	LYS
1	B	260	LYS
1	B	269	ASN
1	B	281	VAL
1	B	302	LYS
1	C	3	ARG
1	C	4	GLU
1	C	16	ARG
1	C	18	LYS
1	C	19	GLU
1	C	25	GLU
1	C	36	ARG
1	C	39	TYR
1	C	40	ASN
1	C	42	GLU
1	C	51	THR
1	C	55	SER
1	C	68	HIS
1	C	76	ARG
1	C	84	ARG
1	C	86	SER
1	C	87	ARG
1	C	93	LYS
1	C	95	ARG
1	C	98	ILE
1	C	101	LEU
1	C	116	LYS
1	C	133	GLU
1	C	134	LYS
1	C	137	LEU

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Mol	Chain	Res	Type
1	C	139	GLU
1	C	150	ILE
1	C	160	GLU
1	C	172	LEU
1	C	181	GLU
1	C	183	GLU
1	C	196	SER
1	C	200	ASN
1	C	202	GLU
1	C	206	LEU
1	C	209	LEU
1	C	215	ARG
1	C	223	VAL
1	C	244	SER
1	C	245	SER
1	C	246	ARG
1	C	248	ILE
1	C	251	LYS
1	C	252	ARG
1	C	253	LYS
1	C	260	LYS
1	C	266	MSE
1	C	274	LEU
1	C	284	ARG
1	C	290	LYS
1	C	305	LYS
1	D	19	GLU
1	D	21	SER
1	D	25	GLU
1	D	28	ASN
1	D	30	ILE
1	D	39	TYR
1	D	40	ASN
1	D	42	GLU
1	D	43	GLU
1	D	48	ILE
1	D	55	SER
1	D	57	THR
1	D	59	ILE
1	D	61	LYS
1	D	68	HIS
1	D	71	THR

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Mol	Chain	Res	Type
1	D	76	ARG
1	D	94	GLU
1	D	96	LYS
1	D	101	LEU
1	D	107	LEU
1	D	116	LYS
1	D	131	SER
1	D	134	LYS
1	D	138	LYS
1	D	140	PHE
1	D	142	ILE
1	D	145	GLU
1	D	150	ILE
1	D	154	LEU
1	D	157	ARG
1	D	158	VAL
1	D	160	GLU
1	D	164	GLU
1	D	168	LEU
1	D	177	LYS
1	D	196	SER
1	D	200	ASN
1	D	202	GLU
1	D	206	LEU
1	D	209	LEU
1	D	215	ARG
1	D	223	VAL
1	D	226	SER
1	D	227	SER
1	D	246	ARG
1	D	248	ILE
1	D	250	ARG
1	D	251	LYS
1	D	253	LYS
1	D	268	GLU
1	D	269	ASN
1	D	281	VAL
1	D	283	MSE
1	D	284	ARG
1	D	305	LYS
1	D	306	ILE
1	D	307	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	68	HIS
1	A	269	ASN
1	B	28	ASN
1	B	269	ASN
1	C	28	ASN
1	C	46	GLN
1	C	68	HIS
1	D	9	ASN
1	D	28	ASN
1	D	68	HIS
1	D	70	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 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	SAM	A	501	-	21,29,29	2.11	4 (19%)	17,42,42	2.23	3 (17%)
2	SAM	B	401	-	21,29,29	2.14	4 (19%)	17,42,42	2.28	4 (23%)
3	BEN	B	402	-	9,9,9	0.79	0	9,11,11	0.65	0
2	SAM	C	401	-	21,29,29	2.05	4 (19%)	17,42,42	2.38	4 (23%)
3	BEN	C	402	-	9,9,9	1.39	1 (11%)	9,11,11	0.95	0
2	SAM	D	401	-	21,29,29	2.09	4 (19%)	17,42,42	2.30	5 (29%)

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	SAM	A	501	-	-	0/8/33/33	0/3/3/3
2	SAM	B	401	-	-	0/8/33/33	0/3/3/3
3	BEN	B	402	-	-	0/4/4/4	0/1/1/1
2	SAM	C	401	-	-	0/8/33/33	0/3/3/3
3	BEN	C	402	-	-	0/4/4/4	0/1/1/1
2	SAM	D	401	-	-	0/8/33/33	0/3/3/3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	SAM	CG-SD	-7.96	1.63	1.80
2	B	401	SAM	CG-SD	-7.77	1.64	1.80
2	C	401	SAM	CG-SD	-7.53	1.64	1.80
2	A	501	SAM	CG-SD	-7.48	1.64	1.80
3	C	402	BEN	C-N2	-2.72	1.27	1.33
2	A	501	SAM	C5-N7	-2.65	1.30	1.39
2	C	401	SAM	C5-N7	-2.60	1.30	1.39
2	D	401	SAM	C5-N7	-2.44	1.31	1.39
2	B	401	SAM	C5-N7	-2.40	1.31	1.39
2	A	501	SAM	C4-N3	-2.30	1.32	1.35
2	D	401	SAM	CE-SD	-2.27	1.62	1.78
2	C	401	SAM	CE-SD	-2.22	1.63	1.78
2	A	501	SAM	CE-SD	-2.19	1.63	1.78
2	C	401	SAM	C4-N3	-2.14	1.32	1.35
2	B	401	SAM	CE-SD	-2.11	1.63	1.78
2	B	401	SAM	C4-N3	-2.11	1.32	1.35
2	D	401	SAM	C4-N3	-2.10	1.32	1.35

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	SAM	N3-C2-N1	-7.99	122.78	128.89
2	A	501	SAM	N3-C2-N1	-7.34	123.28	128.89
2	D	401	SAM	N3-C2-N1	-6.91	123.60	128.89
2	B	401	SAM	N3-C2-N1	-6.15	124.18	128.89
2	B	401	SAM	C4-C5-N7	-4.13	105.68	109.48
2	D	401	SAM	C4-C5-N7	-3.64	106.13	109.48
2	B	401	SAM	C2'-C1'-N9	-3.48	108.97	114.29
2	D	401	SAM	C2'-C1'-N9	-3.31	109.23	114.29
2	A	501	SAM	C4-C5-N7	-3.27	106.47	109.48
2	C	401	SAM	C2'-C1'-N9	-2.95	109.79	114.29
2	B	401	SAM	O3'-C3'-C4'	-2.90	102.36	111.05
2	C	401	SAM	C4'-O4'-C1'	-2.46	107.02	109.72
2	C	401	SAM	O4'-C1'-N9	2.08	112.45	108.10
2	D	401	SAM	C2-N1-C6	2.11	122.55	118.77
2	D	401	SAM	O4'-C1'-N9	2.18	112.66	108.10
2	A	501	SAM	O4'-C1'-N9	2.48	113.28	108.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	SAM	7	0
2	B	401	SAM	3	0
3	B	402	BEN	1	0
2	C	401	SAM	4	0
3	C	402	BEN	2	0
2	D	401	SAM	6	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th 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 ²)	Q<0.9
1	A	301/308 (97%)	-0.35	0 100 100	25, 42, 71, 144	0
1	B	303/308 (98%)	-0.21	1 (0%) 94 95	23, 48, 83, 107	0
1	C	303/308 (98%)	-0.21	1 (0%) 94 95	26, 51, 79, 119	0
1	D	304/308 (98%)	-0.06	3 (0%) 84 86	27, 49, 84, 114	0
All	All	1211/1232 (98%)	-0.21	5 (0%) 93 93	23, 47, 81, 144	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	52	ALA	7.2
1	C	248	ILE	3.9
1	B	142	ILE	2.6
1	D	251	LYS	2.5
1	D	49	ALA	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, 95th 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 ²)	Q<0.9
3	BEN	C	402	9/9	0.90	0.23	5.32	39,44,54,70	0
3	BEN	B	402	9/9	0.94	0.22	2.79	53,57,62,62	0
2	SAM	C	401	27/27	0.95	0.14	0.32	47,55,64,69	0
2	SAM	D	401	27/27	0.95	0.14	0.25	37,50,65,66	0
2	SAM	B	401	27/27	0.95	0.14	-0.09	43,54,63,71	0
2	SAM	A	501	27/27	0.96	0.12	-0.60	29,39,49,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.