



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:06 PM GMT

PDB ID : 1RZR
Title : crystal structure of transcriptional regulator-phosphoprotein-DNA complex
Authors : Schumacher, M.A.; Allen, G.S.; Brennan, R.G.
Deposited on : 2003-12-27
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
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

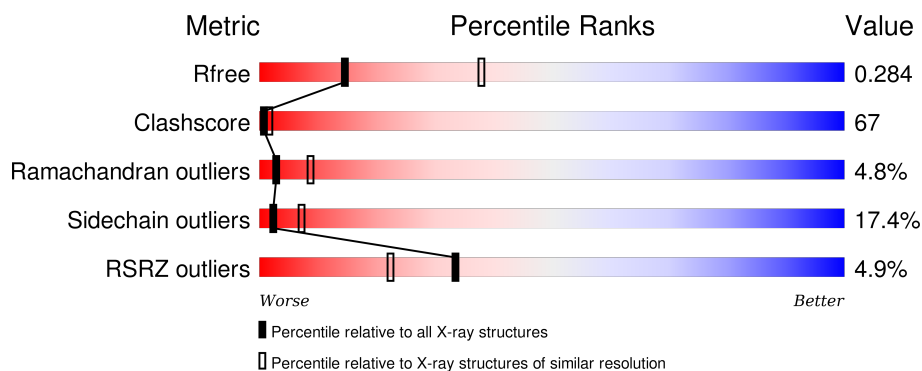
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	E	16	88% 13%
1	H	16	88% 13%
2	B	16	75% 25%
2	R	16	6% 81% 13%
3	A	332	5% 24% 60% 15% .

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Mol	Chain	Length	Quality of chain
3	C	332	
3	G	332	
4	D	332	
5	L	88	
5	S	88	
5	T	88	
5	Y	88	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	SEP	Y	46	-	-	X	-
6	SO4	A	946	-	-	-	X
6	SO4	C	846	-	-	-	X
6	SO4	C	947	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 14194 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 DNA chain called 5'-D(*CP*TP*GP*AP*AP*AP*GP*CP*GP*CP*TP*AP*AP*CP*AP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	16	Total	C	N	O	P	0	0	0
			327	156	66	90	15			
1	E	16	Total	C	N	O	P	0	0	0
			327	156	66	90	15			

- Molecule 2 is a DNA chain called 5'-D(*CP*TP*GP*TP*TP*AP*GP*CP*GP*CP*TP*TP*TP*CP*AP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	R	16	Total	C	N	O	P	0	0	0
			323	156	54	98	15			
2	B	16	Total	C	N	O	P	0	0	0
			323	156	54	98	15			

- Molecule 3 is a protein called Glucose-resistance amylase regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	332	Total	C	N	O	Se	0	0	0
			2564	1610	438	506	10			
3	C	332	Total	C	N	O	Se	0	0	0
			2558	1606	437	505	10			
3	A	332	Total	C	N	O	Se	0	0	0
			2562	1608	437	507	10			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP P46828
A	16	MSE	MET	MODIFIED RESIDUE	UNP P46828
A	88	MSE	MET	MODIFIED RESIDUE	UNP P46828
A	112	MSE	MET	MODIFIED RESIDUE	UNP P46828

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Chain	Residue	Modelled	Actual	Comment	Reference
A	123	MSE	MET	MODIFIED RESIDUE	UNP P46828
A	250	MSE	MET	MODIFIED RESIDUE	UNP P46828
A	282	MSE	MET	MODIFIED RESIDUE	UNP P46828
A	294	MSE	MET	MODIFIED RESIDUE	UNP P46828
A	302	MSE	MET	MODIFIED RESIDUE	UNP P46828
A	309	MSE	MET	MODIFIED RESIDUE	UNP P46828
C	1	MSE	MET	MODIFIED RESIDUE	UNP P46828
C	16	MSE	MET	MODIFIED RESIDUE	UNP P46828
C	88	MSE	MET	MODIFIED RESIDUE	UNP P46828
C	112	MSE	MET	MODIFIED RESIDUE	UNP P46828
C	123	MSE	MET	MODIFIED RESIDUE	UNP P46828
C	250	MSE	MET	MODIFIED RESIDUE	UNP P46828
C	282	MSE	MET	MODIFIED RESIDUE	UNP P46828
C	294	MSE	MET	MODIFIED RESIDUE	UNP P46828
C	302	MSE	MET	MODIFIED RESIDUE	UNP P46828
C	309	MSE	MET	MODIFIED RESIDUE	UNP P46828
G	1	MSE	MET	MODIFIED RESIDUE	UNP P46828
G	16	MSE	MET	MODIFIED RESIDUE	UNP P46828
G	88	MSE	MET	MODIFIED RESIDUE	UNP P46828
G	112	MSE	MET	MODIFIED RESIDUE	UNP P46828
G	123	MSE	MET	MODIFIED RESIDUE	UNP P46828
G	250	MSE	MET	MODIFIED RESIDUE	UNP P46828
G	282	MSE	MET	MODIFIED RESIDUE	UNP P46828
G	294	MSE	MET	MODIFIED RESIDUE	UNP P46828
G	302	MSE	MET	MODIFIED RESIDUE	UNP P46828
G	309	MSE	MET	MODIFIED RESIDUE	UNP P46828

- Molecule 4 is a protein called Glucose-resistance amylase regulator.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	D	332	Total	C	N	O	S	Se	0	0	0
			2558	1606	437	505	1	9			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	16	MSE	MET	MODIFIED RESIDUE	UNP P46828
D	88	MSE	MET	MODIFIED RESIDUE	UNP P46828
D	112	MSE	MET	MODIFIED RESIDUE	UNP P46828
D	123	MSE	MET	MODIFIED RESIDUE	UNP P46828
D	250	MSE	MET	MODIFIED RESIDUE	UNP P46828
D	282	MSE	MET	MODIFIED RESIDUE	UNP P46828

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Chain	Residue	Modelled	Actual	Comment	Reference
D	294	MSE	MET	MODIFIED RESIDUE	UNP P46828
D	302	MSE	MET	MODIFIED RESIDUE	UNP P46828
D	309	MSE	MET	MODIFIED RESIDUE	UNP P46828

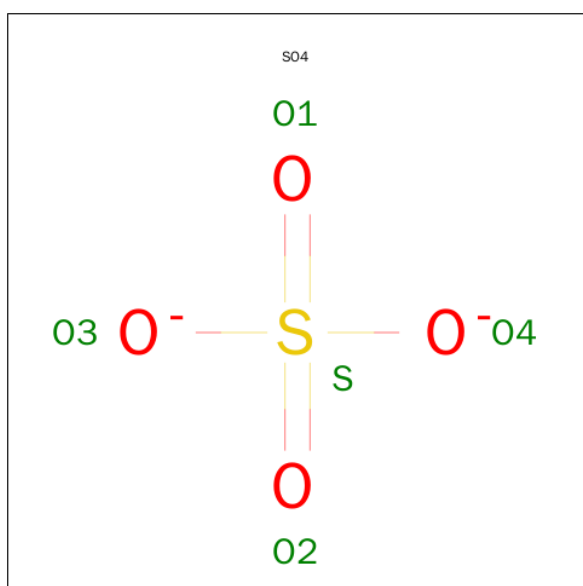
- Molecule 5 is a protein called Phosphocarrier protein HPr.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
5	T	87	Total	C	N	O	P	S	0	0	0
			632	386	104	138	1	3			
5	L	87	Total	C	N	O	P	S	0	0	0
			632	386	104	138	1	3			
5	Y	87	Total	C	N	O	P	S	0	0	0
			632	386	104	138	1	3			
5	S	87	Total	C	N	O	P	S	0	0	0
			632	386	104	138	1	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	46	SEP	SER	MODIFIED RESIDUE	UNP O69250
T	46	SEP	SER	MODIFIED RESIDUE	UNP O69250
L	46	SEP	SER	MODIFIED RESIDUE	UNP O69250
Y	46	SEP	SER	MODIFIED RESIDUE	UNP O69250

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O S 5 4 1	0	0
6	A	1	Total O S 5 4 1	0	0
6	C	1	Total O S 5 4 1	0	0
6	C	1	Total O S 5 4 1	0	0
6	G	1	Total O S 5 4 1	0	0
6	G	1	Total O S 5 4 1	0	0
6	C	1	Total O S 5 4 1	0	0

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Mg 1 1	0	0
7	D	1	Total Mg 1 1	0	0

- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	17	Total O 17 17	0	0
8	B	1	Total O 1 1	0	0
8	C	13	Total O 13 13	0	0
8	D	12	Total O 12 12	0	0
8	E	2	Total O 2 2	0	0
8	G	10	Total O 10 10	0	0
8	H	1	Total O 1 1	0	0
8	L	4	Total O 4 4	0	0
8	R	1	Total O 1 1	0	0

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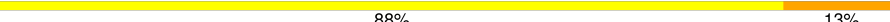
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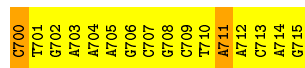
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	S	7	Total 7	O 7	0	0
8	T	9	Total 9	O 9	0	0
8	Y	10	Total 10	O 10	0	0

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.

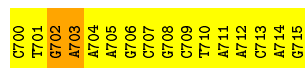
- Molecule 1: 5'-D(*CP*TP*GP*AP*AP*AP*GP*CP*GP*CP*TP*AP*AP*CP*AP*G)-3'

Chain H: 



- Molecule 1: 5'-D(*CP*TP*GP*AP*AP*AP*GP*CP*GP*CP*TP*AP*AP*CP*AP*G)-3'

Chain E: 



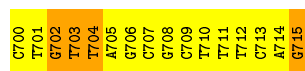
- Molecule 2: 5'-D(*CP*TP*GP*TP*TP*AP*GP*CP*GP*CP*TP*TP*TP*CP*AP*G)-3'

Chain R: 



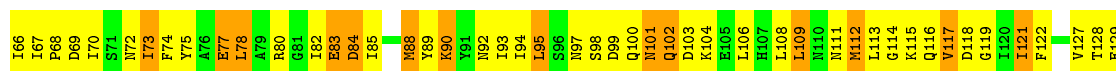
- Molecule 2: 5'-D(*CP*TP*GP*TP*TP*AP*GP*CP*GP*CP*TP*TP*TP*CP*AP*G)-3'

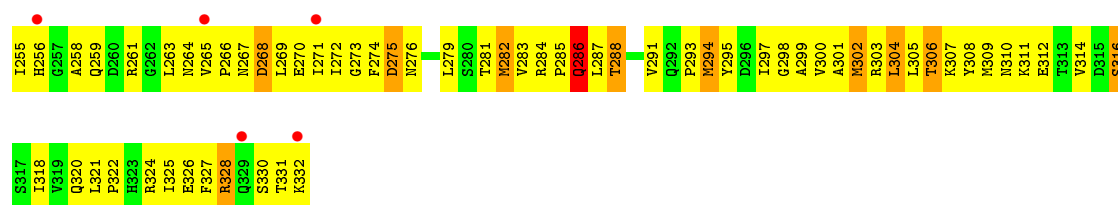
Chain B: 



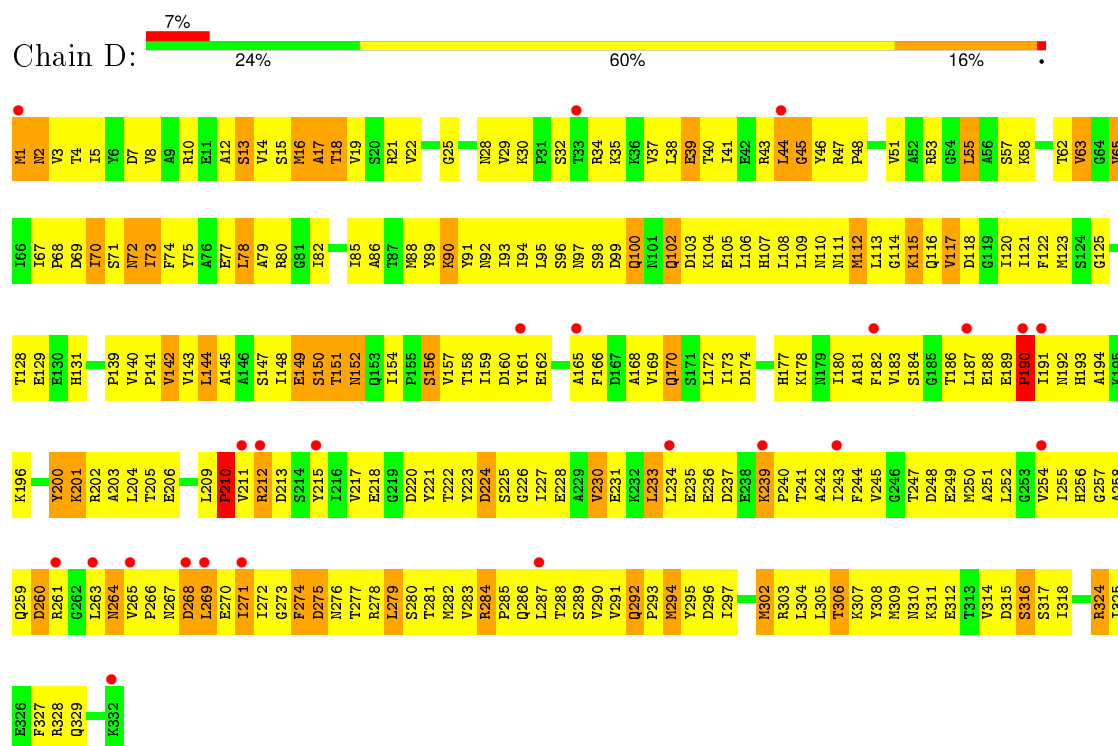
- Molecule 3: Glucose-resistance amylase regulator

Chain G: 

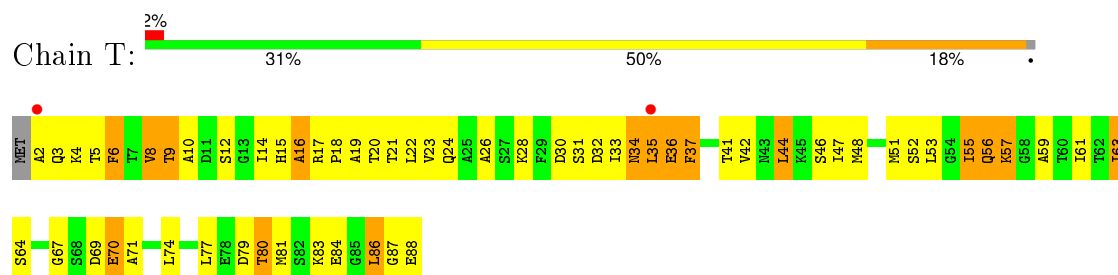




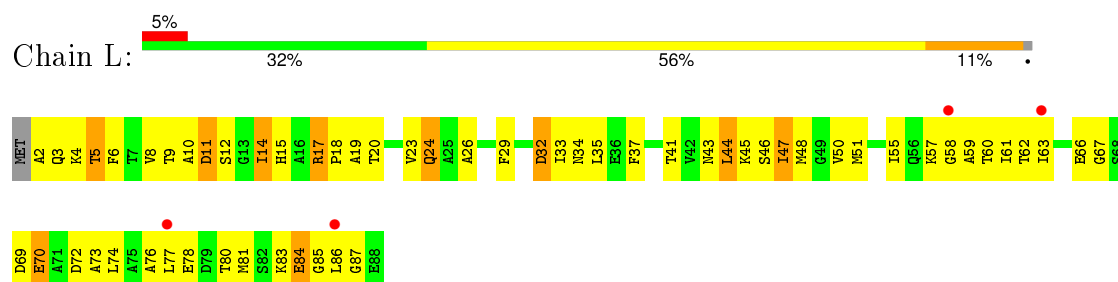
• Molecule 4: Glucose-resistance amylase regulator



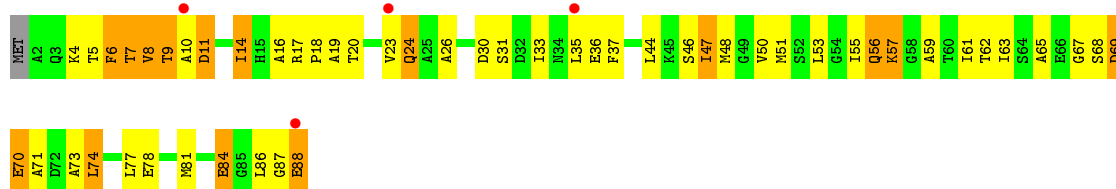
• Molecule 5: Phosphocarrier protein HPr



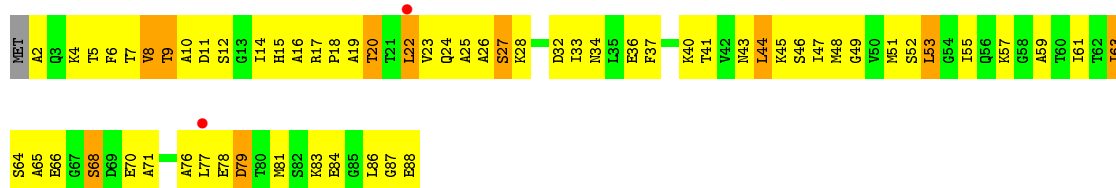
• Molecule 5: Phosphocarrier protein HPr



● Molecule 5: Phosphocarrier protein HPr

Chain Y: 

● Molecule 5: Phosphocarrier protein HPr

Chain S: 

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.71Å 109.24Å 117.81Å 90.00° 90.05° 90.00°	Depositor
Resolution (Å)	78.70 – 2.80 78.71 – 2.80	Depositor EDS
% Data completeness (in resolution range)	86.8 (78.70-2.80) 86.6 (78.71-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.82Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.242 , 0.288 0.240 , 0.284	Depositor DCC
R_{free} test set	5845 reflections (10.17%)	DCC
Wilson B-factor (Å ²)	81.1	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 79.2	EDS
Estimated twinning fraction	0.037 for -k,-h,-l 0.038 for k,h,-l 0.349 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	2 of 57480 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14194	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.32% 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: MG, SO4, SEP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	E	0.75	0/368	0.89	0/566
1	H	1.03	3/368 (0.8%)	0.94	1/566 (0.2%)
2	B	0.70	0/360	0.95	0/554
2	R	0.74	0/360	1.00	0/554
3	A	0.73	7/2590 (0.3%)	0.85	3/3492 (0.1%)
3	C	0.68	3/2586 (0.1%)	0.85	3/3486 (0.1%)
3	G	0.73	4/2593 (0.2%)	0.93	8/3498 (0.2%)
4	D	0.66	3/2586 (0.1%)	0.83	1/3486 (0.0%)
5	L	0.51	0/625	0.75	0/839
5	S	0.54	0/625	0.76	0/839
5	T	0.53	0/625	0.75	0/839
5	Y	0.56	0/625	0.87	1/839 (0.1%)
All	All	0.69	20/14311 (0.1%)	0.86	17/19558 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	E	0	2
1	H	0	1
2	B	0	4
2	R	0	2
4	D	0	1
5	Y	0	1
All	All	0	11

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1	MSE	SE-CE	11.43	2.62	1.95
3	A	129	GLU	CD-OE1	9.85	1.36	1.25
4	D	129	GLU	CD-OE1	9.60	1.36	1.25
3	C	129	GLU	CD-OE1	8.89	1.35	1.25
3	C	129	GLU	CD-OE2	8.75	1.35	1.25
1	H	711	DA	N9-C4	7.94	1.42	1.37
3	G	129	GLU	CD-OE2	6.79	1.33	1.25
4	D	1	MET	SD-CE	6.75	2.15	1.77
1	H	711	DA	N3-C4	6.61	1.38	1.34
3	A	286	GLN	CG-CD	5.87	1.64	1.51
3	A	286	GLN	CB-CG	5.81	1.68	1.52
3	G	2	ASN	CB-CG	-5.76	1.37	1.51
3	G	129	GLU	CD-OE1	5.75	1.31	1.25
3	G	2	ASN	CG-OD1	5.65	1.36	1.24
3	A	302	MSE	SE-CE	-5.50	1.62	1.95
4	D	129	GLU	CG-CD	5.43	1.60	1.51
3	A	129	GLU	CG-CD	5.39	1.60	1.51
3	C	320	GLN	CG-CD	5.20	1.63	1.51
1	H	711	DA	C2-N3	5.11	1.38	1.33
3	A	112	MSE	CG-SE	-5.03	1.78	1.95

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	711	DA	C8-N9-C4	-9.02	102.19	105.80
3	A	236	GLU	N-CA-C	-7.22	91.49	111.00
3	A	95	LEU	CA-CB-CG	6.44	130.10	115.30
3	G	3	VAL	N-CA-C	6.43	128.36	111.00
3	C	1	MSE	CB-CG-SE	-6.39	93.53	112.70
3	G	95	LEU	CA-CB-CG	6.27	129.71	115.30
3	C	129	GLU	OE1-CD-OE2	6.19	130.73	123.30
3	C	87	THR	OG1-CB-CG2	-6.19	95.77	110.00
3	G	109	LEU	CA-CB-CG	-5.89	101.74	115.30
3	G	29	VAL	N-CA-C	-5.84	95.23	111.00
3	G	4	THR	N-CA-C	5.45	125.72	111.00
3	G	21	ARG	NE-CZ-NH2	-5.37	117.61	120.30
5	Y	7	THR	CA-C-O	-5.35	108.87	120.10
3	A	94	ILE	N-CA-C	-5.23	96.87	111.00
4	D	236	GLU	N-CA-C	5.16	124.92	111.00
3	G	1	MSE	CB-CA-C	5.07	120.53	110.40
3	G	47	ARG	N-CA-C	-5.00	97.49	111.00

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	702	DG	Sidechain
2	B	703	DT	Sidechain
2	B	704	DT	Sidechain
2	B	715	DG	Sidechain
4	D	200	TYR	Sidechain
1	E	702	DG	Sidechain
1	E	703	DA	Sidechain
1	H	700	DC	Sidechain
2	R	712	DT	Sidechain
2	R	715	DG	Sidechain
5	Y	7	THR	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	327	0	180	52	0
1	H	327	0	180	56	0
2	B	323	0	184	43	0
2	R	323	0	184	57	0
3	A	2562	0	2587	389	0
3	C	2558	0	2584	386	1
3	G	2564	0	2594	374	1
4	D	2558	0	2584	376	0
5	L	632	0	624	70	0
5	S	632	0	624	69	0
5	T	632	0	624	79	0
5	Y	632	0	624	69	0
6	A	10	0	0	1	0
6	C	15	0	0	1	0
6	G	10	0	0	0	0
7	A	1	0	0	0	0
7	D	1	0	0	0	0
8	A	17	0	0	0	0
8	B	1	0	0	0	0
8	C	13	0	0	0	0
8	D	12	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	E	2	0	0	0	0
8	G	10	0	0	0	0
8	H	1	0	0	0	0
8	L	4	0	0	0	0
8	R	1	0	0	0	0
8	S	7	0	0	0	0
8	T	9	0	0	0	0
8	Y	10	0	0	0	0
All	All	14194	0	13573	1861	1

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 67.

All (1861) 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)
3:C:1:MSE:CE	3:C:1:MSE:SE	2.20	1.40
4:D:1:MET:SD	4:D:1:MET:CE	2.15	1.34
3:G:139:PRO:CG	3:C:1:MSE:HE2	1.66	1.26
3:G:73:ILE:CG2	3:C:278:ARG:HH22	1.53	1.22
3:G:73:ILE:HG22	3:C:278:ARG:NH2	1.54	1.21
3:C:305:LEU:HG	3:C:309:MSE:HE2	1.25	1.16
2:R:700:DC:H2"	2:R:701:DT:H5"	1.16	1.15
4:D:231:GLU:HA	4:D:261:ARG:HH22	1.10	1.14
3:A:284:ARG:HB2	3:A:285:PRO:HD3	1.24	1.14
5:T:36:GLU:HB2	5:T:41:THR:HG22	1.22	1.13
4:D:41:ILE:HG23	4:D:46:TYR:HB3	1.27	1.13
5:Y:18:PRO:HB3	5:Y:86:LEU:HD21	1.24	1.13
3:C:303:ARG:HH12	3:C:307:LYS:HE3	1.18	1.09
3:A:55:LEU:HD12	4:D:55:LEU:HD12	1.33	1.08
3:A:111:ASN:ND2	6:A:946:SO4:O3	1.86	1.08
5:S:26:ALA:HB2	5:S:77:LEU:HD21	1.14	1.08
3:C:231:GLU:HB2	3:C:261:ARG:HH21	1.07	1.08
3:C:255:ILE:HG23	3:C:265:VAL:HG21	1.30	1.08
3:C:212:ARG:H	3:C:212:ARG:HD2	1.14	1.07
4:D:149:GLU:HG2	4:D:154:ILE:HD11	1.36	1.07
3:G:49:ASN:HD21	3:G:52:ALA:HB3	1.20	1.06
3:C:232:LYS:O	3:C:236:GLU:HG2	1.55	1.06
5:S:9:THR:HG22	5:S:87:GLY:HA2	1.37	1.06
2:B:713:DC:H2"	2:B:714:DA:H5"	1.37	1.06
5:Y:14:ILE:O	5:Y:14:ILE:HD13	1.55	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:139:PRO:HG3	3:C:1:MSE:HE2	1.07	1.05
5:T:79:ASP:HB3	5:T:83:LYS:HE2	1.38	1.04
5:Y:9:THR:HG22	5:Y:87:GLY:HA2	1.39	1.04
3:G:284:ARG:HB2	3:G:285:PRO:HD3	1.38	1.03
3:G:139:PRO:CG	3:C:1:MSE:CE	2.37	1.01
3:C:22:VAL:HG11	3:C:37:VAL:HG11	1.39	1.01
4:D:82:ILE:HG23	4:D:302:MSE:HG2	1.39	1.01
5:T:26:ALA:HB2	5:T:77:LEU:HD21	1.42	1.00
3:A:12:ALA:HA	3:A:36:LYS:HE3	1.36	1.00
5:T:14:ILE:HD12	5:T:55:ILE:HG21	1.40	1.00
4:D:288:THR:HG23	4:D:327:PHE:HA	1.42	1.00
3:A:7:ASP:HB3	3:A:44:LEU:HD21	1.40	0.99
3:C:148:ILE:HG12	3:C:190:PRO:HB2	1.45	0.98
4:D:231:GLU:HA	4:D:261:ARG:NH2	1.77	0.98
3:A:212:ARG:HD2	3:A:212:ARG:H	1.27	0.98
3:A:1:MSE:CE	3:A:1:MSE:SE	2.62	0.97
4:D:69:ASP:OD2	4:D:71:SER:HB3	1.64	0.97
4:D:284:ARG:HB3	4:D:285:PRO:HD3	1.43	0.97
4:D:63:VAL:HG21	4:D:302:MSE:HE1	1.45	0.97
3:A:326:GLU:HB3	3:A:328:ARG:HH12	1.26	0.97
3:G:284:ARG:HH21	3:C:284:ARG:HA	1.29	0.96
4:D:204:LEU:HD23	4:D:211:VAL:HG12	1.48	0.96
2:R:700:DC:C2'	2:R:701:DT:H5''	1.95	0.96
1:E:712:DA:H2''	1:E:713:DC:H5''	1.44	0.95
3:G:47:ARG:HH22	3:C:113:LEU:HD12	1.29	0.95
3:G:90:LYS:O	3:G:90:LYS:HG2	1.66	0.95
3:G:139:PRO:HG3	3:C:1:MSE:CE	1.95	0.95
3:A:152:ASN:HD22	3:A:318:ILE:HG12	1.32	0.94
4:D:169:VAL:HG23	4:D:172:LEU:HD12	1.50	0.94
4:D:182:PHE:HE1	4:D:184:SER:HG	1.02	0.94
1:H:709:DC:H5'	1:H:709:DC:H6	1.30	0.93
5:S:70:GLU:HG3	5:S:71:ALA:H	1.30	0.93
2:R:702:DG:H2''	2:R:703:DT:H5'	1.48	0.93
4:D:180:ILE:HG22	4:D:242:ALA:HB3	1.49	0.93
3:C:74:PHE:HE2	3:C:294:MSE:HG2	1.32	0.93
3:C:191:ILE:HD11	3:C:196:LYS:NZ	1.84	0.93
3:A:1:MSE:HG2	3:A:47:ARG:HH11	1.33	0.92
3:G:49:ASN:HD21	3:G:52:ALA:CB	1.81	0.92
3:C:74:PHE:CE2	3:C:294:MSE:HG2	2.04	0.92
3:C:288:THR:HG23	3:C:327:PHE:HA	1.52	0.92
3:C:148:ILE:HG12	3:C:190:PRO:CB	2.00	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:11:GLU:HG2	3:A:40:THR:HG22	1.50	0.92
2:B:701:DT:H2"	2:B:702:DG:H5'	1.52	0.91
3:C:180:ILE:HD11	3:C:204:LEU:HD21	1.51	0.91
3:A:63:VAL:HG21	3:A:302:MSE:HE1	1.53	0.91
3:G:220:ASP:OD2	3:G:225:SER:HB3	1.69	0.91
3:G:73:ILE:HD11	3:G:277:THR:HG22	1.52	0.90
3:A:121:ILE:HD11	3:A:302:MSE:HE2	1.51	0.90
3:A:121:ILE:CD1	3:A:302:MSE:HE2	2.00	0.90
3:A:11:GLU:OE1	3:A:43:ARG:HD3	1.71	0.90
3:A:293:PRO:O	3:A:297:ILE:HG12	1.72	0.90
3:G:73:ILE:HG22	3:C:278:ARG:HH22	0.75	0.90
3:A:67:ILE:HD11	3:A:75:TYR:HB3	1.51	0.90
3:C:264:ASN:HD22	3:C:267:ASN:H	1.20	0.89
4:D:121:ILE:CD1	4:D:302:MSE:HE3	2.03	0.89
2:B:713:DC:C2'	2:B:714:DA:H5"	2.04	0.88
3:C:144:LEU:HD21	3:C:154:ILE:HG23	1.55	0.88
3:A:252:LEU:HD12	3:A:283:VAL:HG22	1.54	0.88
3:C:264:ASN:ND2	3:C:267:ASN:H	1.72	0.88
1:E:706:DG:OP1	1:E:706:DG:H4'	1.74	0.88
3:A:3:VAL:HG11	3:A:44:LEU:HG	1.55	0.88
3:G:293:PRO:HB2	3:G:296:ASP:HB2	1.56	0.87
4:D:264:ASN:HD21	4:D:267:ASN:HB2	1.37	0.87
3:G:73:ILE:HG13	3:G:74:PHE:N	1.89	0.87
5:L:11:ASP:HA	5:L:57:LYS:HE3	1.57	0.87
3:C:212:ARG:N	3:C:212:ARG:HD2	1.89	0.87
2:R:711:DT:H2"	2:R:712:DT:C6	2.09	0.86
4:D:154:ILE:O	4:D:154:ILE:HD12	1.76	0.86
3:A:1:MSE:HG2	3:A:47:ARG:NH1	1.90	0.85
2:R:705:DA:H2"	2:R:706:DG:O4'	1.74	0.85
3:G:65:VAL:HG12	3:G:121:ILE:HB	1.58	0.85
3:G:173:ILE:HD11	3:G:204:LEU:HD23	1.56	0.85
4:D:180:ILE:O	4:D:180:ILE:HD12	1.75	0.85
4:D:74:PHE:CE2	4:D:294:MSE:HG2	2.12	0.85
3:G:101:ASN:ND2	3:G:103:ASP:OD2	2.09	0.85
4:D:144:LEU:HB3	4:D:147:SER:OG	1.77	0.85
2:B:704:DT:H1'	2:B:705:DA:H5"	1.56	0.85
4:D:82:ILE:HG23	4:D:302:MSE:CG	2.06	0.84
3:G:70:ILE:HG23	3:G:97:ASN:OD1	1.76	0.84
3:G:274:PHE:O	3:G:275:ASP:HB2	1.77	0.84
3:C:105:GLU:OE1	3:C:122:PHE:HZ	1.60	0.84
1:E:714:DA:H2"	1:E:715:DG:H5"	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:143:VAL:HG23	3:G:156:SER:HA	1.58	0.84
2:R:712:DT:H2'	2:R:713:DC:C6	2.12	0.84
3:G:43:ARG:HH21	3:G:44:LEU:HB2	1.41	0.84
5:S:26:ALA:HB2	5:S:77:LEU:CD2	2.04	0.83
3:G:42:GLU:OE2	3:G:42:GLU:HA	1.78	0.83
1:H:707:DC:H6	1:H:707:DC:H5''	1.42	0.83
4:D:62:THR:HA	4:D:92:ASN:O	1.78	0.83
3:G:139:PRO:HG2	3:C:1:MSE:CE	2.09	0.83
3:A:29:VAL:HB	3:A:34:ARG:NH2	1.94	0.83
4:D:202:ARG:O	4:D:206:GLU:HB2	1.78	0.83
3:A:51:VAL:HG13	4:D:51:VAL:HG13	1.60	0.83
3:G:154:ILE:HD12	3:G:154:ILE:H	1.44	0.83
3:C:277:THR:HB	3:C:279:LEU:HD11	1.60	0.83
3:C:212:ARG:H	3:C:212:ARG:CD	1.91	0.83
5:T:36:GLU:CB	5:T:41:THR:HG22	2.05	0.82
3:C:252:LEU:HG	3:C:283:VAL:CG1	2.09	0.82
4:D:284:ARG:HB3	4:D:285:PRO:CD	2.09	0.82
2:R:712:DT:H2''	2:R:713:DC:O4'	1.79	0.82
5:Y:11:ASP:HA	5:Y:57:LYS:HE2	1.59	0.82
4:D:106:LEU:HD11	4:D:131:HIS:CD2	2.15	0.82
3:A:326:GLU:HB3	3:A:328:ARG:NH1	1.95	0.82
5:T:19:ALA:O	5:T:23:VAL:HG23	1.80	0.82
2:B:713:DC:H2''	2:B:714:DA:C5'	2.10	0.82
5:L:9:THR:O	5:L:57:LYS:HE2	1.80	0.82
3:C:231:GLU:HB2	3:C:261:ARG:NH2	1.92	0.82
1:E:714:DA:H2''	1:E:715:DG:O4'	1.80	0.82
3:A:284:ARG:HB2	3:A:285:PRO:CD	2.08	0.82
3:G:47:ARG:NH2	3:C:113:LEU:HD12	1.94	0.82
4:D:302:MSE:HE2	4:D:302:MSE:HA	1.61	0.82
3:A:259:GLN:HG3	3:A:284:ARG:NH2	1.94	0.81
3:C:28:ASN:O	3:C:29:VAL:HG23	1.80	0.81
2:R:700:DC:H2'	2:R:701:DT:C5	2.16	0.81
3:A:177:HIS:ND1	3:A:241:THR:HB	1.96	0.81
3:G:49:ASN:ND2	3:G:52:ALA:HB3	1.95	0.81
4:D:182:PHE:HB2	4:D:200:TYR:CE2	2.15	0.81
3:G:47:ARG:HH22	3:C:113:LEU:CD1	1.93	0.81
3:G:284:ARG:HB2	3:G:285:PRO:CD	2.11	0.81
3:A:41:ILE:HG12	3:A:46:TYR:HB3	1.63	0.81
5:L:37:PHE:HE2	5:L:59:ALA:HB1	1.44	0.80
5:S:27:SER:HA	5:S:45:LYS:HD3	1.62	0.80
3:A:180:ILE:HG22	3:A:242:ALA:HB3	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:180:ILE:HG22	3:C:242:ALA:HB3	1.63	0.80
2:B:701:DT:H2"	2:B:702:DG:C5'	2.11	0.80
3:A:217:VAL:HG11	3:A:233:LEU:HG	1.64	0.80
2:B:712:DT:H2'	2:B:713:DC:C5	2.16	0.80
4:D:259:GLN:HB2	4:D:284:ARG:NH2	1.97	0.80
5:T:32:ASP:O	5:T:33:ILE:HG13	1.82	0.80
5:Y:44:LEU:O	5:Y:44:LEU:HD13	1.82	0.80
3:A:288:THR:HG23	3:A:330:SER:HB3	1.64	0.79
3:A:305:LEU:HG	3:A:309:MSE:HE3	1.62	0.79
2:B:705:DA:H2"	2:B:706:DG:O4'	1.82	0.79
4:D:44:LEU:HD12	4:D:44:LEU:O	1.82	0.79
3:C:2:ASN:OD1	3:C:2:ASN:O	1.99	0.79
4:D:144:LEU:HD22	4:D:144:LEU:H	1.47	0.79
3:C:29:VAL:HG12	3:C:34:ARG:HB2	1.63	0.79
3:G:73:ILE:HG12	3:G:277:THR:HG21	1.65	0.79
3:C:252:LEU:HG	3:C:283:VAL:HG11	1.63	0.79
5:T:79:ASP:O	5:T:83:LYS:HG2	1.83	0.79
3:G:43:ARG:HH21	3:G:44:LEU:CB	1.95	0.79
3:G:73:ILE:HD11	3:G:277:THR:CG2	2.14	0.78
5:S:9:THR:HG22	5:S:87:GLY:CA	2.11	0.78
3:G:144:LEU:HD22	3:G:144:LEU:N	1.98	0.78
3:G:276:ASN:HD21	3:G:328:ARG:HH22	1.31	0.78
3:A:29:VAL:HB	3:A:34:ARG:HH21	1.49	0.78
3:A:36:LYS:O	3:A:39:GLU:HG3	1.83	0.78
4:D:22:VAL:HG21	4:D:37:VAL:HG11	1.66	0.78
3:C:303:ARG:HH11	3:C:303:ARG:HG3	1.48	0.78
3:C:35:LYS:O	3:C:39:GLU:HB2	1.82	0.78
3:A:247:THR:HG22	3:A:249:GLU:N	1.98	0.78
3:C:105:GLU:OE1	3:C:122:PHE:CZ	2.37	0.78
5:S:19:ALA:O	5:S:23:VAL:HG23	1.83	0.78
3:G:247:THR:HG22	3:G:250:MSE:H	1.48	0.77
3:C:190:PRO:O	3:C:194:ALA:HB3	1.84	0.77
3:C:194:ALA:O	3:C:198:LYS:HG3	1.84	0.77
3:G:102:GLN:O	3:G:106:LEU:HD13	1.83	0.77
4:D:41:ILE:CG2	4:D:46:TYR:HB3	2.13	0.77
4:D:255:ILE:HG23	4:D:265:VAL:HG21	1.65	0.77
3:G:284:ARG:HE	3:C:284:ARG:HG2	1.50	0.77
1:E:703:DA:N6	3:A:17:ALA:HB2	1.99	0.77
4:D:184:SER:HB2	4:D:192:ASN:ND2	1.99	0.77
5:Y:37:PHE:HB2	5:Y:61:ILE:HG22	1.66	0.77
1:E:714:DA:C2'	1:E:715:DG:H5"	2.14	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:132:VAL:HG12	3:A:136:LYS:HE2	1.67	0.77
4:D:304:LEU:HB2	5:Y:48:MET:HE3	1.66	0.77
3:G:63:VAL:HG21	3:G:302:MSE:HE1	1.66	0.76
1:H:709:DC:H5'	1:H:709:DC:C6	2.18	0.76
4:D:303:ARG:HH21	4:D:306:THR:HB	1.49	0.76
4:D:90:LYS:O	4:D:90:LYS:HG2	1.86	0.76
4:D:201:LYS:HD3	4:D:202:ARG:H	1.50	0.76
3:G:296:ASP:CG	5:L:51:MET:HG2	2.05	0.76
3:C:243:ILE:HG22	3:C:244:PHE:N	1.99	0.76
4:D:168:ALA:HB1	4:D:272:ILE:HG21	1.66	0.76
4:D:73:ILE:HD13	4:D:73:ILE:N	2.01	0.76
3:G:73:ILE:C	3:G:73:ILE:HD12	2.06	0.76
2:B:706:DG:H2''	2:B:707:DC:C5	2.21	0.76
5:L:67:GLY:O	5:L:70:GLU:HG3	1.86	0.76
3:G:139:PRO:HG2	3:C:1:MSE:HE1	1.66	0.75
3:G:217:VAL:CG1	3:G:233:LEU:HD21	2.16	0.75
1:H:714:DA:H2'	1:H:715:DG:C8	2.21	0.75
3:G:284:ARG:NE	3:C:284:ARG:HG2	2.00	0.75
3:A:170:GLN:HE21	3:A:170:GLN:HA	1.51	0.75
4:D:144:LEU:HD23	4:D:154:ILE:HD13	1.65	0.75
3:G:213:ASP:O	3:G:216:ILE:HG22	1.86	0.75
4:D:302:MSE:HE1	4:D:305:LEU:HD23	1.69	0.75
4:D:263:LEU:HD12	4:D:268:ASP:OD1	1.86	0.75
1:H:707:DC:H2''	3:G:55:LEU:HD22	1.68	0.75
3:G:216:ILE:HG23	3:G:216:ILE:O	1.87	0.75
1:E:704:DA:H2''	1:E:705:DA:OP2	1.87	0.75
3:G:226:GLY:O	3:G:230:VAL:HG23	1.87	0.75
3:A:148:ILE:HD12	3:A:148:ILE:H	1.50	0.75
5:S:63:ILE:HD12	5:S:77:LEU:HD13	1.68	0.75
5:S:70:GLU:HG3	5:S:71:ALA:N	2.02	0.75
3:G:113:LEU:HD13	3:C:47:ARG:HH12	1.52	0.74
5:Y:18:PRO:CB	5:Y:86:LEU:HD21	2.11	0.74
3:C:303:ARG:NH1	3:C:307:LYS:HE3	1.98	0.74
5:Y:14:ILE:HG23	5:Y:55:ILE:HB	1.69	0.74
3:G:230:VAL:HG21	3:G:254:VAL:HA	1.69	0.74
1:H:708:DG:H2''	1:H:709:DC:C5'	2.17	0.74
5:S:26:ALA:CB	5:S:77:LEU:HD21	2.07	0.74
3:A:1:MSE:HG3	4:D:139:PRO:HG2	1.67	0.74
5:L:80:THR:HA	5:L:83:LYS:HG2	1.68	0.74
3:G:230:VAL:CG2	3:G:254:VAL:HA	2.17	0.74
5:S:33:ILE:HG21	5:S:44:LEU:HD12	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:82:ILE:HD11	4:D:123:MSE:CE	2.18	0.74
3:G:173:ILE:HD11	3:G:204:LEU:CD2	2.17	0.74
3:C:121:ILE:CD1	3:C:302:MSE:HE2	2.16	0.74
3:G:317:SER:C	3:G:318:ILE:HD12	2.07	0.74
1:H:707:DC:H5''	1:H:707:DC:C6	2.23	0.74
3:C:152:ASN:N	3:C:152:ASN:HD22	1.85	0.74
3:G:259:GLN:OE1	3:G:284:ARG:HD2	1.88	0.73
4:D:67:ILE:HD11	4:D:75:TYR:HB3	1.70	0.73
3:A:143:VAL:HG11	3:A:305:LEU:HB2	1.69	0.73
3:A:50:ALA:HB3	4:D:115:LYS:HA	1.68	0.73
3:A:324:ARG:HB3	3:A:324:ARG:NH1	2.03	0.73
4:D:287:LEU:HD12	4:D:288:THR:H	1.53	0.73
3:G:304:LEU:HD23	3:G:305:LEU:N	2.04	0.73
3:C:102:GLN:CA	3:C:102:GLN:HE21	1.99	0.73
3:G:150:SER:O	3:G:152:ASN:OD1	2.07	0.73
4:D:192:ASN:HA	4:D:196:LYS:HB2	1.68	0.73
3:A:247:THR:HG22	3:A:249:GLU:H	1.53	0.73
2:B:712:DT:H2'	2:B:713:DC:C6	2.22	0.73
5:Y:33:ILE:HG23	5:Y:65:ALA:HB2	1.69	0.73
3:C:121:ILE:HD11	3:C:302:MSE:HE2	1.70	0.73
3:G:43:ARG:NH2	3:G:44:LEU:HB2	2.03	0.73
3:A:187:LEU:O	3:A:193:HIS:HB3	1.89	0.73
3:A:88:MSE:HE1	5:S:20:THR:HG22	1.71	0.73
4:D:70:ILE:H	4:D:97:ASN:HD21	1.37	0.73
4:D:106:LEU:HD11	4:D:131:HIS:HD2	1.51	0.73
5:T:22:LEU:CD1	5:T:77:LEU:HD22	2.19	0.73
1:E:702:DG:H2'	3:A:15:SER:HB3	1.71	0.72
1:E:708:DG:H1'	1:E:709:DC:H5''	1.70	0.72
4:D:102:GLN:OE1	4:D:103:ASP:N	2.20	0.72
3:A:11:GLU:HG2	3:A:40:THR:CG2	2.19	0.72
3:A:212:ARG:HD2	3:A:212:ARG:N	2.03	0.72
3:A:230:VAL:HG22	3:A:254:VAL:HA	1.70	0.72
3:A:38:LEU:O	3:A:38:LEU:HD23	1.89	0.72
4:D:172:LEU:HD22	4:D:242:ALA:HB1	1.72	0.72
2:R:706:DG:H2''	2:R:707:DC:C5	2.25	0.72
5:L:8:VAL:HG12	5:L:59:ALA:O	1.88	0.72
3:A:259:GLN:HG3	3:A:284:ARG:CZ	2.20	0.72
3:A:15:SER:O	3:A:19:VAL:HG23	1.90	0.72
4:D:304:LEU:HD13	5:Y:48:MET:HE1	1.72	0.72
3:C:109:LEU:O	3:C:109:LEU:HD12	1.90	0.72
3:A:305:LEU:HD12	3:A:305:LEU:O	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Y:26:ALA:HB2	5:Y:44:LEU:HD12	1.71	0.72
4:D:47:ARG:HG3	4:D:47:ARG:O	1.90	0.72
3:C:191:ILE:HD11	3:C:196:LYS:HZ2	1.55	0.72
3:G:143:VAL:HG12	3:G:305:LEU:HD13	1.71	0.72
3:C:322:PRO:HG2	5:T:52:SER:O	1.90	0.71
5:Y:30:ASP:OD2	5:Y:69:ASP:OD2	2.07	0.71
4:D:290:VAL:HA	4:D:325:ILE:HG22	1.70	0.71
3:C:233:LEU:HD22	3:C:240:PRO:HG2	1.72	0.71
3:G:193:HIS:CD2	3:G:194:ALA:N	2.58	0.71
3:A:282:MSE:HE3	4:D:279:LEU:HD22	1.72	0.71
4:D:191:ILE:HD11	4:D:196:LYS:HE3	1.72	0.71
1:H:706:DG:H2"	1:H:707:DC:C5	2.25	0.71
3:A:274:PHE:O	3:A:275:ASP:HB2	1.90	0.71
2:R:711:DT:H2'	2:R:712:DT:H72	1.72	0.71
4:D:144:LEU:N	4:D:144:LEU:HD22	2.04	0.71
5:S:9:THR:CG2	5:S:87:GLY:HA2	2.19	0.71
3:C:150:SER:O	3:C:152:ASN:ND2	2.24	0.71
5:T:42:VAL:HG11	5:T:53:LEU:HD21	1.73	0.71
3:A:230:VAL:CG2	3:A:254:VAL:HA	2.21	0.71
1:H:712:DA:H2"	1:H:713:DC:H5"	1.72	0.71
4:D:304:LEU:HB2	5:Y:48:MET:CE	2.20	0.71
4:D:121:ILE:HD11	4:D:302:MSE:HE3	1.71	0.71
3:A:231:GLU:OE1	3:A:261:ARG:HD3	1.90	0.71
3:C:158:THR:OG1	3:C:161:TYR:HE1	1.74	0.71
3:A:197:VAL:HG12	3:A:201:LYS:HE2	1.73	0.70
3:G:115:LYS:HA	3:C:50:ALA:HB3	1.74	0.70
3:A:216:ILE:O	3:A:216:ILE:HG23	1.90	0.70
4:D:144:LEU:CD2	4:D:154:ILE:HD13	2.21	0.70
2:R:703:DT:H71	3:C:17:ALA:HB2	1.73	0.70
4:D:121:ILE:HD11	4:D:302:MSE:CE	2.21	0.70
1:H:711:DA:H2	2:R:704:DT:H3	1.36	0.70
3:C:185:GLY:HA3	3:C:221:TYR:CE1	2.26	0.70
4:D:154:ILE:O	4:D:154:ILE:CD1	2.40	0.70
5:T:37:PHE:HB2	5:T:61:ILE:HG22	1.74	0.70
3:A:307:LYS:HE2	5:S:48:MET:HE2	1.73	0.70
3:A:46:TYR:HE1	3:A:48:PRO:HG3	1.56	0.70
3:A:252:LEU:CD1	3:A:283:VAL:HG22	2.21	0.70
2:B:702:DG:H2"	2:B:703:DT:OP2	1.89	0.70
3:A:3:VAL:HG11	3:A:44:LEU:CG	2.22	0.69
2:B:704:DT:C1'	2:B:705:DA:H5"	2.22	0.69
5:L:20:THR:HG23	5:L:47:ILE:HD11	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:711:DA:H2''	1:H:712:DA:C8	2.27	0.69
3:G:69:ASP:OD1	3:C:80:ARG:NH1	2.26	0.69
5:T:36:GLU:HB2	5:T:41:THR:CG2	2.12	0.69
3:C:288:THR:CG2	3:C:327:PHE:HA	2.22	0.69
3:C:295:TYR:CD1	5:T:16:ALA:HA	2.27	0.69
5:T:30:ASP:HB2	5:T:69:ASP:OD1	1.91	0.69
3:A:102:GLN:OE1	3:A:103:ASP:N	2.24	0.69
3:G:88:MSE:HE2	5:L:24:GLN:CD	2.12	0.69
4:D:264:ASN:ND2	4:D:267:ASN:HB2	2.07	0.69
3:G:26:ASN:OD1	3:G:27:PRO:HD2	1.93	0.69
3:C:82:ILE:HD11	3:C:123:MSE:HE1	1.75	0.69
3:G:217:VAL:HG12	3:G:233:LEU:HD21	1.74	0.69
3:A:180:ILE:HD11	3:A:204:LEU:HD21	1.75	0.69
5:S:43:ASN:OD1	5:S:45:LYS:HB2	1.93	0.69
2:R:700:DC:H2''	2:R:701:DT:C5'	2.09	0.68
3:G:264:ASN:N	3:G:268:ASP:OD1	2.24	0.68
5:Y:55:ILE:HD13	5:Y:61:ILE:HG21	1.74	0.68
2:R:711:DT:H2''	2:R:712:DT:C5	2.29	0.68
3:G:149:GLU:CG	3:G:154:ILE:HD11	2.23	0.68
5:T:2:ALA:N	5:T:74:LEU:HD11	2.07	0.68
3:A:137:LYS:HA	3:A:137:LYS:HE2	1.75	0.68
3:A:3:VAL:CG1	3:A:44:LEU:HG	2.22	0.68
3:A:259:GLN:CG	3:A:284:ARG:HH22	2.06	0.68
1:E:715:DG:H1	2:B:700:DC:H42	1.42	0.68
3:C:259:GLN:HB2	3:C:284:ARG:NH2	2.08	0.68
5:T:22:LEU:HD11	5:T:77:LEU:HD22	1.75	0.68
1:H:703:DA:N1	2:R:712:DT:O4	2.27	0.68
3:G:73:ILE:CD1	3:G:277:THR:CG2	2.71	0.68
5:S:44:LEU:HD22	5:S:44:LEU:O	1.92	0.68
5:S:10:ALA:HB2	5:S:86:LEU:HA	1.75	0.68
1:E:707:DC:H2''	3:A:55:LEU:CD2	2.24	0.68
3:C:108:LEU:O	3:C:112:MSE:HB2	1.92	0.68
1:E:707:DC:H2''	3:A:55:LEU:HD22	1.75	0.68
5:T:42:VAL:CG1	5:T:53:LEU:HD21	2.24	0.68
3:A:70:ILE:H	3:A:97:ASN:ND2	1.91	0.68
4:D:113:LEU:O	4:D:116:GLN:NE2	2.27	0.68
3:C:60:THR:OG1	3:C:62:THR:HG23	1.93	0.68
5:T:32:ASP:C	5:T:33:ILE:HG13	2.12	0.68
4:D:187:LEU:O	4:D:193:HIS:HB2	1.94	0.68
3:A:226:GLY:O	3:A:230:VAL:HG23	1.95	0.67
3:G:8:VAL:HG13	3:G:40:THR:HG22	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:192:ASN:N	3:A:192:ASN:HD22	1.93	0.67
4:D:239:LYS:N	4:D:239:LYS:HD3	2.09	0.67
4:D:274:PHE:O	4:D:275:ASP:HB2	1.92	0.67
5:L:37:PHE:CE2	5:L:59:ALA:HB1	2.29	0.67
4:D:3:VAL:CG1	4:D:7:ASP:HB2	2.24	0.67
3:C:137:LYS:HA	3:C:137:LYS:HE3	1.75	0.67
4:D:85:ILE:CG2	4:D:302:MSE:HB3	2.24	0.67
3:G:317:SER:O	3:G:318:ILE:HD12	1.95	0.67
2:R:712:DT:H2'	2:R:713:DC:H6	1.60	0.67
3:G:3:VAL:HG13	3:G:7:ASP:OD2	1.94	0.67
1:E:702:DG:H2'	3:A:15:SER:CB	2.25	0.67
4:D:74:PHE:CD2	4:D:294:MSE:HG2	2.28	0.67
3:G:43:ARG:NH2	3:G:44:LEU:HD22	2.09	0.67
3:A:208:GLY:O	3:A:210:PRO:HD3	1.94	0.67
3:G:303:ARG:O	3:G:306:THR:OG1	2.12	0.67
1:H:707:DC:C2'	3:G:55:LEU:HD22	2.25	0.67
2:B:704:DT:C2'	2:B:705:DA:H5''	2.25	0.66
3:C:165:ALA:HB3	3:C:199:GLY:HA3	1.75	0.66
4:D:63:VAL:HG21	4:D:302:MSE:CE	2.24	0.66
3:G:231:GLU:HB2	3:G:261:ARG:NH2	2.09	0.66
3:G:73:ILE:CG1	3:G:74:PHE:N	2.57	0.66
3:A:82:ILE:CG2	3:A:302:MSE:HE3	2.26	0.66
3:A:191:ILE:C	3:A:192:ASN:HD22	1.98	0.66
3:C:265:VAL:HB	3:C:266:PRO:HD3	1.76	0.66
3:G:276:ASN:ND2	3:G:328:ARG:HH22	1.93	0.66
1:E:703:DA:H1'	1:E:704:DA:H5'	1.77	0.66
4:D:201:LYS:HD3	4:D:202:ARG:N	2.11	0.66
3:C:22:VAL:HG11	3:C:37:VAL:CG1	2.19	0.66
3:G:55:LEU:HD12	3:C:55:LEU:HD12	1.77	0.66
3:A:251:ALA:O	3:A:255:ILE:HG13	1.94	0.66
5:Y:37:PHE:HE2	5:Y:59:ALA:HB1	1.60	0.66
5:T:80:THR:O	5:T:84:GLU:HB2	1.95	0.66
3:A:121:ILE:HD12	3:A:302:MSE:HE2	1.77	0.66
1:H:701:DT:OP2	3:G:29:VAL:HA	1.96	0.66
4:D:34:ARG:O	4:D:38:LEU:HB2	1.95	0.66
2:R:700:DC:H2'	2:R:701:DT:H72	1.77	0.66
3:C:191:ILE:HD11	3:C:196:LYS:HZ1	1.60	0.66
3:G:88:MSE:HE2	5:L:24:GLN:OE1	1.96	0.66
3:A:50:ALA:CB	4:D:115:LYS:HA	2.26	0.66
3:C:102:GLN:HE21	3:C:102:GLN:HA	1.58	0.66
3:G:85:ILE:HD11	5:L:47:ILE:CD1	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:43:ARG:HE	3:G:44:LEU:N	1.93	0.66
5:Y:35:LEU:HB2	5:Y:44:LEU:HD23	1.78	0.66
4:D:186:THR:HG22	4:D:187:LEU:N	2.11	0.66
3:G:6:TYR:O	3:G:9:ALA:HB3	1.95	0.66
3:G:122:PHE:O	3:G:144:LEU:HA	1.96	0.66
4:D:73:ILE:HD13	4:D:73:ILE:H	1.60	0.66
3:A:159:ILE:HD12	3:A:321:LEU:O	1.95	0.66
3:G:187:LEU:HD21	3:G:216:ILE:HD11	1.78	0.66
2:R:700:DC:H2'	2:R:701:DT:C7	2.25	0.65
4:D:118:ASP:O	4:D:309:MSE:SE	2.64	0.65
3:C:3:VAL:HG13	3:C:7:ASP:HB3	1.77	0.65
3:C:82:ILE:HG23	3:C:302:MSE:CE	2.26	0.65
1:E:700:DC:H2'	1:E:701:DT:C6	2.31	0.65
3:G:183:VAL:HG22	3:G:229:ALA:HB1	1.78	0.65
3:A:213:ASP:O	3:A:216:ILE:HG22	1.95	0.65
5:S:33:ILE:CG2	5:S:44:LEU:HD12	2.27	0.65
3:G:282:MSE:HG2	3:C:252:LEU:HD22	1.77	0.65
3:A:305:LEU:HG	3:A:309:MSE:CE	2.27	0.65
3:A:186:THR:HA	3:A:218:GLU:OE1	1.96	0.65
3:A:192:ASN:O	3:A:197:VAL:HG23	1.96	0.65
3:C:3:VAL:HG13	3:C:7:ASP:CB	2.26	0.65
3:C:144:LEU:HD21	3:C:154:ILE:CG2	2.27	0.65
1:H:703:DA:OP2	1:H:703:DA:H2'	1.96	0.65
1:E:709:DC:H2'	1:E:710:DT:H72	1.79	0.65
1:E:714:DA:H2''	1:E:715:DG:C5'	2.26	0.65
3:C:226:GLY:HA3	3:C:253:GLY:HA3	1.79	0.65
3:A:265:VAL:HB	3:A:266:PRO:HD3	1.77	0.65
2:R:712:DT:H4'	2:R:712:DT:OP1	1.97	0.65
3:C:292:GLN:O	3:C:294:MSE:HE2	1.95	0.65
1:E:703:DA:H62	3:A:17:ALA:HB2	1.60	0.65
1:E:709:DC:H6	1:E:709:DC:H5'	1.62	0.65
3:A:149:GLU:HG2	3:A:154:ILE:CD1	2.26	0.65
4:D:3:VAL:HG12	4:D:7:ASP:HB2	1.78	0.64
3:C:144:LEU:HD22	3:C:144:LEU:N	2.12	0.64
4:D:265:VAL:HB	4:D:266:PRO:HD3	1.79	0.64
2:B:708:DG:H1'	2:B:709:DC:H5''	1.80	0.64
4:D:69:ASP:CG	4:D:71:SER:HB3	2.17	0.64
3:C:230:VAL:CG2	3:C:254:VAL:HA	2.27	0.64
4:D:248:ASP:O	4:D:251:ALA:HB3	1.96	0.64
4:D:227:ILE:O	4:D:231:GLU:HG2	1.97	0.64
4:D:261:ARG:HG2	4:D:261:ARG:HH11	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:180:ILE:HA	3:G:242:ALA:O	1.98	0.64
5:T:9:THR:HG21	5:T:88:GLU:HG3	1.80	0.64
3:A:12:ALA:HA	3:A:36:LYS:CE	2.22	0.64
5:Y:14:ILE:O	5:Y:14:ILE:CD1	2.39	0.64
3:C:148:ILE:HG12	3:C:190:PRO:HB3	1.80	0.64
1:E:715:DG:H1	2:B:700:DC:N4	1.96	0.64
3:A:49:ASN:OD1	3:A:52:ALA:N	2.27	0.64
3:A:324:ARG:HG2	3:A:325:ILE:N	2.11	0.64
4:D:317:SER:O	4:D:318:ILE:HD12	1.98	0.64
3:A:247:THR:HG21	3:A:249:GLU:HB3	1.80	0.64
3:C:307:LYS:NZ	3:C:314:VAL:HG11	2.13	0.64
3:G:169:VAL:HG21	3:G:200:TYR:HA	1.79	0.64
3:G:64:GLY:HA3	3:G:112:MSE:HG2	1.80	0.64
2:B:702:DG:H2'	2:B:703:DT:H72	1.79	0.64
3:G:149:GLU:HG3	3:G:154:ILE:HD11	1.77	0.64
3:A:151:THR:OG1	3:A:153:GLN:HB2	1.98	0.64
1:E:706:DG:H2''	1:E:707:DC:C6	2.33	0.64
3:C:232:LYS:O	3:C:236:GLU:CG	2.41	0.64
3:A:212:ARG:HD3	3:A:215:TYR:CD2	2.32	0.64
5:S:20:THR:O	5:S:24:GLN:HB2	1.98	0.64
2:B:701:DT:OP2	4:D:29:VAL:HA	1.98	0.63
4:D:57:SER:C	4:D:58:LYS:HD2	2.18	0.63
3:A:279:LEU:HA	3:A:282:MSE:HB2	1.78	0.63
3:G:247:THR:CG2	3:G:250:MSE:H	2.11	0.63
5:L:67:GLY:H	5:L:70:GLU:CG	2.09	0.63
3:C:315:ASP:CG	3:C:316:SER:H	2.00	0.63
5:S:47:ILE:HD12	5:S:51:MET:CE	2.28	0.63
5:T:47:ILE:HG22	5:T:51:MET:CE	2.27	0.63
3:A:38:LEU:C	3:A:38:LEU:HD23	2.18	0.63
5:Y:44:LEU:HG	5:Y:63:ILE:CD1	2.27	0.63
5:L:73:ALA:O	5:L:76:ALA:HB3	1.99	0.63
3:G:177:HIS:HE1	3:G:241:THR:HG22	1.64	0.63
3:A:41:ILE:HD13	3:A:41:ILE:C	2.18	0.63
3:C:62:THR:HA	3:C:92:ASN:O	1.97	0.63
3:C:305:LEU:CG	3:C:309:MSE:HE2	2.16	0.63
4:D:78:LEU:HG	4:D:123:MSE:SE	2.49	0.63
4:D:182:PHE:CE1	4:D:184:SER:HB3	2.33	0.63
3:G:204:LEU:HB3	3:G:209:LEU:O	1.97	0.63
3:G:80:ARG:HD2	3:C:70:ILE:HD11	1.80	0.63
5:Y:6:PHE:HD2	5:Y:88:GLU:HA	1.64	0.63
5:T:10:ALA:HB2	5:T:86:LEU:HA	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:252:LEU:HD13	4:D:282:MSE:HE2	1.80	0.63
5:T:14:ILE:HD12	5:T:55:ILE:CG2	2.25	0.63
3:A:179:ASN:HB3	3:A:215:TYR:HE2	1.64	0.63
4:D:166:PHE:CE2	4:D:202:ARG:CZ	2.81	0.63
3:G:43:ARG:HH21	3:G:44:LEU:CG	2.11	0.63
3:C:243:ILE:CG2	3:C:244:PHE:N	2.61	0.63
3:G:204:LEU:HD12	3:G:211:VAL:CG1	2.28	0.63
3:A:261:ARG:HG3	3:A:261:ARG:HH11	1.63	0.63
3:G:80:ARG:O	3:G:84:ASP:HB2	1.99	0.62
4:D:296:ASP:OD1	5:Y:51:MET:SD	2.57	0.62
4:D:252:LEU:HA	4:D:255:ILE:HD12	1.81	0.62
5:T:2:ALA:N	5:T:74:LEU:CD1	2.62	0.62
3:C:277:THR:O	3:C:279:LEU:HD12	1.99	0.62
3:C:231:GLU:CB	3:C:261:ARG:HH21	1.98	0.62
3:G:80:ARG:CD	3:C:70:ILE:HD11	2.29	0.62
3:A:288:THR:HB	3:A:327:PHE:HA	1.82	0.62
1:E:702:DG:N7	3:A:21:ARG:NH2	2.44	0.62
1:H:703:DA:H62	3:G:17:ALA:HB2	1.64	0.62
5:T:67:GLY:O	5:T:70:GLU:HB2	1.99	0.62
5:T:6:PHE:N	5:T:6:PHE:CD1	2.67	0.62
3:A:222:THR:OG1	3:A:225:SER:HB3	1.99	0.62
3:A:1:MSE:CG	3:A:47:ARG:NH1	2.60	0.62
3:G:47:ARG:NH2	3:C:113:LEU:HB2	2.13	0.62
3:C:144:LEU:HB3	3:C:147:SER:HB2	1.82	0.62
3:A:67:ILE:O	3:A:97:ASN:HA	1.99	0.62
3:G:155:PRO:O	3:G:156:SER:HB3	1.99	0.62
4:D:103:ASP:OD2	4:D:104:LYS:HG3	2.00	0.62
5:S:14:ILE:HD12	5:S:55:ILE:HD13	1.80	0.62
3:C:148:ILE:O	3:C:148:ILE:HG23	1.98	0.62
3:C:109:LEU:O	3:C:113:LEU:HG	2.00	0.62
3:C:94:ILE:CG2	3:C:112:MSE:HE1	2.29	0.62
3:G:73:ILE:CG1	3:G:277:THR:HG21	2.29	0.62
5:T:47:ILE:O	5:T:51:MET:HE2	1.99	0.62
1:H:712:DA:C2'	1:H:713:DC:H5''	2.28	0.62
4:D:275:ASP:HA	4:D:292:GLN:HB3	1.82	0.62
3:A:235:GLU:C	3:A:236:GLU:O	2.35	0.62
1:H:714:DA:H2'	1:H:715:DG:H8	1.65	0.62
3:C:303:ARG:HA	3:C:306:THR:OG1	2.00	0.62
3:G:284:ARG:CB	3:G:285:PRO:HD3	2.22	0.62
4:D:122:PHE:HD1	4:D:144:LEU:HD12	1.64	0.62
3:C:186:THR:HG23	3:C:189:GLU:HB2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:168:ALA:HB2	3:C:290:VAL:HG21	1.82	0.62
3:A:54:GLY:HA2	3:A:59:LYS:O	2.00	0.62
3:G:324:ARG:NH2	3:G:326:GLU:OE2	2.29	0.62
3:G:64:GLY:N	3:G:117:VAL:HG11	2.14	0.62
3:G:154:ILE:CD1	3:G:154:ILE:O	2.48	0.62
3:A:103:ASP:OD1	3:A:104:LYS:N	2.33	0.62
4:D:264:ASN:HD21	4:D:268:ASP:H	1.48	0.61
1:H:714:DA:H4'	1:H:714:DA:OP1	1.98	0.61
3:A:152:ASN:HD22	3:A:318:ILE:CG1	2.10	0.61
1:H:705:DA:H2''	1:H:706:DG:O5'	2.00	0.61
4:D:43:ARG:HH11	4:D:43:ARG:HG2	1.64	0.61
3:C:275:ASP:OD2	3:C:292:GLN:NE2	2.33	0.61
2:R:700:DC:H2'	2:R:701:DT:C6	2.34	0.61
4:D:82:ILE:HD11	4:D:123:MSE:HE1	1.81	0.61
3:G:43:ARG:HE	3:G:44:LEU:CA	2.13	0.61
3:A:88:MSE:CE	5:S:20:THR:HG22	2.30	0.61
3:A:332:LYS:N	3:A:332:LYS:HD3	2.14	0.61
3:A:24:ASN:N	3:A:24:ASN:HD22	1.97	0.61
3:G:73:ILE:O	3:G:73:ILE:HD12	2.01	0.61
3:A:259:GLN:HG3	3:A:284:ARG:HH22	1.61	0.61
3:G:49:ASN:O	3:G:49:ASN:ND2	2.33	0.61
3:C:37:VAL:HG13	3:C:38:LEU:N	2.16	0.61
3:A:149:GLU:HG2	3:A:154:ILE:HD11	1.82	0.61
3:C:73:ILE:HD12	3:C:74:PHE:N	2.15	0.61
5:L:8:VAL:HA	5:L:86:LEU:O	2.01	0.61
3:C:238:GLU:OE1	3:C:238:GLU:HA	2.00	0.61
3:G:1:MSE:HG2	3:G:2:ASN:O	1.99	0.61
4:D:121:ILE:HD11	4:D:302:MSE:HA	1.82	0.61
3:A:279:LEU:O	3:A:283:VAL:HG23	2.01	0.61
3:A:180:ILE:CG2	3:A:242:ALA:HB3	2.31	0.61
3:A:18:THR:O	3:A:22:VAL:HG13	2.00	0.61
1:E:703:DA:H2''	1:E:704:DA:OP2	1.99	0.61
3:C:32:SER:O	3:C:36:LYS:HB2	2.00	0.61
2:B:702:DG:O6	4:D:21:ARG:NH2	2.34	0.61
3:A:122:PHE:O	3:A:144:LEU:HA	2.00	0.61
4:D:284:ARG:CB	4:D:285:PRO:HD3	2.26	0.61
4:D:173:ILE:HD12	4:D:209:LEU:HD12	1.83	0.61
3:C:258:ALA:HB1	3:C:269:LEU:HD21	1.81	0.61
3:G:83:GLU:HB2	3:G:93:ILE:HD11	1.82	0.61
3:G:287:LEU:HD22	3:G:288:THR:N	2.16	0.61
5:Y:17:ARG:HB2	5:Y:18:PRO:HD3	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:284:ARG:HB2	3:C:285:PRO:CD	2.31	0.60
4:D:222:THR:OG1	4:D:225:SER:HB3	2.00	0.60
3:C:12:ALA:HB2	3:C:37:VAL:HG23	1.81	0.60
3:A:224:ASP:O	3:A:227:ILE:HG12	2.01	0.60
3:A:286:GLN:O	3:A:328:ARG:HB2	2.01	0.60
3:G:247:THR:CG2	3:G:248:ASP:N	2.64	0.60
3:G:307:LYS:NZ	5:L:48:MET:HE3	2.16	0.60
2:B:706:DG:H2''	2:B:707:DC:C6	2.36	0.60
4:D:72:ASN:HD22	4:D:73:ILE:HD13	1.67	0.60
3:C:102:GLN:NE2	3:C:102:GLN:N	2.50	0.60
4:D:3:VAL:HG13	4:D:7:ASP:OD2	2.02	0.60
4:D:191:ILE:HG23	4:D:192:ASN:OD1	2.02	0.60
3:C:263:LEU:N	3:C:263:LEU:HD12	2.16	0.60
3:G:318:ILE:O	3:G:318:ILE:HG22	2.01	0.60
1:H:709:DC:H2'	1:H:710:DT:H71	1.84	0.60
3:G:208:GLY:O	3:G:209:LEU:HD23	2.02	0.60
4:D:90:LYS:CG	4:D:90:LYS:O	2.50	0.60
3:C:3:VAL:O	3:C:46:TYR:HD2	1.85	0.60
3:A:288:THR:CG2	3:A:328:ARG:H	2.14	0.60
5:T:3:GLN:N	5:T:74:LEU:HD11	2.16	0.60
3:A:114:GLY:O	3:A:116:GLN:HG2	2.02	0.60
3:C:188:GLU:CD	3:C:188:GLU:H	2.05	0.60
3:C:195:LYS:HD2	3:C:195:LYS:N	2.16	0.60
3:A:192:ASN:HA	3:A:196:LYS:HB2	1.83	0.60
5:T:67:GLY:H	5:T:70:GLU:HB2	1.67	0.60
1:E:706:DG:H2''	1:E:707:DC:C5	2.37	0.60
3:C:265:VAL:CG1	3:C:271:ILE:HD12	2.32	0.60
4:D:159:ILE:HG22	4:D:160:ASP:N	2.17	0.60
1:E:712:DA:C2'	1:E:713:DC:H5''	2.26	0.60
3:G:220:ASP:OD2	3:G:225:SER:CB	2.46	0.60
3:G:180:ILE:HG22	3:G:242:ALA:HB3	1.82	0.60
4:D:74:PHE:HE2	4:D:294:MSE:HG2	1.59	0.60
3:A:166:PHE:HE2	3:A:202:ARG:HG2	1.67	0.60
3:G:298:GLY:O	3:G:299:ALA:C	2.36	0.60
4:D:144:LEU:O	4:D:157:VAL:HG12	2.02	0.60
4:D:121:ILE:HD12	4:D:302:MSE:HE3	1.81	0.60
3:G:304:LEU:HA	5:L:48:MET:HE2	1.82	0.60
3:C:98:SER:O	3:C:99:ASP:HB2	2.02	0.60
3:A:284:ARG:HG2	4:D:256:HIS:CE1	2.37	0.59
3:C:263:LEU:HD23	3:C:269:LEU:HG	1.84	0.59
3:A:29:VAL:HB	3:A:34:ARG:CZ	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:183:VAL:CG1	4:D:250:MSE:HE2	2.31	0.59
3:G:60:THR:O	3:G:61:THR:OG1	2.18	0.59
1:H:708:DG:H2''	1:H:709:DC:H5'	1.83	0.59
4:D:191:ILE:O	4:D:196:LYS:HG3	2.03	0.59
3:G:83:GLU:HB2	3:G:93:ILE:CD1	2.32	0.59
3:A:304:LEU:HG	5:S:48:MET:HE1	1.84	0.59
1:H:708:DG:H2''	1:H:709:DC:H5''	1.83	0.59
3:C:100:GLN:HE22	3:C:125:GLY:H	1.49	0.59
3:C:192:ASN:HA	3:C:196:LYS:HB2	1.84	0.59
3:C:102:GLN:CA	3:C:102:GLN:NE2	2.65	0.59
4:D:103:ASP:OD2	4:D:104:LYS:N	2.35	0.59
5:T:57:LYS:O	5:T:57:LYS:HD3	2.02	0.59
3:G:284:ARG:NH2	3:C:284:ARG:HA	2.11	0.59
3:A:161:TYR:O	3:A:162:GLU:C	2.40	0.59
4:D:73:ILE:CD1	4:D:73:ILE:H	2.15	0.59
3:G:229:ALA:O	3:G:233:LEU:HG	2.02	0.59
5:T:20:THR:O	5:T:24:GLN:HG3	2.02	0.59
3:G:194:ALA:O	3:G:198:LYS:NZ	2.24	0.59
3:C:30:LYS:HB3	3:C:33:THR:OG1	2.01	0.59
3:C:82:ILE:HG23	3:C:302:MSE:HE3	1.83	0.59
4:D:70:ILE:H	4:D:97:ASN:ND2	1.99	0.59
3:C:200:TYR:O	3:C:203:ALA:HB3	2.02	0.59
3:C:271:ILE:H	3:C:271:ILE:HD13	1.67	0.59
3:C:255:ILE:HG22	3:C:284:ARG:NH2	2.17	0.59
5:L:2:ALA:N	5:L:74:LEU:HD22	2.17	0.59
3:G:162:GLU:OE1	3:G:202:ARG:NH2	2.31	0.59
3:A:82:ILE:HG23	3:A:302:MSE:HE3	1.85	0.59
3:G:276:ASN:HD21	3:G:328:ARG:NH2	1.98	0.59
2:B:704:DT:H2''	2:B:705:DA:C5'	2.33	0.59
4:D:38:LEU:HD23	4:D:38:LEU:O	2.02	0.59
4:D:145:ALA:HA	4:D:157:VAL:HG13	1.85	0.58
4:D:166:PHE:HE2	4:D:202:ARG:HG2	1.68	0.58
3:C:109:LEU:HD22	3:C:135:LEU:HD12	1.84	0.58
1:H:707:DC:H2''	3:G:55:LEU:CD2	2.32	0.58
4:D:317:SER:C	4:D:318:ILE:HD12	2.24	0.58
3:A:180:ILE:HA	3:A:242:ALA:O	2.03	0.58
3:C:307:LYS:HG2	3:C:312:GLU:OE2	2.03	0.58
4:D:85:ILE:HG22	4:D:302:MSE:HB3	1.85	0.58
3:C:106:LEU:HD23	3:C:134:GLU:OE2	2.02	0.58
3:G:325:ILE:HG22	3:G:326:GLU:N	2.18	0.58
5:S:25:ALA:HA	5:S:28:LYS:HE2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:8:VAL:CG1	5:S:59:ALA:HB3	2.33	0.58
3:A:128:THR:O	3:A:131:HIS:HB2	2.03	0.58
3:G:220:ASP:O	3:G:250:MSE:SE	2.71	0.58
4:D:273:GLY:O	4:D:290:VAL:HG23	2.03	0.58
5:S:4:LYS:HD2	5:S:6:PHE:CZ	2.38	0.58
3:G:113:LEU:O	3:G:116:GLN:NE2	2.35	0.58
3:C:221:TYR:HD1	3:C:250:MSE:HE2	1.68	0.58
3:G:193:HIS:HD2	3:G:194:ALA:N	2.00	0.58
4:D:288:THR:CG2	4:D:327:PHE:HA	2.25	0.58
3:C:307:LYS:HB3	3:C:312:GLU:HG3	1.84	0.58
4:D:247:THR:O	4:D:251:ALA:HB2	2.04	0.58
3:C:37:VAL:HG13	3:C:38:LEU:H	1.69	0.58
3:C:300:VAL:HG23	5:T:51:MET:HE3	1.86	0.58
3:C:204:LEU:HD12	3:C:211:VAL:HG21	1.84	0.58
3:C:96:SER:OG	3:C:108:LEU:HD22	2.03	0.58
5:Y:9:THR:CG2	5:Y:87:GLY:HA2	2.25	0.58
4:D:191:ILE:CD1	4:D:196:LYS:HE3	2.34	0.58
2:R:706:DG:H4'	2:R:706:DG:OP1	2.02	0.58
3:G:127:VAL:HG21	3:G:149:GLU:HB3	1.86	0.58
5:T:8:VAL:HA	5:T:86:LEU:O	2.02	0.58
3:G:202:ARG:O	3:G:206:GLU:HB2	2.04	0.58
3:G:74:PHE:CE2	3:G:294:MSE:HG2	2.38	0.58
3:A:247:THR:CG2	3:A:249:GLU:HB3	2.33	0.58
3:C:212:ARG:O	3:C:215:TYR:HB2	2.04	0.58
4:D:86:ALA:HB2	4:D:302:MSE:SE	2.54	0.58
3:G:141:PRO:O	3:G:142:VAL:HG23	2.04	0.58
3:A:206:GLU:C	3:A:208:GLY:H	2.05	0.58
4:D:88:MSE:HE2	5:Y:24:GLN:HG3	1.85	0.58
4:D:212:ARG:HD3	4:D:215:TYR:CD2	2.38	0.58
1:H:710:DT:H5''	3:C:53:ARG:NH2	2.19	0.58
2:R:711:DT:C2'	2:R:712:DT:C5	2.86	0.58
5:T:48:MET:O	5:T:52:SER:OG	2.22	0.58
3:G:254:VAL:HG12	3:G:271:ILE:CD1	2.33	0.58
3:G:252:LEU:HD21	3:G:283:VAL:HG22	1.85	0.58
5:T:26:ALA:HB2	5:T:77:LEU:CD2	2.27	0.57
5:T:47:ILE:HG22	5:T:51:MET:HE2	1.84	0.57
3:C:197:VAL:HG12	3:C:201:LYS:HD3	1.85	0.57
3:C:202:ARG:O	3:C:206:GLU:HB2	2.03	0.57
3:A:259:GLN:HG3	3:A:284:ARG:NH1	2.18	0.57
1:H:702:DG:H5''	3:G:15:SER:OG	2.04	0.57
3:G:99:ASP:O	3:G:101:ASN:N	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:103:ASP:OD2	3:G:104:LYS:N	2.37	0.57
4:D:158:THR:OG1	4:D:159:ILE:N	2.37	0.57
5:Y:37:PHE:CE2	5:Y:59:ALA:HB1	2.38	0.57
4:D:85:ILE:HG13	5:Y:47:ILE:HD12	1.84	0.57
1:H:702:DG:H2''	1:H:703:DA:C8	2.40	0.57
3:C:187:LEU:HD11	3:C:218:GLU:HG2	1.85	0.57
3:G:113:LEU:CD2	3:G:139:PRO:HD2	2.34	0.57
3:A:173:ILE:HD11	3:A:204:LEU:HD23	1.87	0.57
3:C:288:THR:HG23	3:C:327:PHE:CA	2.31	0.57
2:B:700:DC:H2''	2:B:701:DT:O5'	2.04	0.57
3:C:112:MSE:HE3	3:C:112:MSE:HA	1.86	0.57
5:Y:14:ILE:HD11	5:Y:50:VAL:HG12	1.86	0.57
3:A:68:PRO:HD3	3:A:123:MSE:O	2.04	0.57
3:G:43:ARG:NH2	3:G:44:LEU:HD13	2.19	0.57
4:D:73:ILE:N	4:D:73:ILE:CD1	2.67	0.57
3:A:304:LEU:HD22	3:A:308:TYR:CE2	2.39	0.57
3:G:113:LEU:HD22	3:G:139:PRO:HD2	1.86	0.57
4:D:41:ILE:HG23	4:D:46:TYR:CB	2.17	0.57
3:G:113:LEU:HD13	3:C:47:ARG:NH1	2.20	0.57
4:D:1:MET:O	4:D:3:VAL:HG23	2.03	0.57
1:E:703:DA:H2''	1:E:704:DA:H5'	1.87	0.57
3:G:65:VAL:HG22	3:G:94:ILE:O	2.05	0.57
3:C:160:ASP:OD1	3:C:163:GLN:HG2	2.05	0.57
5:S:79:ASP:O	5:S:83:LYS:HB2	2.05	0.57
1:H:710:DT:H5''	3:C:53:ARG:CZ	2.34	0.57
5:S:27:SER:HA	5:S:45:LYS:CD	2.35	0.57
3:A:36:LYS:O	3:A:40:THR:HG23	2.05	0.57
5:T:22:LEU:HD12	5:T:77:LEU:HD22	1.87	0.57
4:D:258:ALA:HB2	4:D:269:LEU:HD21	1.87	0.57
3:C:61:THR:N	3:C:118:ASP:OD2	2.35	0.57
3:G:151:THR:OG1	3:G:153:GLN:HG3	2.05	0.57
3:C:303:ARG:HD2	3:C:303:ARG:O	2.04	0.57
3:G:255:ILE:HG23	3:G:265:VAL:HG11	1.87	0.57
3:C:12:ALA:CB	3:C:37:VAL:HG23	2.34	0.57
4:D:142:VAL:HG23	4:D:143:VAL:N	2.19	0.57
3:A:169:VAL:HG12	3:A:173:ILE:HG12	1.87	0.57
4:D:144:LEU:HB3	4:D:147:SER:HG	1.68	0.57
1:E:700:DC:C6	1:E:701:DT:H72	2.40	0.57
3:C:182:PHE:CZ	3:C:184:SER:HB3	2.39	0.57
1:H:706:DG:OP1	1:H:706:DG:H4'	2.04	0.56
3:C:123:MSE:HA	3:C:147:SER:OG	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:230:VAL:HG21	4:D:257:GLY:HA3	1.86	0.56
3:C:102:GLN:O	3:C:106:LEU:HD13	2.05	0.56
3:C:162:GLU:OE2	3:C:199:GLY:HA2	2.04	0.56
3:C:274:PHE:O	3:C:275:ASP:HB2	2.04	0.56
3:C:67:ILE:HG22	3:C:123:MSE:SE	2.55	0.56
3:C:155:PRO:HG3	3:C:317:SER:HB2	1.87	0.56
3:A:182:PHE:HB2	3:A:200:TYR:CD2	2.41	0.56
3:A:3:VAL:CG1	3:A:44:LEU:CD2	2.84	0.56
1:E:714:DA:H2''	1:E:715:DG:C4'	2.36	0.56
3:G:204:LEU:HD12	3:G:211:VAL:HG11	1.87	0.56
3:G:177:HIS:CE1	3:G:241:THR:HG22	2.39	0.56
5:S:4:LYS:HZ2	5:S:78:GLU:HG3	1.69	0.56
3:C:148:ILE:O	3:C:148:ILE:CG2	2.54	0.56
3:C:1:MSE:SE	3:C:47:ARG:NH2	2.89	0.56
4:D:149:GLU:CG	4:D:154:ILE:HD11	2.24	0.56
3:G:254:VAL:HG12	3:G:271:ILE:HD13	1.86	0.56
5:Y:11:ASP:HA	5:Y:57:LYS:CE	2.31	0.56
3:A:193:HIS:HA	3:A:197:VAL:CG2	2.35	0.56
4:D:187:LEU:C	4:D:189:GLU:H	2.09	0.56
4:D:100:GLN:NE2	4:D:125:GLY:HA3	2.20	0.56
4:D:2:ASN:OD1	4:D:2:ASN:C	2.44	0.56
3:A:259:GLN:CG	3:A:284:ARG:NH2	2.65	0.56
3:G:265:VAL:HB	3:G:285:PRO:HG2	1.88	0.56
3:A:63:VAL:HG22	3:A:93:ILE:HD12	1.86	0.56
3:G:70:ILE:HG21	3:G:95:LEU:HD21	1.87	0.56
3:C:102:GLN:CD	3:C:102:GLN:H	2.09	0.56
4:D:290:VAL:HG22	4:D:325:ILE:CG2	2.36	0.56
2:R:701:DT:H2''	2:R:702:DG:H8	1.70	0.56
4:D:184:SER:HB2	4:D:192:ASN:HD22	1.68	0.56
2:B:703:DT:O4	4:D:17:ALA:HB2	2.05	0.56
3:A:157:VAL:HG11	3:A:301:ALA:HA	1.88	0.56
3:A:80:ARG:NH1	5:S:17:ARG:HD2	2.20	0.56
3:C:38:LEU:HA	3:C:41:ILE:HD12	1.88	0.56
2:B:701:DT:H3'	4:D:18:THR:HG21	1.87	0.56
1:H:712:DA:H2'	1:H:713:DC:C6	2.40	0.56
5:L:4:LYS:HG2	5:L:5:THR:N	2.20	0.56
3:G:64:GLY:HA3	3:G:112:MSE:CG	2.36	0.55
3:C:277:THR:O	3:C:278:ARG:C	2.44	0.55
1:H:708:DG:C2'	1:H:709:DC:H5''	2.36	0.55
3:G:247:THR:HG22	3:G:250:MSE:N	2.19	0.55
3:G:82:ILE:HD11	3:G:121:ILE:HG21	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:8:VAL:HG13	5:S:59:ALA:HB3	1.88	0.55
3:A:65:VAL:HG22	3:A:95:LEU:HB2	1.88	0.55
4:D:108:LEU:O	4:D:112:MSE:HB2	2.06	0.55
3:C:271:ILE:HD13	3:C:330:SER:OG	2.06	0.55
4:D:244:PHE:HD1	4:D:272:ILE:HG22	1.71	0.55
5:Y:8:VAL:O	5:Y:57:LYS:O	2.23	0.55
3:G:139:PRO:CB	3:C:1:MSE:HE2	2.34	0.55
1:H:714:DA:H2''	1:H:715:DG:O4'	2.06	0.55
1:H:702:DG:H2''	1:H:703:DA:OP2	2.05	0.55
3:A:324:ARG:HH11	3:A:324:ARG:HB3	1.71	0.55
5:Y:33:ILE:HG12	5:Y:65:ALA:HB1	1.87	0.55
5:T:2:ALA:O	5:T:64:SER:HA	2.07	0.55
4:D:186:THR:HA	4:D:218:GLU:OE1	2.06	0.55
4:D:245:VAL:CG1	4:D:250:MSE:HG3	2.36	0.55
4:D:275:ASP:OD1	4:D:292:GLN:HG2	2.06	0.55
3:G:92:ASN:HD21	3:C:111:ASN:ND2	2.04	0.55
3:G:297:ILE:O	3:G:301:ALA:N	2.30	0.55
3:A:318:ILE:N	3:A:318:ILE:HD12	2.21	0.55
3:A:298:GLY:O	3:A:299:ALA:C	2.40	0.55
3:C:204:LEU:HD13	3:C:211:VAL:HG13	1.89	0.55
3:A:302:MSE:O	3:A:305:LEU:HB3	2.07	0.55
3:A:3:VAL:HG11	3:A:44:LEU:CD2	2.37	0.55
4:D:37:VAL:HA	4:D:40:THR:HB	1.88	0.55
4:D:264:ASN:OD1	4:D:267:ASN:ND2	2.38	0.55
1:E:709:DC:OP1	4:D:48:PRO:HA	2.06	0.55
3:C:73:ILE:HD13	3:C:277:THR:HG21	1.87	0.55
1:E:700:DC:H2''	1:E:701:DT:H5'	1.88	0.55
5:L:18:PRO:HA	5:L:84:GLU:OE2	2.07	0.55
3:G:230:VAL:HG22	3:G:254:VAL:HG13	1.89	0.55
3:G:5:ILE:HG23	3:G:6:TYR:N	2.21	0.55
3:A:177:HIS:CE1	3:A:241:THR:HB	2.41	0.55
3:C:263:LEU:HG	3:C:268:ASP:OD1	2.06	0.55
4:D:182:PHE:HE1	4:D:184:SER:OG	1.80	0.55
4:D:290:VAL:HG22	4:D:325:ILE:HG22	1.89	0.55
1:H:711:DA:N1	2:R:704:DT:O4	2.40	0.55
3:A:131:HIS:O	3:A:134:GLU:HB3	2.07	0.55
2:R:700:DC:C2'	2:R:701:DT:C6	2.90	0.55
3:A:82:ILE:HD11	3:A:123:MSE:HE1	1.89	0.55
3:A:288:THR:CG2	3:A:330:SER:HB3	2.35	0.54
3:G:265:VAL:O	3:G:269:LEU:O	2.25	0.54
4:D:241:THR:O	4:D:269:LEU:HA	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:80:ARG:HH12	5:L:17:ARG:NH1	2.05	0.54
3:G:73:ILE:CD1	3:G:77:GLU:OE2	2.56	0.54
3:A:221:TYR:O	3:A:249:GLU:HG2	2.07	0.54
3:G:255:ILE:HG23	3:G:265:VAL:HG21	1.87	0.54
5:L:15:HIS:O	5:L:18:PRO:HD2	2.07	0.54
3:C:107:HIS:O	3:C:110:ASN:HB2	2.07	0.54
3:A:192:ASN:ND2	3:A:192:ASN:N	2.54	0.54
4:D:271:ILE:HD13	4:D:271:ILE:H	1.71	0.54
4:D:243:ILE:HG22	4:D:244:PHE:H	1.73	0.54
3:G:180:ILE:HD11	3:G:204:LEU:CD2	2.37	0.54
3:C:243:ILE:CG2	3:C:244:PHE:H	2.20	0.54
3:A:177:HIS:NE2	3:A:270:GLU:OE2	2.38	0.54
5:L:14:ILE:HG13	5:L:55:ILE:HG21	1.88	0.54
5:Y:6:PHE:HE1	5:Y:63:ILE:HG22	1.72	0.54
5:T:44:LEU:O	5:T:44:LEU:HD22	2.07	0.54
3:G:310:ASN:O	3:G:312:GLU:N	2.40	0.54
2:B:703:DT:H71	4:D:17:ALA:HB2	1.90	0.54
3:A:128:THR:H	3:A:131:HIS:CD2	2.26	0.54
3:A:106:LEU:O	3:A:110:ASN:ND2	2.40	0.54
3:C:17:ALA:O	3:C:21:ARG:HG3	2.07	0.54
3:C:303:ARG:HH11	3:C:303:ARG:CG	2.19	0.54
3:C:235:GLU:CD	3:C:235:GLU:H	2.10	0.54
3:C:257:GLY:O	3:C:261:ARG:HG2	2.08	0.54
3:A:11:GLU:OE2	3:A:43:ARG:NH1	2.40	0.54
1:E:700:DC:O5'	3:A:29:VAL:HA	2.08	0.54
3:C:148:ILE:CG1	3:C:190:PRO:HB2	2.28	0.54
3:G:216:ILE:O	3:G:216:ILE:CG2	2.54	0.54
3:C:98:SER:O	3:C:104:LYS:HD2	2.07	0.54
4:D:245:VAL:HG11	4:D:251:ALA:HA	1.89	0.54
3:C:165:ALA:O	3:C:169:VAL:HG12	2.07	0.54
3:A:245:VAL:HG11	3:A:251:ALA:N	2.21	0.54
4:D:58:LYS:N	4:D:58:LYS:HD2	2.23	0.54
3:C:144:LEU:CD2	3:C:154:ILE:HG23	2.34	0.54
5:S:18:PRO:CB	5:S:86:LEU:HD21	2.37	0.54
3:C:40:THR:O	3:C:44:LEU:HD23	2.08	0.54
3:G:73:ILE:HD12	3:G:77:GLU:OE2	2.06	0.54
3:G:274:PHE:O	3:G:275:ASP:CB	2.50	0.54
4:D:85:ILE:HG21	4:D:302:MSE:HB3	1.89	0.54
3:C:319:VAL:HG21	5:T:48:MET:HE1	1.90	0.54
4:D:177:HIS:CD2	4:D:177:HIS:H	2.25	0.54
3:C:230:VAL:HG23	3:C:254:VAL:HA	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:29:VAL:CB	3:A:34:ARG:HH21	2.18	0.54
4:D:204:LEU:HG	4:D:209:LEU:O	2.08	0.54
3:G:208:GLY:C	3:G:210:PRO:HD3	2.28	0.54
3:C:94:ILE:HG21	3:C:112:MSE:HE1	1.89	0.54
4:D:275:ASP:O	4:D:276:ASN:HB3	2.08	0.54
4:D:98:SER:HB2	4:D:105:GLU:HG2	1.89	0.54
3:C:69:ASP:OD2	3:C:71:SER:HB3	2.07	0.54
3:A:173:ILE:HD12	3:A:209:LEU:HD12	1.89	0.54
3:A:276:ASN:OD1	3:A:328:ARG:NH2	2.39	0.54
2:B:712:DT:C2'	2:B:713:DC:C6	2.90	0.54
3:A:121:ILE:HG13	3:A:305:LEU:HD23	1.89	0.54
2:R:714:DA:H2''	2:R:715:DG:C8	2.43	0.54
3:G:315:ASP:O	3:G:316:SER:HB2	2.08	0.54
3:A:270:GLU:HB3	3:A:331:THR:HB	1.89	0.53
3:G:265:VAL:HB	3:G:266:PRO:HD3	1.90	0.53
3:A:184:SER:OG	3:A:185:GLY:N	2.41	0.53
3:A:166:PHE:CE2	3:A:202:ARG:HG2	2.42	0.53
3:G:73:ILE:HG13	3:G:74:PHE:H	1.72	0.53
3:C:143:VAL:HG12	3:C:305:LEU:HD13	1.90	0.53
2:B:701:DT:H1'	2:B:702:DG:H5''	1.90	0.53
3:G:144:LEU:N	3:G:144:LEU:CD2	2.68	0.53
5:S:23:VAL:HG12	5:S:23:VAL:O	2.07	0.53
3:G:192:ASN:HA	3:G:196:LYS:HB2	1.91	0.53
3:C:209:LEU:O	3:C:210:PRO:C	2.47	0.53
4:D:230:VAL:HG13	4:D:254:VAL:HG13	1.89	0.53
3:A:179:ASN:HB3	3:A:215:TYR:CE2	2.43	0.53
4:D:205:THR:HG22	4:D:210:PRO:HA	1.89	0.53
3:G:121:ILE:HD11	3:G:302:MSE:HA	1.89	0.53
3:G:180:ILE:HD11	3:G:204:LEU:HD21	1.91	0.53
3:G:43:ARG:HH21	3:G:44:LEU:HD13	1.73	0.53
3:G:73:ILE:CD1	3:G:277:THR:HG22	2.29	0.53
3:C:67:ILE:HA	3:C:123:MSE:HG3	1.91	0.53
1:H:705:DA:H1'	1:H:706:DG:O4'	2.08	0.53
5:T:32:ASP:O	5:T:33:ILE:CG1	2.56	0.53
5:S:18:PRO:HB2	5:S:86:LEU:HD21	1.90	0.53
3:A:128:THR:H	3:A:131:HIS:HD2	1.55	0.53
4:D:88:MSE:HE2	5:Y:24:GLN:CG	2.37	0.53
5:S:36:GLU:HG2	5:S:41:THR:OG1	2.08	0.53
4:D:324:ARG:HE	5:Y:56:GLN:HG2	1.74	0.53
5:L:81:MET:HE2	5:L:87:GLY:HA3	1.90	0.53
3:G:73:ILE:CD1	3:G:277:THR:HG21	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Y:6:PHE:CD1	5:Y:6:PHE:N	2.77	0.53
3:A:92:ASN:ND2	4:D:111:ASN:OD1	2.40	0.53
3:C:300:VAL:CG2	5:T:51:MET:HE3	2.39	0.53
3:A:187:LEU:H	3:A:218:GLU:CD	2.12	0.53
3:A:300:VAL:HG13	5:S:48:MET:HG2	1.89	0.53
4:D:4:THR:HG22	4:D:7:ASP:OD2	2.08	0.53
3:G:140:VAL:O	3:G:141:PRO:O	2.26	0.53
4:D:239:LYS:H	4:D:239:LYS:HD3	1.74	0.53
3:C:279:LEU:HD12	3:C:280:SER:N	2.24	0.53
3:A:276:ASN:ND2	3:A:291:VAL:HG22	2.24	0.53
3:C:127:VAL:O	3:C:127:VAL:HG12	2.09	0.53
3:C:243:ILE:HG22	3:C:244:PHE:H	1.74	0.53
3:C:152:ASN:N	3:C:152:ASN:ND2	2.56	0.53
5:S:76:ALA:HA	5:S:79:ASP:HB3	1.89	0.53
3:A:22:VAL:HG21	3:A:37:VAL:CG1	2.39	0.53
3:G:69:ASP:OD1	5:T:17:ARG:NH2	2.42	0.53
3:G:22:VAL:HG23	3:G:23:VAL:N	2.23	0.53
4:D:212:ARG:HG3	4:D:212:ARG:HH11	1.72	0.53
1:E:701:DT:OP1	3:A:33:THR:HG21	2.09	0.53
4:D:62:THR:HG22	4:D:117:VAL:HG12	1.91	0.53
4:D:128:THR:O	4:D:131:HIS:HB2	2.08	0.53
3:A:50:ALA:HB1	4:D:115:LYS:HD2	1.91	0.53
5:T:12:SER:O	5:T:15:HIS:HD2	1.91	0.53
4:D:180:ILE:C	4:D:180:ILE:HD12	2.29	0.52
3:A:70:ILE:HG12	3:A:70:ILE:O	2.08	0.52
3:G:11:GLU:CB	3:G:40:THR:HG23	2.40	0.52
4:D:43:ARG:HG2	4:D:43:ARG:NH1	2.23	0.52
5:Y:56:GLN:CD	5:Y:56:GLN:H	2.12	0.52
3:C:146:ALA:HB2	3:C:297:ILE:HG21	1.91	0.52
3:G:128:THR:O	3:G:131:HIS:HB2	2.09	0.52
4:D:69:ASP:HA	4:D:97:ASN:HD22	1.73	0.52
4:D:114:GLY:C	4:D:116:GLN:H	2.12	0.52
4:D:104:LYS:O	4:D:107:HIS:HB3	2.09	0.52
5:T:87:GLY:C	5:T:88:GLU:HG2	2.29	0.52
4:D:15:SER:O	4:D:19:VAL:HG23	2.10	0.52
4:D:172:LEU:HD22	4:D:242:ALA:CB	2.40	0.52
3:G:141:PRO:O	3:G:142:VAL:CG2	2.58	0.52
3:A:216:ILE:CG2	3:A:216:ILE:O	2.58	0.52
3:C:112:MSE:O	3:C:115:LYS:N	2.42	0.52
3:C:188:GLU:N	3:C:188:GLU:CD	2.62	0.52
5:T:34:ASN:HA	5:T:44:LEU:H	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:220:ASP:O	3:C:225:SER:CB	2.57	0.52
4:D:261:ARG:CG	4:D:261:ARG:HH11	2.23	0.52
3:A:291:VAL:CG2	3:A:326:GLU:HG2	2.39	0.52
3:C:307:LYS:HD3	3:C:314:VAL:CB	2.39	0.52
3:G:65:VAL:O	3:G:65:VAL:HG23	2.09	0.52
3:A:208:GLY:C	3:A:210:PRO:HD3	2.30	0.52
3:C:162:GLU:O	3:C:165:ALA:HB3	2.09	0.52
4:D:252:LEU:HD13	4:D:279:LEU:HD11	1.90	0.52
3:C:307:LYS:HE2	3:C:314:VAL:HG21	1.91	0.52
5:S:26:ALA:O	5:S:45:LYS:HD3	2.09	0.52
5:Y:46:SEP:O3P	5:Y:48:MET:HB3	2.10	0.52
3:C:300:VAL:O	3:C:301:ALA:C	2.48	0.52
4:D:244:PHE:CD1	4:D:272:ILE:HG22	2.45	0.52
5:L:18:PRO:HA	5:L:84:GLU:CD	2.30	0.52
1:H:712:DA:H2''	1:H:713:DC:C5'	2.40	0.52
4:D:3:VAL:CG1	4:D:7:ASP:CB	2.88	0.52
2:R:701:DT:H2''	2:R:702:DG:C8	2.44	0.52
4:D:280:SER:OG	4:D:287:LEU:HB3	2.10	0.52
3:G:85:ILE:HD11	5:L:47:ILE:HD13	1.91	0.52
3:C:151:THR:OG1	3:C:153:GLN:HB2	2.09	0.52
5:Y:84:GLU:HA	5:Y:84:GLU:OE1	2.10	0.52
1:H:709:DC:OP2	3:C:5:ILE:HG22	2.09	0.52
3:C:109:LEU:CD2	3:C:135:LEU:HD12	2.40	0.52
4:D:182:PHE:CE1	4:D:184:SER:CB	2.92	0.52
4:D:22:VAL:HG21	4:D:37:VAL:CG1	2.38	0.52
3:C:264:ASN:ND2	3:C:267:ASN:N	2.52	0.52
4:D:293:PRO:O	4:D:294:MSE:C	2.48	0.52
3:C:104:LYS:O	3:C:108:LEU:HG	2.09	0.52
4:D:98:SER:O	4:D:99:ASP:HB2	2.10	0.52
5:L:32:ASP:CB	5:L:66:GLU:HG3	2.39	0.52
3:G:185:GLY:HA3	3:G:221:TYR:CE1	2.45	0.52
4:D:277:THR:O	4:D:279:LEU:N	2.42	0.52
3:A:180:ILE:H	3:A:180:ILE:HD13	1.74	0.52
3:C:235:GLU:O	3:C:236:GLU:C	2.47	0.52
3:C:296:ASP:O	3:C:300:VAL:HG23	2.10	0.52
3:G:80:ARG:HD3	3:C:70:ILE:CD1	2.39	0.52
5:L:2:ALA:O	5:L:3:GLN:HB3	2.09	0.52
3:G:115:LYS:O	3:G:116:GLN:HB2	2.10	0.52
3:C:194:ALA:C	3:C:195:LYS:HD2	2.30	0.52
3:A:294:MSE:O	3:A:297:ILE:HB	2.10	0.52
3:G:145:ALA:O	3:G:147:SER:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:68:PRO:HB2	3:C:75:TYR:CE2	2.45	0.52
3:A:223:TYR:CD2	4:D:282:MSE:HG2	2.45	0.52
3:A:288:THR:HG22	3:A:328:ARG:H	1.75	0.52
3:A:38:LEU:O	3:A:41:ILE:HG23	2.10	0.52
2:B:709:DC:H5'	2:B:709:DC:H6	1.75	0.52
4:D:169:VAL:HG13	4:D:170:GLN:N	2.25	0.52
4:D:201:LYS:CD	4:D:202:ARG:N	2.73	0.52
3:A:191:ILE:HG22	3:A:192:ASN:ND2	2.25	0.52
3:G:145:ALA:O	3:G:146:ALA:C	2.49	0.52
3:C:82:ILE:HD11	3:C:123:MSE:CE	2.40	0.51
5:S:43:ASN:HB3	5:S:46:SEP:HB2	1.91	0.51
3:C:265:VAL:HG13	3:C:271:ILE:HD12	1.91	0.51
3:A:22:VAL:HG12	3:A:29:VAL:HG11	1.92	0.51
3:G:296:ASP:O	3:G:300:VAL:HG23	2.10	0.51
3:G:208:GLY:C	3:G:209:LEU:HD23	2.30	0.51
5:Y:63:ILE:HG23	5:Y:63:ILE:O	2.11	0.51
3:A:89:TYR:CG	3:A:306:THR:HG21	2.45	0.51
5:T:9:THR:CG2	5:T:88:GLU:HG3	2.40	0.51
3:C:277:THR:HG22	3:C:278:ARG:N	2.26	0.51
3:G:245:VAL:HB	3:G:251:ALA:HB2	1.91	0.51
3:G:285:PRO:O	3:G:286:GLN:C	2.49	0.51
3:C:36:LYS:O	3:C:39:GLU:HB3	2.10	0.51
4:D:302:MSE:HA	4:D:302:MSE:CE	2.35	0.51
1:H:704:DA:H61	2:R:711:DT:H3	1.58	0.51
3:G:83:GLU:HG3	3:G:84:ASP:N	2.25	0.51
3:C:159:ILE:HG13	3:C:159:ILE:O	2.11	0.51
3:C:295:TYR:CD1	3:C:295:TYR:C	2.83	0.51
3:A:121:ILE:HG13	3:A:305:LEU:CD2	2.40	0.51
5:L:47:ILE:O	5:L:51:MET:HB2	2.11	0.51
3:A:49:ASN:HD21	4:D:116:GLN:HG3	1.75	0.51
3:C:295:TYR:CD1	3:C:295:TYR:O	2.63	0.51
3:A:220:ASP:O	3:A:250:MSE:SE	2.78	0.51
3:A:37:VAL:O	3:A:41:ILE:HG22	2.10	0.51
3:G:53:ARG:O	3:G:53:ARG:HG2	2.11	0.51
4:D:287:LEU:HD12	4:D:288:THR:N	2.22	0.51
4:D:22:VAL:HG11	4:D:37:VAL:HG13	1.92	0.51
5:L:72:ASP:O	5:L:76:ALA:HB2	2.11	0.51
3:C:111:ASN:ND2	6:C:947:SO4:O1	2.44	0.51
4:D:5:ILE:HD11	4:D:19:VAL:CG1	2.40	0.51
3:C:173:ILE:HD13	3:C:207:SER:OG	2.11	0.51
3:A:64:GLY:HA3	3:A:112:MSE:SE	2.61	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:30:LYS:HG2	4:D:32:SER:H	1.74	0.51
3:G:180:ILE:H	3:G:180:ILE:HD13	1.74	0.51
3:G:204:LEU:CD1	3:G:211:VAL:HG13	2.41	0.51
3:A:261:ARG:NH1	3:A:261:ARG:HG3	2.26	0.51
5:L:19:ALA:O	5:L:23:VAL:HG23	2.10	0.51
4:D:259:GLN:C	4:D:261:ARG:H	2.14	0.51
3:A:275:ASP:O	3:A:276:ASN:HB3	2.10	0.51
4:D:182:PHE:HB2	4:D:200:TYR:CD2	2.46	0.51
3:C:204:LEU:HD12	3:C:211:VAL:CG2	2.41	0.51
3:G:159:ILE:CD1	3:G:321:LEU:O	2.58	0.51
1:H:702:DG:H5''	3:G:15:SER:CB	2.39	0.51
4:D:292:GLN:O	4:D:292:GLN:HG3	2.11	0.51
3:C:160:ASP:C	3:C:162:GLU:H	2.14	0.51
5:S:4:LYS:NZ	5:S:78:GLU:OE1	2.43	0.51
5:L:26:ALA:HB1	5:L:33:ILE:HD12	1.92	0.51
4:D:152:ASN:N	4:D:152:ASN:HD22	2.08	0.51
2:R:702:DG:H2'	2:R:703:DT:H72	1.91	0.51
4:D:259:GLN:NE2	4:D:260:ASP:HA	2.26	0.51
4:D:264:ASN:C	4:D:264:ASN:HD22	2.09	0.51
5:T:12:SER:O	5:T:15:HIS:CD2	2.63	0.51
5:L:10:ALA:HB2	5:L:85:GLY:O	2.10	0.51
3:C:212:ARG:O	3:C:215:TYR:N	2.43	0.51
3:A:3:VAL:HG13	3:A:44:LEU:HD21	1.93	0.51
3:C:168:ALA:CB	3:C:244:PHE:HE2	2.24	0.51
3:A:194:ALA:O	3:A:195:LYS:HD2	2.11	0.51
5:Y:67:GLY:O	5:Y:68:SER:C	2.48	0.51
4:D:291:VAL:HB	4:D:324:ARG:O	2.11	0.51
3:A:25:GLY:O	3:A:26:ASN:C	2.49	0.51
1:H:714:DA:N1	2:R:701:DT:O2	2.44	0.51
3:A:73:ILE:HG22	3:A:74:PHE:N	2.24	0.51
5:Y:68:SER:OG	5:Y:69:ASP:N	2.43	0.51
3:G:67:ILE:HD11	3:G:75:TYR:HB3	1.92	0.51
3:G:116:GLN:HG3	3:C:49:ASN:HD21	1.76	0.50
3:A:247:THR:CG2	3:A:248:ASP:N	2.73	0.50
4:D:273:GLY:O	4:D:289:SER:HA	2.12	0.50
3:C:265:VAL:O	3:C:269:LEU:O	2.29	0.50
2:B:709:DC:OP2	3:A:5:ILE:HB	2.11	0.50
4:D:293:PRO:O	4:D:295:TYR:N	2.44	0.50
3:G:154:ILE:N	3:G:154:ILE:HD12	2.17	0.50
3:C:319:VAL:HG21	5:T:48:MET:CE	2.41	0.50
3:G:99:ASP:C	3:G:101:ASN:H	2.14	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:706:DG:C2'	2:B:707:DC:C5	2.94	0.50
3:G:83:GLU:O	3:G:84:ASP:C	2.48	0.50
5:S:18:PRO:HA	5:S:84:GLU:OE2	2.12	0.50
5:S:4:LYS:HG2	5:S:5:THR:N	2.26	0.50
3:C:283:VAL:HG23	3:C:286:GLN:HA	1.94	0.50
5:S:2:ALA:HA	5:S:65:ALA:O	2.11	0.50
5:L:46:SEP:O	5:L:50:VAL:HG23	2.11	0.50
2:R:710:DT:H2''	2:R:711:DT:C6	2.46	0.50
2:R:713:DC:H2'	2:R:714:DA:C8	2.46	0.50
4:D:223:TYR:O	4:D:226:GLY:N	2.39	0.50
3:A:4:THR:HG23	3:A:7:ASP:H	1.75	0.50
3:C:157:VAL:HG21	3:C:301:ALA:HA	1.92	0.50
3:G:204:LEU:HD12	3:G:211:VAL:HG13	1.94	0.50
3:G:61:THR:N	3:G:118:ASP:OD2	2.42	0.50
3:A:66:ILE:HG13	3:A:112:MSE:HE1	1.94	0.50
3:A:101:ASN:O	3:A:105:GLU:HG3	2.12	0.50
3:G:142:VAL:HG12	3:G:143:VAL:N	2.26	0.50
3:G:11:GLU:HB2	3:G:40:THR:HG23	1.94	0.50
4:D:2:ASN:O	4:D:2:ASN:OD1	2.29	0.50
3:A:271:ILE:H	3:A:331:THR:HG22	1.76	0.50
5:T:47:ILE:HG22	5:T:51:MET:HE1	1.94	0.50
3:C:134:GLU:HA	3:C:134:GLU:OE1	2.12	0.50
3:A:187:LEU:HB2	3:A:218:GLU:OE2	2.12	0.50
3:A:193:HIS:ND1	3:A:194:ALA:N	2.60	0.50
3:G:215:TYR:CZ	3:G:240:PRO:HG3	2.46	0.50
4:D:259:GLN:HB2	4:D:284:ARG:HH22	1.76	0.50
4:D:157:VAL:O	4:D:158:THR:HB	2.12	0.50
4:D:303:ARG:HH21	4:D:306:THR:CB	2.22	0.50
4:D:269:LEU:O	4:D:269:LEU:HD12	2.12	0.50
4:D:107:HIS:O	4:D:110:ASN:N	2.41	0.50
4:D:187:LEU:HD21	4:D:193:HIS:HD2	1.77	0.50
2:R:701:DT:H2'	3:C:18:THR:HG23	1.94	0.50
3:A:247:THR:HG22	3:A:248:ASP:N	2.26	0.50
3:C:38:LEU:O	3:C:38:LEU:HD23	2.11	0.50
3:G:47:ARG:HH22	3:C:113:LEU:HB2	1.76	0.50
1:H:700:DC:H3'	3:G:29:VAL:HA	1.92	0.50
3:G:154:ILE:HD13	3:G:154:ILE:O	2.11	0.50
3:G:37:VAL:O	3:G:41:ILE:HG13	2.12	0.50
3:G:252:LEU:HG	3:G:283:VAL:HG21	1.93	0.50
5:L:32:ASP:HB2	5:L:66:GLU:HG3	1.94	0.50
3:C:307:LYS:HD3	3:C:314:VAL:HB	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:234:LEU:HB3	3:C:235:GLU:OE1	2.12	0.49
3:C:22:VAL:HG23	3:C:23:VAL:N	2.26	0.49
3:G:85:ILE:HG22	3:G:302:MSE:HG3	1.94	0.49
3:C:182:PHE:HD1	3:C:216:ILE:HG23	1.76	0.49
3:A:193:HIS:CE1	3:A:194:ALA:HB2	2.46	0.49
3:G:166:PHE:C	3:G:166:PHE:CD1	2.85	0.49
3:C:11:GLU:HG3	3:C:44:LEU:HD21	1.94	0.49
3:C:248:ASP:OD1	3:C:275:ASP:HB2	2.12	0.49
3:A:252:LEU:HD21	3:A:256:HIS:CD2	2.47	0.49
4:D:277:THR:C	4:D:279:LEU:H	2.15	0.49
3:A:200:TYR:CE1	3:A:204:LEU:HD12	2.47	0.49
5:S:63:ILE:CD1	5:S:77:LEU:HD13	2.39	0.49
3:G:49:ASN:ND2	3:G:52:ALA:CB	2.62	0.49
1:E:700:DC:O5'	3:A:28:ASN:O	2.25	0.49
3:A:43:ARG:HH11	3:A:43:ARG:HG3	1.77	0.49
2:R:706:DG:H2''	2:R:707:DC:C6	2.47	0.49
3:G:204:LEU:CD1	3:G:211:VAL:CG1	2.90	0.49
3:G:43:ARG:HE	3:G:44:LEU:HB2	1.77	0.49
3:C:29:VAL:CG1	3:C:34:ARG:HB2	2.38	0.49
3:G:136:LYS:NZ	3:G:153:GLN:OE1	2.22	0.49
3:C:259:GLN:HE22	3:C:284:ARG:HD2	1.77	0.49
5:T:23:VAL:O	5:T:26:ALA:N	2.43	0.49
3:G:82:ILE:CD1	3:G:121:ILE:HG21	2.41	0.49
1:H:702:DG:H5''	3:G:15:SER:HB3	1.94	0.49
1:E:708:DG:C2'	1:E:709:DC:H5''	2.42	0.49
3:G:127:VAL:HG11	3:G:149:GLU:CB	2.43	0.49
3:A:324:ARG:HH11	3:A:324:ARG:CB	2.26	0.49
5:Y:77:LEU:O	5:Y:81:MET:HG2	2.13	0.49
4:D:249:GLU:C	4:D:251:ALA:H	2.15	0.49
4:D:98:SER:C	4:D:100:GLN:H	2.16	0.49
4:D:230:VAL:HG22	4:D:254:VAL:HA	1.94	0.49
4:D:82:ILE:HD11	4:D:123:MSE:HE3	1.93	0.49
3:C:121:ILE:HD12	3:C:302:MSE:HE2	1.94	0.49
1:H:708:DG:H1'	3:C:52:ALA:HB1	1.93	0.49
3:A:170:GLN:O	3:A:171:SER:C	2.51	0.49
3:A:287:LEU:HD12	3:A:288:THR:N	2.26	0.49
3:A:46:TYR:CE1	3:A:48:PRO:HG3	2.41	0.49
4:D:310:ASN:O	4:D:311:LYS:HB2	2.12	0.49
3:G:282:MSE:HG2	3:C:252:LEU:CD2	2.43	0.49
4:D:149:GLU:HG3	4:D:149:GLU:O	2.13	0.49
3:A:4:THR:OG1	3:A:5:ILE:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:49:GLY:O	5:S:53:LEU:HD22	2.13	0.49
4:D:255:ILE:CG2	4:D:265:VAL:HG21	2.41	0.49
3:A:291:VAL:HG21	3:A:326:GLU:HG2	1.93	0.49
4:D:144:LEU:N	4:D:144:LEU:CD2	2.75	0.49
3:A:38:LEU:HA	3:A:41:ILE:CG2	2.42	0.49
4:D:75:TYR:O	4:D:79:ALA:N	2.40	0.49
2:R:712:DT:C2'	2:R:713:DC:O4'	2.58	0.49
3:G:151:THR:CB	3:G:153:GLN:HE21	2.25	0.49
3:G:157:VAL:HG21	3:G:301:ALA:HA	1.95	0.49
3:C:1:MSE:SE	3:C:47:ARG:HH21	2.46	0.49
3:C:82:ILE:CG2	3:C:302:MSE:HE3	2.42	0.49
2:R:711:DT:C2'	2:R:712:DT:C6	2.91	0.49
4:D:109:LEU:O	4:D:113:LEU:HG	2.12	0.49
3:A:193:HIS:HA	3:A:197:VAL:HG21	1.93	0.49
3:A:306:THR:O	3:A:310:ASN:ND2	2.46	0.49
3:G:22:VAL:CG2	3:G:23:VAL:N	2.75	0.49
4:D:245:VAL:HG21	4:D:251:ALA:HA	1.94	0.49
3:G:223:TYR:CE1	3:G:227:ILE:HD11	2.48	0.49
3:A:180:ILE:N	3:A:180:ILE:HD13	2.27	0.49
5:S:63:ILE:HG13	5:S:64:SER:N	2.28	0.49
5:S:77:LEU:O	5:S:81:MET:HG2	2.12	0.49
3:G:251:ALA:O	3:G:255:ILE:HG13	2.13	0.49
2:B:711:DT:H2"	2:B:712:DT:O4'	2.13	0.49
3:G:144:LEU:HD22	3:G:144:LEU:H	1.76	0.49
3:G:4:THR:HG23	3:G:7:ASP:CG	2.32	0.49
3:A:28:ASN:O	3:A:29:VAL:HG23	2.13	0.49
3:C:22:VAL:CG2	3:C:23:VAL:N	2.76	0.49
5:L:67:GLY:H	5:L:70:GLU:CD	2.15	0.49
3:A:187:LEU:CD1	3:A:218:GLU:HB2	2.43	0.49
3:A:247:THR:CG2	3:A:249:GLU:H	2.23	0.48
3:A:284:ARG:CB	3:A:285:PRO:HD3	2.15	0.48
5:T:35:LEU:C	5:T:35:LEU:HD23	2.33	0.48
4:D:144:LEU:CD2	4:D:144:LEU:H	2.22	0.48
3:G:85:ILE:HD11	5:L:47:ILE:HD11	1.95	0.48
2:R:712:DT:C4'	2:R:712:DT:OP1	2.60	0.48
4:D:295:TYR:CD1	5:Y:16:ALA:HA	2.48	0.48
3:G:43:ARG:HH21	3:G:44:LEU:HD22	1.78	0.48
3:A:270:GLU:OE1	3:A:331:THR:HB	2.13	0.48
3:A:14:VAL:HG21	3:A:37:VAL:HG22	1.95	0.48
3:G:303:ARG:CG	5:L:47:ILE:HG22	2.42	0.48
3:G:154:ILE:HD12	3:G:154:ILE:O	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:67:GLY:N	5:L:70:GLU:CG	2.74	0.48
3:A:303:ARG:O	3:A:306:THR:OG1	2.24	0.48
4:D:186:THR:CG2	4:D:187:LEU:N	2.75	0.48
4:D:16:MSE:HE3	4:D:16:MSE:HB3	1.72	0.48
1:H:709:DC:H2'	1:H:710:DT:C7	2.43	0.48
2:R:701:DT:H6	2:R:701:DT:H5'	1.79	0.48
4:D:228:GLU:HA	4:D:231:GLU:HG3	1.94	0.48
3:A:265:VAL:HG11	3:A:285:PRO:CB	2.44	0.48
3:A:271:ILE:N	3:A:331:THR:CG2	2.76	0.48
4:D:85:ILE:CG1	5:Y:47:ILE:HD12	2.43	0.48
4:D:292:GLN:OE1	4:D:297:ILE:HD11	2.12	0.48
3:G:5:ILE:CG2	3:G:6:TYR:N	2.76	0.48
3:G:146:ALA:H	3:G:297:ILE:HG21	1.76	0.48
2:R:711:DT:H2'	2:R:712:DT:C7	2.43	0.48
1:H:706:DG:H2''	1:H:707:DC:C6	2.47	0.48
3:G:226:GLY:O	3:G:230:VAL:CG2	2.60	0.48
5:Y:69:ASP:OD1	5:Y:69:ASP:C	2.51	0.48
3:A:17:ALA:O	3:A:21:ARG:N	2.30	0.48
4:D:67:ILE:O	4:D:97:ASN:HA	2.13	0.48
5:L:44:LEU:CD1	5:L:77:LEU:HD13	2.43	0.48
3:C:130:GLU:OE2	3:C:133:GLU:OE1	2.31	0.48
4:D:159:ILE:CG2	4:D:160:ASP:N	2.76	0.48
3:A:3:VAL:CG1	3:A:44:LEU:CG	2.89	0.48
4:D:243:ILE:HG22	4:D:244:PHE:N	2.29	0.48
3:C:160:ASP:C	3:C:162:GLU:N	2.66	0.48
4:D:5:ILE:CG2	4:D:16:MSE:HE1	2.44	0.48
3:G:33:THR:O	3:G:34:ARG:C	2.52	0.48
3:C:53:ARG:O	3:C:54:GLY:C	2.52	0.48
3:G:49:ASN:HB2	3:C:116:GLN:NE2	2.28	0.48
3:A:70:ILE:N	3:A:97:ASN:ND2	2.60	0.48
3:G:82:ILE:HG23	3:G:302:MSE:CE	2.44	0.48
3:A:186:THR:HB	3:A:189:GLU:HG3	1.96	0.48
3:C:315:ASP:CG	3:C:316:SER:N	2.66	0.48
3:C:121:ILE:HG13	3:C:305:LEU:HD22	1.94	0.48
3:A:271:ILE:N	3:A:271:ILE:HD12	2.29	0.48
3:G:43:ARG:HH21	3:G:44:LEU:CD1	2.26	0.48
3:G:83:GLU:HG2	3:C:97:ASN:ND2	2.28	0.48
5:T:8:VAL:CG2	5:T:57:LYS:HA	2.44	0.48
3:A:113:LEU:O	3:A:116:GLN:NE2	2.46	0.48
3:G:44:LEU:O	3:G:44:LEU:HD12	2.13	0.48
4:D:290:VAL:HG13	4:D:325:ILE:HG23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:209:LEU:O	3:C:210:PRO:O	2.31	0.48
3:G:34:ARG:O	3:G:38:LEU:HD12	2.14	0.48
3:G:114:GLY:C	3:G:116:GLN:HE21	2.17	0.48
3:C:82:ILE:HG23	3:C:302:MSE:HE2	1.93	0.48
3:A:17:ALA:O	3:A:20:SER:HB3	2.13	0.48
3:A:1:MSE:CE	3:A:1:MSE:HB3	2.44	0.48
4:D:178:LYS:O	4:D:209:LEU:HD13	2.13	0.48
4:D:242:ALA:HA	4:D:270:GLU:H	1.79	0.48
3:G:93:ILE:HG13	3:G:93:ILE:O	2.14	0.48
3:G:60:THR:O	3:G:62:THR:HG22	2.14	0.48
5:L:34:ASN:ND2	5:L:41:THR:HG21	2.29	0.48
4:D:12:ALA:HB3	4:D:14:VAL:HG22	1.96	0.48
3:C:234:LEU:CD1	3:C:261:ARG:HG3	2.44	0.47
3:A:12:ALA:N	3:A:40:THR:HG21	2.29	0.47
3:C:158:THR:HG1	3:C:161:TYR:HE1	1.60	0.47
3:C:24:ASN:HD21	3:C:53:ARG:NH2	2.11	0.47
3:C:324:ARG:CG	3:C:325:ILE:N	2.76	0.47
3:C:325:ILE:HD13	3:C:327:PHE:HE1	1.80	0.47
3:A:39:GLU:HG3	3:A:40:THR:H	1.79	0.47
1:E:703:DA:C2'	1:E:704:DA:H5'	2.44	0.47
3:G:88:MSE:HG2	3:G:89:TYR:CD2	2.49	0.47
4:D:252:LEU:HD21	4:D:283:VAL:HG22	1.96	0.47
3:A:328:ARG:HH11	3:A:328:ARG:HG2	1.78	0.47
3:G:263:LEU:N	3:G:263:LEU:HD12	2.28	0.47
4:D:295:TYR:C	4:D:295:TYR:CD1	2.87	0.47
3:C:2:ASN:O	3:C:4:THR:N	2.46	0.47
5:T:46:SEP:O3P	5:T:48:MET:HB2	2.14	0.47
3:A:234:LEU:HD12	3:A:261:ARG:HH12	1.79	0.47
3:G:241:THR:HG22	3:G:241:THR:O	2.13	0.47
3:C:220:ASP:O	3:C:225:SER:HB3	2.14	0.47
4:D:261:ARG:CG	4:D:261:ARG:NH1	2.78	0.47
3:A:258:ALA:HB1	3:A:263:LEU:HB2	1.97	0.47
5:S:12:SER:O	5:S:15:HIS:HD2	1.97	0.47
3:C:303:ARG:O	3:C:306:THR:OG1	2.33	0.47
3:G:282:MSE:HG3	3:C:223:TYR:CD2	2.49	0.47
1:E:704:DA:H2	2:B:711:DT:H3	1.60	0.47
4:D:209:LEU:O	4:D:210:PRO:O	2.31	0.47
3:C:106:LEU:HG	3:C:134:GLU:HG2	1.96	0.47
3:A:188:GLU:O	3:A:193:HIS:HD2	1.98	0.47
3:C:87:THR:HG22	3:C:88:MSE:N	2.30	0.47
3:G:116:GLN:CG	3:C:49:ASN:ND2	2.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:709:DC:C2'	1:H:710:DT:C6	2.98	0.47
2:R:702:DG:C5'	3:C:15:SER:HB2	2.45	0.47
3:A:168:ALA:HB1	3:A:272:ILE:CD1	2.44	0.47
3:C:245:VAL:HG21	3:C:251:ALA:HA	1.96	0.47
3:C:284:ARG:CB	3:C:285:PRO:CD	2.93	0.47
4:D:209:LEU:N	4:D:210:PRO:CD	2.77	0.47
3:A:318:ILE:N	3:A:318:ILE:CD1	2.78	0.47
5:T:17:ARG:HB2	5:T:18:PRO:HD3	1.96	0.47
4:D:249:GLU:C	4:D:251:ALA:N	2.68	0.47
3:G:224:ASP:O	3:G:228:GLU:HG3	2.14	0.47
5:Y:71:ALA:O	5:Y:74:LEU:N	2.47	0.47
3:C:248:ASP:OD1	3:C:274:PHE:O	2.33	0.47
3:A:222:THR:O	3:A:223:TYR:C	2.53	0.47
5:L:69:ASP:O	5:L:70:GLU:C	2.52	0.47
3:C:169:VAL:O	3:C:170:GLN:C	2.54	0.47
3:G:73:ILE:CG2	3:C:278:ARG:NH2	2.38	0.47
3:A:264:ASN:OD1	3:A:266:PRO:HD2	2.15	0.47
3:A:41:ILE:HD13	3:A:41:ILE:O	2.15	0.47
5:Y:9:THR:O	5:Y:10:ALA:C	2.52	0.47
3:A:77:GLU:HG3	3:A:294:MSE:HE2	1.97	0.47
3:C:214:SER:C	3:C:216:ILE:H	2.19	0.47
3:A:304:LEU:CD2	3:A:308:TYR:CE2	2.97	0.47
3:C:160:ASP:HB3	3:C:163:GLN:HB2	1.96	0.47
3:G:62:THR:HA	3:G:92:ASN:O	2.15	0.47
3:C:121:ILE:HG13	3:C:305:LEU:CD2	2.45	0.47
4:D:255:ILE:HG12	4:D:271:ILE:CD1	2.44	0.47
4:D:265:VAL:HB	4:D:285:PRO:HG2	1.97	0.47
5:T:26:ALA:CB	5:T:77:LEU:HD21	2.29	0.47
4:D:181:ALA:CB	4:D:233:LEU:HD11	2.45	0.47
3:G:217:VAL:HG11	3:G:233:LEU:HD11	1.96	0.47
3:G:128:THR:H	3:G:131:HIS:CG	2.32	0.47
3:C:307:LYS:HZ2	3:C:314:VAL:HG11	1.79	0.46
5:T:79:ASP:HB3	5:T:83:LYS:CE	2.28	0.46
3:A:82:ILE:HG23	3:A:302:MSE:CE	2.44	0.46
3:G:50:ALA:HB3	3:C:115:LYS:HD3	1.96	0.46
4:D:187:LEU:C	4:D:189:GLU:N	2.68	0.46
4:D:187:LEU:O	4:D:189:GLU:N	2.48	0.46
3:C:169:VAL:O	3:C:172:LEU:HB2	2.15	0.46
3:C:208:GLY:C	3:C:209:LEU:HD12	2.36	0.46
3:G:108:LEU:O	3:G:112:MSE:HB2	2.14	0.46
3:C:154:ILE:HD12	3:C:155:PRO:CD	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:714:DA:C2'	2:R:715:DG:C8	2.99	0.46
5:Y:31:SER:HA	5:Y:67:GLY:HA3	1.97	0.46
5:T:17:ARG:N	5:T:18:PRO:CD	2.78	0.46
3:A:162:GLU:OE1	3:A:198:LYS:HE3	2.15	0.46
3:G:132:VAL:O	3:G:132:VAL:HG12	2.15	0.46
3:A:241:THR:O	3:A:269:LEU:HA	2.16	0.46
3:A:248:ASP:OD1	3:A:274:PHE:O	2.33	0.46
5:T:36:GLU:HA	5:T:41:THR:HA	1.97	0.46
5:S:22:LEU:HD11	5:S:81:MET:HE2	1.97	0.46
3:C:288:THR:H	3:C:330:SER:HB3	1.80	0.46
3:G:83:GLU:HA	3:G:93:ILE:HD13	1.97	0.46
3:G:4:THR:N	3:G:7:ASP:OD2	2.41	0.46
4:D:140:VAL:HB	4:D:141:PRO:HD2	1.96	0.46
3:G:263:LEU:CD2	3:G:269:LEU:HD22	2.46	0.46
4:D:122:PHE:O	4:D:144:LEU:HA	2.16	0.46
3:C:37:VAL:C	3:C:39:GLU:N	2.68	0.46
3:A:234:LEU:HD12	3:A:261:ARG:NH1	2.31	0.46
3:C:159:ILE:HG22	3:C:321:LEU:O	2.16	0.46
3:A:158:THR:HG23	3:A:159:ILE:N	2.31	0.46
3:C:68:PRO:HG2	3:C:75:TYR:CZ	2.50	0.46
4:D:307:LYS:O	4:D:308:TYR:C	2.54	0.46
5:S:65:ALA:O	5:S:70:GLU:HB2	2.16	0.46
3:G:156:SER:N	3:G:317:SER:O	2.43	0.46
4:D:258:ALA:O	4:D:263:LEU:HB3	2.16	0.46
3:G:8:VAL:HG13	3:G:40:THR:CG2	2.43	0.46
3:G:113:LEU:CD1	3:C:47:ARG:HH12	2.25	0.46
3:C:143:VAL:CG1	3:C:305:LEU:HD13	2.45	0.46
2:B:701:DT:C2'	2:B:702:DG:C5'	2.88	0.46
3:G:180:ILE:HD11	3:G:204:LEU:CD1	2.45	0.46
1:E:708:DG:C1'	1:E:709:DC:H5''	2.40	0.46
5:Y:6:PHE:HE1	5:Y:63:ILE:CG2	2.27	0.46
3:A:245:VAL:HG11	3:A:251:ALA:CA	2.46	0.46
3:A:124:SER:OG	3:A:125:GLY:N	2.49	0.46
4:D:304:LEU:HG	4:D:308:TYR:CE2	2.51	0.46
3:A:305:LEU:HD11	3:A:309:MSE:HE2	1.97	0.46
3:A:324:ARG:CG	3:A:325:ILE:N	2.78	0.46
3:C:307:LYS:CD	3:C:314:VAL:HG21	2.46	0.46
3:G:284:ARG:CB	3:G:285:PRO:CD	2.88	0.46
5:T:22:LEU:HD13	5:T:80:THR:HG22	1.98	0.46
4:D:234:LEU:HD21	4:D:269:LEU:HD23	1.97	0.46
1:H:703:DA:H62	3:G:17:ALA:CB	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:62:THR:CG2	4:D:94:ILE:HG13	2.46	0.46
3:A:57:SER:O	3:A:58:LYS:HB2	2.15	0.46
5:L:4:LYS:HD3	5:L:78:GLU:OE1	2.15	0.46
4:D:18:THR:O	4:D:22:VAL:HG23	2.16	0.46
3:G:43:ARG:NE	3:G:44:LEU:HB2	2.31	0.46
3:A:224:ASP:C	3:A:226:GLY:N	2.69	0.46
3:A:226:GLY:O	3:A:227:ILE:C	2.55	0.46
3:A:115:LYS:O	3:A:116:GLN:HB2	2.15	0.46
4:D:112:MSE:HE3	4:D:112:MSE:HA	1.98	0.46
3:C:67:ILE:HD12	3:C:95:LEU:HD11	1.97	0.46
3:A:170:GLN:NE2	3:A:170:GLN:HA	2.26	0.46
4:D:170:GLN:HE21	4:D:173:ILE:HG13	1.80	0.46
5:L:17:ARG:N	5:L:18:PRO:CD	2.79	0.46
4:D:237:ASP:O	4:D:239:LYS:N	2.49	0.46
4:D:98:SER:C	4:D:100:GLN:N	2.69	0.46
3:C:183:VAL:HA	3:C:217:VAL:O	2.15	0.46
1:H:709:DC:H2'	1:H:710:DT:C5	2.51	0.45
1:E:706:DG:OP1	1:E:706:DG:C4'	2.53	0.45
3:C:285:PRO:O	3:C:286:GLN:C	2.54	0.45
3:A:8:VAL:CG2	3:A:44:LEU:HD23	2.47	0.45
4:D:78:LEU:HD11	4:D:123:MSE:HE1	1.98	0.45
4:D:166:PHE:CD2	4:D:203:ALA:HB2	2.52	0.45
3:G:80:ARG:HD3	3:C:70:ILE:HD11	1.98	0.45
3:G:84:ASP:OD1	3:G:295:TYR:OH	2.34	0.45
3:A:310:ASN:O	3:A:311:LYS:HB2	2.16	0.45
3:C:159:ILE:HD12	3:C:323:HIS:HB3	1.98	0.45
3:A:145:ALA:O	3:A:146:ALA:C	2.54	0.45
2:R:707:DC:C2	3:C:55:LEU:HD13	2.51	0.45
3:A:137:LYS:CA	3:A:137:LYS:HE2	2.44	0.45
4:D:310:ASN:C	4:D:312:GLU:H	2.19	0.45
5:S:9:THR:H	5:S:87:GLY:HA3	1.81	0.45
2:R:713:DC:C2'	2:R:714:DA:C8	3.00	0.45
3:A:148:ILE:HD13	3:A:190:PRO:HB2	1.98	0.45
3:A:224:ASP:O	3:A:226:GLY:N	2.49	0.45
3:A:160:ASP:HB2	3:A:320:GLN:OE1	2.16	0.45
3:A:267:ASN:O	3:A:268:ASP:C	2.54	0.45
5:S:11:ASP:HA	5:S:57:LYS:HE2	1.98	0.45
3:A:271:ILE:N	3:A:331:THR:HG22	2.32	0.45
3:A:284:ARG:HG2	4:D:256:HIS:HE1	1.81	0.45
3:A:39:GLU:HG3	3:A:40:THR:N	2.31	0.45
5:L:11:ASP:OD1	5:L:57:LYS:NZ	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:705:DA:H2"	2:B:706:DG:O5'	2.17	0.45
3:C:169:VAL:HG11	3:C:203:ALA:CB	2.46	0.45
3:A:154:ILE:O	3:A:154:ILE:HD12	2.17	0.45
3:G:1:MSE:C	3:G:2:ASN:O	2.54	0.45
3:G:128:THR:H	3:G:131:HIS:CD2	2.35	0.45
3:C:285:PRO:HG2	3:C:285:PRO:O	2.17	0.45
3:A:29:VAL:HB	3:A:34:ARG:NE	2.31	0.45
3:C:19:VAL:O	3:C:22:VAL:HG22	2.15	0.45
4:D:166:PHE:O	4:D:170:GLN:HB2	2.17	0.45
4:D:209:LEU:O	4:D:210:PRO:C	2.55	0.45
3:C:204:LEU:HD13	3:C:211:VAL:CG1	2.46	0.45
3:G:247:THR:HG22	3:G:249:GLU:N	2.31	0.45
1:H:700:DC:H42	2:R:715:DG:H1	1.63	0.45
3:A:304:LEU:HD22	3:A:308:TYR:HE2	1.80	0.45
3:C:170:GLN:HE21	3:C:170:GLN:CA	2.30	0.45
5:S:76:ALA:O	5:S:79:ASP:HB3	2.17	0.45
3:G:116:GLN:HG3	3:C:49:ASN:ND2	2.32	0.45
3:C:6:TYR:HB2	3:C:16:MSE:SE	2.66	0.45
3:A:330:SER:OG	3:A:331:THR:HG23	2.15	0.45
3:A:12:ALA:HB3	3:A:14:VAL:HG22	1.98	0.45
3:A:29:VAL:CG2	3:A:34:ARG:HH21	2.29	0.45
3:A:12:ALA:HB2	3:A:40:THR:HG21	1.98	0.45
4:D:290:VAL:CA	4:D:325:ILE:HG22	2.44	0.45
3:G:4:THR:OG1	3:G:5:ILE:N	2.50	0.45
3:A:144:LEU:HD11	3:A:154:ILE:CD1	2.47	0.45
5:Y:14:ILE:HG12	5:Y:19:ALA:HB2	1.99	0.45
1:E:714:DA:C3'	1:E:715:DG:H5"	2.46	0.45
3:C:106:LEU:O	3:C:107:HIS:C	2.54	0.45
3:G:39:GLU:C	3:G:41:ILE:N	2.67	0.45
3:C:170:GLN:O	3:C:171:SER:C	2.54	0.45
4:D:228:GLU:HA	4:D:231:GLU:CG	2.47	0.45
4:D:304:LEU:HB2	5:Y:48:MET:HE1	1.99	0.45
4:D:209:LEU:N	4:D:210:PRO:HD3	2.31	0.45
3:A:50:ALA:CB	4:D:115:LYS:HD2	2.47	0.45
3:A:230:VAL:HG21	3:A:254:VAL:HA	1.98	0.45
3:G:22:VAL:O	3:G:25:GLY:N	2.48	0.45
4:D:276:ASN:OD1	4:D:328:ARG:NH2	2.48	0.45
2:R:709:DC:H5"	2:R:709:DC:H6	1.82	0.45
3:A:149:GLU:HG3	3:A:149:GLU:O	2.16	0.45
5:S:47:ILE:HG23	5:S:51:MET:HE3	1.98	0.45
5:L:43:ASN:C	5:L:45:LYS:H	2.19	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:119:GLY:C	3:A:120:ILE:HG13	2.36	0.45
3:G:115:LYS:HZ1	3:C:92:ASN:CG	2.20	0.45
3:C:144:LEU:HD22	3:C:144:LEU:H	1.80	0.45
5:S:43:ASN:OD1	5:S:45:LYS:N	2.43	0.45
1:E:700:DC:H5''	3:A:28:ASN:C	2.37	0.45
3:C:189:GLU:O	3:C:192:ASN:HB2	2.16	0.45
3:A:212:ARG:HD3	3:A:215:TYR:CG	2.52	0.45
4:D:180:ILE:HD11	4:D:204:LEU:HD13	1.98	0.45
5:L:44:LEU:HA	5:L:44:LEU:HD23	1.85	0.45
5:S:66:GLU:N	5:S:66:GLU:OE1	2.50	0.45
2:R:702:DG:C2'	2:R:703:DT:H5'	2.35	0.45
3:C:303:ARG:NH1	3:C:303:ARG:CG	2.80	0.45
3:C:263:LEU:CD2	3:C:269:LEU:HG	2.47	0.45
3:G:278:ARG:O	3:G:279:LEU:C	2.56	0.45
3:A:4:THR:HG22	3:A:7:ASP:OD2	2.17	0.45
4:D:181:ALA:HB1	4:D:233:LEU:HD11	1.99	0.45
3:C:204:LEU:CD1	3:C:211:VAL:CG1	2.95	0.45
1:H:703:DA:H2	2:R:712:DT:H3	1.65	0.45
3:G:98:SER:O	3:G:99:ASP:HB2	2.17	0.45
3:C:159:ILE:O	3:C:161:TYR:CD1	2.70	0.45
3:C:201:LYS:O	3:C:202:ARG:C	2.50	0.45
4:D:252:LEU:HG	4:D:283:VAL:HG22	1.98	0.44
3:C:291:VAL:N	3:C:324:ARG:O	2.48	0.44
3:C:327:PHE:CD1	3:C:327:PHE:N	2.85	0.44
5:Y:46:SEP:O	5:Y:50:VAL:HG23	2.17	0.44
3:A:305:LEU:CG	3:A:309:MSE:HE3	2.41	0.44
4:D:72:ASN:ND2	4:D:73:ILE:HD13	2.31	0.44
3:A:157:VAL:HG22	3:A:157:VAL:O	2.17	0.44
5:S:34:ASN:HD21	5:S:41:THR:CG2	2.30	0.44
3:A:121:ILE:HD12	3:A:302:MSE:CE	2.44	0.44
4:D:62:THR:O	4:D:117:VAL:HG12	2.17	0.44
4:D:109:LEU:HD12	4:D:120:ILE:HD13	1.99	0.44
5:L:8:VAL:HG11	5:L:55:ILE:HG23	1.99	0.44
3:C:160:ASP:O	3:C:162:GLU:N	2.50	0.44
3:C:315:ASP:O	3:C:316:SER:HB3	2.17	0.44
3:C:30:LYS:HA	3:C:31:PRO:HD3	1.79	0.44
5:S:37:PHE:HE2	5:S:59:ALA:HB1	1.83	0.44
3:A:211:VAL:O	3:A:211:VAL:HG23	2.17	0.44
4:D:327:PHE:CD1	4:D:327:PHE:N	2.84	0.44
3:G:82:ILE:HG23	3:G:302:MSE:HE2	1.99	0.44
2:R:710:DT:O4'	3:G:56:ALA:HB1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:22:VAL:HG21	3:G:37:VAL:CG1	2.47	0.44
3:C:278:ARG:HB3	3:C:282:MSE:CE	2.48	0.44
3:A:149:GLU:HG2	3:A:154:ILE:HD12	1.98	0.44
3:G:287:LEU:HD11	3:G:289:SER:HB3	2.00	0.44
3:G:66:ILE:HG23	3:G:108:LEU:HD12	1.99	0.44
3:A:204:LEU:HD23	3:A:204:LEU:HA	1.79	0.44
3:G:263:LEU:HB3	3:G:268:ASP:HB2	1.99	0.44
3:A:68:PRO:O	3:A:97:ASN:HB3	2.17	0.44
3:G:141:PRO:C	3:G:142:VAL:HG23	2.37	0.44
3:G:43:ARG:HH21	3:G:44:LEU:CD2	2.30	0.44
5:L:12:SER:O	5:L:15:HIS:HD2	2.01	0.44
3:C:2:ASN:OD1	3:C:2:ASN:C	2.55	0.44
3:C:158:THR:OG1	3:C:161:TYR:CE1	2.62	0.44
5:L:3:GLN:N	5:L:74:LEU:HD21	2.33	0.44
4:D:315:ASP:O	4:D:316:SER:HB2	2.18	0.44
4:D:89:TYR:O	4:D:91:TYR:HD1	2.00	0.44
4:D:283:VAL:O	4:D:284:ARG:O	2.36	0.44
3:C:265:VAL:HA	3:C:269:LEU:CD1	2.48	0.44
4:D:183:VAL:HG12	4:D:250:MSE:HE2	1.99	0.44
3:C:67:ILE:HD13	3:C:67:ILE:H	1.82	0.44
1:E:706:DG:C2'	1:E:707:DC:C5	3.01	0.44
3:A:22:VAL:HG21	3:A:37:VAL:HG11	1.99	0.44
5:Y:46:SEP:O3P	5:Y:48:MET:CB	2.65	0.44
4:D:165:ALA:HA	4:D:244:PHE:CZ	2.53	0.44
3:A:70:ILE:O	3:A:70:ILE:CG1	2.65	0.44
3:G:99:ASP:C	3:G:101:ASN:N	2.70	0.44
5:L:18:PRO:HA	5:L:84:GLU:OE1	2.18	0.44
3:C:181:ALA:HB1	3:C:233:LEU:HD11	1.99	0.44
3:G:33:THR:O	3:G:35:LYS:N	2.50	0.44
3:A:295:TYR:CD1	5:S:16:ALA:HA	2.53	0.44
3:C:154:ILE:HD12	3:C:155:PRO:HD2	2.00	0.44
3:C:252:LEU:CG	3:C:283:VAL:CG1	2.90	0.44
5:T:56:GLN:CD	5:T:56:GLN:H	2.21	0.44
3:A:29:VAL:CG1	3:A:34:ARG:HE	2.31	0.44
3:A:43:ARG:HG3	3:A:43:ARG:NH1	2.33	0.44
2:B:709:DC:H2'	2:B:710:DT:H72	2.00	0.44
1:E:701:DT:P	3:A:30:LYS:HB2	2.58	0.44
3:G:303:ARG:HD3	5:L:46:SEP:O3P	2.18	0.44
4:D:193:HIS:ND1	4:D:194:ALA:N	2.66	0.44
5:T:63:ILE:O	5:T:63:ILE:HG22	2.17	0.44
4:D:255:ILE:HG23	4:D:265:VAL:CG2	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:279:LEU:C	4:D:279:LEU:HD12	2.38	0.44
3:A:252:LEU:CD2	4:D:282:MSE:HB3	2.48	0.44
4:D:285:PRO:O	4:D:286:GLN:C	2.56	0.44
3:A:274:PHE:O	3:A:275:ASP:CB	2.62	0.44
3:C:263:LEU:CD1	3:C:263:LEU:N	2.79	0.44
3:A:22:VAL:HG21	3:A:37:VAL:HG12	2.00	0.44
5:T:26:ALA:HB2	5:T:77:LEU:HD11	2.00	0.44
4:D:201:LYS:HE3	4:D:202:ARG:HA	2.00	0.44
2:B:701:DT:H2'	4:D:18:THR:HG23	2.00	0.44
3:G:247:THR:HG23	3:G:248:ASP:N	2.33	0.44
2:R:713:DC:OP1	2:R:713:DC:H4'	2.18	0.44
2:B:704:DT:H1'	2:B:705:DA:C5'	2.37	0.44
3:C:182:PHE:CE1	3:C:184:SER:HB3	2.53	0.44
3:G:39:GLU:O	3:G:40:THR:C	2.56	0.44
4:D:311:LYS:O	4:D:312:GLU:C	2.56	0.44
3:C:58:LYS:O	3:C:59:LYS:HG2	2.18	0.44
3:G:113:LEU:CB	3:C:47:ARG:HH11	2.30	0.43
4:D:277:THR:C	4:D:279:LEU:N	2.71	0.43
3:G:275:ASP:O	3:G:276:ASN:HB3	2.18	0.43
3:A:39:GLU:O	3:A:42:GLU:HB3	2.17	0.43
3:A:3:VAL:HG21	3:A:44:LEU:HG	2.00	0.43
3:G:43:ARG:CZ	3:G:44:LEU:HB2	2.46	0.43
3:G:149:GLU:OE1	3:G:154:ILE:HD11	2.18	0.43
5:T:37:PHE:CE2	5:T:59:ALA:HB1	2.53	0.43
4:D:150:SER:O	4:D:152:ASN:ND2	2.50	0.43
3:A:244:PHE:HA	3:A:272:ILE:HG23	1.99	0.43
3:C:307:LYS:HD3	3:C:314:VAL:HG21	2.00	0.43
3:C:251:ALA:O	3:C:254:VAL:HB	2.18	0.43
5:T:84:GLU:HA	5:T:84:GLU:OE1	2.18	0.43
3:G:159:ILE:HA	3:G:159:ILE:HD12	1.70	0.43
3:G:180:ILE:HD11	3:G:204:LEU:HD11	1.99	0.43
5:Y:33:ILE:HG12	5:Y:65:ALA:CB	2.48	0.43
3:A:85:ILE:O	3:A:89:TYR:HD2	2.01	0.43
4:D:35:LYS:HD3	4:D:38:LEU:HD13	2.00	0.43
3:A:158:THR:OG1	3:A:161:TYR:HE1	2.01	0.43
4:D:220:ASP:O	4:D:225:SER:OG	2.28	0.43
4:D:212:ARG:HG3	4:D:212:ARG:NH1	2.33	0.43
3:C:125:GLY:O	3:C:189:GLU:OE2	2.35	0.43
3:C:190:PRO:O	3:C:194:ALA:CB	2.62	0.43
3:G:89:TYR:O	3:G:90:LYS:HD3	2.18	0.43
3:A:188:GLU:O	3:A:193:HIS:CD2	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:T:15:HIS:O	5:T:18:PRO:HD2	2.18	0.43
4:D:247:THR:HB	4:D:250:MSE:HG2	2.00	0.43
3:G:4:THR:CG2	3:G:7:ASP:CG	2.87	0.43
3:G:145:ALA:C	3:G:147:SER:N	2.71	0.43
2:R:700:DC:C3'	2:R:701:DT:H5''	2.42	0.43
3:A:272:ILE:O	3:A:272:ILE:HG23	2.18	0.43
3:G:286:GLN:HB3	3:G:328:ARG:HD3	2.00	0.43
3:A:12:ALA:CA	3:A:40:THR:HG21	2.48	0.43
3:A:212:ARG:HH11	3:A:212:ARG:HG3	1.83	0.43
4:D:169:VAL:CG2	4:D:172:LEU:HD12	2.35	0.43
4:D:204:LEU:HD23	4:D:211:VAL:CG1	2.33	0.43
4:D:258:ALA:CB	4:D:269:LEU:HD21	2.47	0.43
1:H:702:DG:C5'	3:G:15:SER:HB3	2.48	0.43
3:C:151:THR:O	3:C:152:ASN:C	2.56	0.43
5:Y:20:THR:O	5:Y:24:GLN:HB2	2.18	0.43
5:S:7:THR:OG1	5:S:88:GLU:OXT	2.33	0.43
2:R:702:DG:H2'	2:R:703:DT:C7	2.49	0.43
1:E:703:DA:H1'	1:E:704:DA:C5'	2.48	0.43
4:D:303:ARG:HG2	5:Y:48:MET:HB2	2.00	0.43
5:T:23:VAL:O	5:T:24:GLN:C	2.56	0.43
4:D:173:ILE:CD1	4:D:209:LEU:HD12	2.46	0.43
4:D:182:PHE:CZ	4:D:184:SER:HB3	2.53	0.43
3:A:245:VAL:O	3:A:273:GLY:HA2	2.19	0.43
3:C:227:ILE:HD13	3:C:253:GLY:O	2.19	0.43
3:A:57:SER:C	3:A:59:LYS:H	2.22	0.43
5:Y:4:LYS:O	5:Y:62:THR:HG23	2.18	0.43
3:A:204:LEU:O	3:A:209:LEU:N	2.42	0.43
4:D:224:ASP:C	4:D:226:GLY:H	2.22	0.43
4:D:41:ILE:O	4:D:45:GLY:N	2.50	0.43
3:C:41:ILE:HG22	3:C:42:GLU:N	2.33	0.43
3:G:80:ARG:CD	3:C:70:ILE:CD1	2.95	0.43
3:A:85:ILE:HD11	5:S:20:THR:CG2	2.48	0.43
4:D:190:PRO:O	4:D:194:ALA:HB3	2.19	0.43
4:D:70:ILE:HG23	4:D:70:ILE:O	2.18	0.43
4:D:243:ILE:N	4:D:270:GLU:O	2.52	0.43
3:A:143:VAL:CG1	3:A:305:LEU:HB2	2.43	0.43
2:R:712:DT:C5	2:R:713:DC:C4	3.07	0.43
4:D:115:LYS:HB3	4:D:115:LYS:NZ	2.34	0.43
5:Y:73:ALA:O	5:Y:77:LEU:HG	2.17	0.43
5:T:2:ALA:HB2	5:T:70:GLU:OE2	2.19	0.43
3:G:255:ILE:CG2	3:G:265:VAL:HG21	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:263:LEU:HD23	3:G:269:LEU:HD22	2.00	0.43
3:C:324:ARG:NE	5:T:56:GLN:HG2	2.34	0.43
4:D:156:SER:OG	4:D:157:VAL:N	2.52	0.43
3:A:8:VAL:HG13	3:A:40:THR:OG1	2.19	0.43
3:A:212:ARG:NH1	3:A:212:ARG:HG3	2.33	0.43
3:G:217:VAL:HG11	3:G:233:LEU:HD21	1.99	0.43
5:T:46:SEP:P	5:T:48:MET:HB2	2.59	0.43
4:D:276:ASN:O	4:D:276:ASN:CG	2.56	0.43
5:L:3:GLN:HA	5:L:74:LEU:HD11	2.00	0.43
3:C:237:ASP:C	3:C:239:LYS:H	2.22	0.43
5:L:61:ILE:HG13	5:L:63:ILE:CD1	2.49	0.43
3:A:265:VAL:HG21	3:A:285:PRO:HG2	2.00	0.43
3:G:259:GLN:CD	3:G:284:ARG:HH11	2.22	0.43
3:A:16:MSE:O	3:A:20:SER:N	2.45	0.43
3:C:264:ASN:HD22	3:C:267:ASN:N	2.02	0.43
4:D:264:ASN:C	4:D:264:ASN:ND2	2.72	0.43
3:G:80:ARG:NH1	5:L:17:ARG:NH1	2.66	0.43
3:G:298:GLY:O	3:G:299:ALA:O	2.37	0.43
5:L:43:ASN:C	5:L:45:LYS:N	2.71	0.43
3:A:242:ALA:HB2	3:A:270:GLU:HB2	2.00	0.43
3:A:75:TYR:O	3:A:76:ALA:C	2.57	0.43
1:E:709:DC:H2''	1:E:710:DT:O5'	2.19	0.43
3:C:2:ASN:O	3:C:4:THR:HG22	2.19	0.43
3:A:193:HIS:HA	3:A:197:VAL:HG23	1.99	0.43
5:S:14:ILE:HD11	5:S:61:ILE:HD13	2.01	0.43
3:G:325:ILE:HG22	3:G:326:GLU:H	1.83	0.43
3:G:309:MSE:C	3:G:311:LYS:H	2.21	0.43
5:S:22:LEU:CD1	5:S:81:MET:HE2	2.49	0.42
3:G:144:LEU:HD23	3:G:156:SER:HB3	2.00	0.42
3:C:169:VAL:O	3:C:172:LEU:N	2.50	0.42
3:C:303:ARG:NH1	3:C:303:ARG:HG3	2.25	0.42
3:A:5:ILE:HA	3:A:5:ILE:HD12	1.85	0.42
5:Y:23:VAL:HG22	5:Y:50:VAL:HG21	2.01	0.42
3:A:93:ILE:HG23	3:A:94:ILE:N	2.33	0.42
4:D:102:GLN:CD	4:D:102:GLN:N	2.73	0.42
3:C:178:LYS:HA	3:C:209:LEU:CD2	2.49	0.42
3:C:178:LYS:HG3	3:C:209:LEU:HD23	2.01	0.42
3:A:100:GLN:OE1	3:A:125:GLY:N	2.51	0.42
5:Y:53:LEU:HA	5:Y:53:LEU:HD23	1.90	0.42
4:D:255:ILE:HD11	4:D:287:LEU:HD13	2.01	0.42
5:S:43:ASN:C	5:S:45:LYS:N	2.73	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:82:ILE:O	4:D:302:MSE:HG3	2.19	0.42
5:T:53:LEU:HB2	5:T:55:ILE:HG13	2.01	0.42
5:Y:31:SER:OG	5:Y:70:GLU:N	2.52	0.42
5:S:47:ILE:HG23	5:S:51:MET:CE	2.49	0.42
3:C:238:GLU:O	3:C:239:LYS:C	2.57	0.42
5:T:35:LEU:C	5:T:35:LEU:CD2	2.87	0.42
3:A:35:LYS:O	3:A:39:GLU:N	2.49	0.42
4:D:233:LEU:CD2	4:D:240:PRO:HG2	2.50	0.42
3:G:143:VAL:CG2	3:G:144:LEU:N	2.82	0.42
4:D:294:MSE:H	4:D:294:MSE:HG3	1.71	0.42
3:G:127:VAL:HG11	3:G:149:GLU:HB2	2.01	0.42
3:C:162:GLU:OE2	3:C:199:GLY:CA	2.66	0.42
3:G:201:LYS:O	3:G:202:ARG:C	2.57	0.42
3:G:78:LEU:HD21	3:G:146:ALA:CB	2.49	0.42
3:G:224:ASP:O	3:G:227:ILE:N	2.53	0.42
3:G:30:LYS:HG3	3:G:31:PRO:HD2	2.00	0.42
4:D:252:LEU:CG	4:D:283:VAL:HG22	2.50	0.42
3:A:173:ILE:HD11	3:A:204:LEU:CD2	2.49	0.42
3:A:91:TYR:CE2	3:A:309:MSE:SE	3.23	0.42
3:G:106:LEU:CD2	3:G:130:GLU:OE1	2.67	0.42
3:C:182:PHE:HD2	3:C:244:PHE:HD1	1.68	0.42
3:G:183:VAL:CG2	3:G:229:ALA:HB1	2.49	0.42
3:G:150:SER:O	3:G:152:ASN:N	2.53	0.42
3:G:69:ASP:OD2	3:G:72:ASN:N	2.52	0.42
3:C:270:GLU:OE2	3:C:331:THR:HG23	2.18	0.42
3:C:144:LEU:CD2	3:C:155:PRO:O	2.68	0.42
3:G:286:GLN:O	3:G:328:ARG:HB2	2.20	0.42
3:C:131:HIS:O	3:C:135:LEU:N	2.41	0.42
3:G:159:ILE:HD12	3:G:321:LEU:O	2.19	0.42
1:E:711:DA:N1	2:B:705:DA:C2	2.88	0.42
3:C:158:THR:O	3:C:320:GLN:HA	2.19	0.42
4:D:186:THR:HG22	4:D:187:LEU:H	1.82	0.42
3:A:144:LEU:HD11	3:A:154:ILE:HD11	2.01	0.42
3:G:287:LEU:CD1	3:G:289:SER:HB3	2.48	0.42
5:Y:5:THR:HG23	5:Y:61:ILE:O	2.20	0.42
3:A:212:ARG:O	3:A:215:TYR:HB2	2.20	0.42
3:G:296:ASP:HB3	3:G:321:LEU:HD23	2.01	0.42
5:L:8:VAL:HG11	5:L:59:ALA:HB3	2.02	0.42
5:Y:44:LEU:HG	5:Y:63:ILE:HD13	2.00	0.42
3:G:11:GLU:HB3	3:G:40:THR:HG23	2.02	0.42
3:A:206:GLU:C	3:A:208:GLY:N	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:159:ILE:CD1	3:A:321:LEU:O	2.65	0.42
3:G:325:ILE:CG2	3:G:326:GLU:N	2.82	0.42
3:C:265:VAL:O	3:C:266:PRO:C	2.56	0.42
3:A:33:THR:O	3:A:37:VAL:HG23	2.20	0.42
3:A:123:MSE:HB2	3:A:145:ALA:O	2.20	0.42
4:D:106:LEU:O	4:D:109:LEU:HB3	2.19	0.42
5:L:8:VAL:O	5:L:58:GLY:N	2.46	0.42
5:L:67:GLY:N	5:L:70:GLU:OE1	2.48	0.42
3:A:231:GLU:O	3:A:232:LYS:C	2.58	0.42
4:D:193:HIS:C	4:D:193:HIS:ND1	2.73	0.42
3:G:4:THR:HG22	3:G:7:ASP:OD2	2.19	0.42
2:B:714:DA:H5'	2:B:714:DA:H8	1.85	0.42
1:E:703:DA:C1'	1:E:704:DA:H5'	2.46	0.42
5:L:11:ASP:CA	5:L:57:LYS:HE3	2.38	0.42
3:C:165:ALA:CB	3:C:199:GLY:HA3	2.48	0.42
5:L:73:ALA:O	5:L:76:ALA:N	2.51	0.42
5:S:6:PHE:CD1	5:S:6:PHE:N	2.87	0.42
3:G:33:THR:C	3:G:35:LYS:N	2.72	0.42
5:L:6:PHE:HE1	5:L:63:ILE:HB	1.84	0.42
3:G:212:ARG:C	3:G:214:SER:N	2.73	0.42
3:A:252:LEU:CD2	3:A:256:HIS:CD2	3.02	0.42
5:T:42:VAL:HG13	5:T:53:LEU:HD21	2.01	0.42
3:G:106:LEU:N	3:G:106:LEU:HD12	2.34	0.42
4:D:245:VAL:HG11	4:D:251:ALA:CA	2.50	0.42
3:A:158:THR:O	3:A:159:ILE:HD13	2.19	0.42
3:G:243:ILE:HG22	3:G:244:PHE:N	2.35	0.42
1:H:709:DC:H2'	1:H:710:DT:C6	2.54	0.41
3:A:265:VAL:HG11	3:A:285:PRO:HB2	2.02	0.41
5:S:22:LEU:HD23	5:S:44:LEU:HD21	2.01	0.41
3:G:279:LEU:O	3:G:282:MSE:N	2.53	0.41
5:Y:6:PHE:HA	5:Y:88:GLU:O	2.20	0.41
5:L:29:PHE:HB3	5:L:69:ASP:OD1	2.20	0.41
3:A:185:GLY:O	3:A:186:THR:C	2.59	0.41
3:A:194:ALA:C	3:A:195:LYS:HD2	2.41	0.41
3:A:304:LEU:CD2	3:A:308:TYR:HE2	2.32	0.41
3:G:324:ARG:HH21	3:G:326:GLU:CD	2.17	0.41
3:G:1:MSE:O	3:G:2:ASN:C	2.59	0.41
5:T:4:LYS:HE3	5:T:5:THR:O	2.21	0.41
3:C:318:ILE:N	3:C:318:ILE:HD12	2.34	0.41
3:A:168:ALA:HB1	3:A:272:ILE:HD11	2.01	0.41
3:A:288:THR:HA	3:A:328:ARG:HG3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:707:DC:C2'	3:A:55:LEU:HD22	2.49	0.41
3:A:3:VAL:HG13	3:A:44:LEU:CD2	2.49	0.41
3:A:74:PHE:CD2	3:A:294:MSE:HG2	2.55	0.41
3:G:119:GLY:HA3	3:G:305:LEU:HD21	2.02	0.41
2:R:709:DC:OP2	3:G:5:ILE:HB	2.20	0.41
3:C:82:ILE:CG2	3:C:302:MSE:CE	2.98	0.41
3:A:252:LEU:O	3:A:252:LEU:HD23	2.19	0.41
4:D:279:LEU:C	4:D:281:THR:N	2.73	0.41
3:A:169:VAL:O	3:A:170:GLN:C	2.58	0.41
3:A:30:LYS:O	3:A:34:ARG:N	2.43	0.41
3:G:22:VAL:HG21	3:G:37:VAL:HG11	2.02	0.41
5:L:74:LEU:C	5:L:76:ALA:N	2.74	0.41
3:G:287:LEU:C	3:G:287:LEU:HD22	2.40	0.41
3:G:223:TYR:O	3:G:253:GLY:HA3	2.20	0.41
3:C:15:SER:OG	3:C:16:MSE:N	2.52	0.41
3:A:243:ILE:O	3:A:272:ILE:HG22	2.21	0.41
3:C:283:VAL:O	3:C:284:ARG:O	2.38	0.41
3:C:324:ARG:NH1	3:C:326:GLU:OE1	2.52	0.41
3:G:279:LEU:O	3:G:280:SER:C	2.58	0.41
3:C:191:ILE:HG13	3:C:192:ASN:N	2.34	0.41
4:D:204:LEU:HD12	4:D:204:LEU:HA	1.90	0.41
2:B:701:DT:C2'	2:B:702:DG:H5''	2.51	0.41
3:C:204:LEU:CD1	3:C:211:VAL:HG11	2.49	0.41
4:D:187:LEU:O	4:D:193:HIS:CB	2.64	0.41
4:D:247:THR:HG22	4:D:249:GLU:N	2.36	0.41
3:A:154:ILE:HA	3:A:155:PRO:HD3	1.87	0.41
4:D:10:ARG:O	4:D:13:SER:N	2.50	0.41
3:C:312:GLU:HG3	3:C:314:VAL:HG23	2.01	0.41
1:E:705:DA:OP2	1:E:705:DA:H8	2.04	0.41
5:Y:46:SEP:P	5:Y:48:MET:HB3	2.60	0.41
4:D:143:VAL:HG12	4:D:305:LEU:HD13	2.02	0.41
4:D:305:LEU:O	4:D:309:MSE:HG3	2.20	0.41
4:D:166:PHE:CE2	4:D:202:ARG:HG2	2.54	0.41
4:D:201:LYS:CG	4:D:202:ARG:N	2.83	0.41
4:D:233:LEU:HD13	4:D:243:ILE:HD12	2.01	0.41
3:C:127:VAL:HA	3:C:131:HIS:ND1	2.36	0.41
3:G:47:ARG:HH22	3:C:113:LEU:CB	2.33	0.41
4:D:182:PHE:C	4:D:182:PHE:CD1	2.92	0.41
3:C:158:THR:OG1	3:C:159:ILE:N	2.52	0.41
5:L:73:ALA:HA	5:L:76:ALA:HB3	2.01	0.41
5:T:63:ILE:HD13	5:T:81:MET:CE	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:108:LEU:HD23	3:G:108:LEU:HA	1.84	0.41
3:C:5:ILE:HG23	3:C:6:TYR:N	2.35	0.41
2:B:714:DA:H2'	2:B:715:DG:C8	2.55	0.41
4:D:302:MSE:CE	4:D:305:LEU:HD23	2.46	0.41
5:T:23:VAL:HG11	5:T:47:ILE:HD13	2.03	0.41
4:D:201:LYS:O	4:D:204:LEU:N	2.47	0.41
3:G:144:LEU:H	3:G:144:LEU:CD2	2.33	0.41
1:H:706:DG:C2'	1:H:707:DC:C5	3.00	0.41
3:G:130:GLU:HG2	3:G:130:GLU:O	2.19	0.41
3:A:163:GLN:O	3:A:166:PHE:N	2.53	0.41
5:Y:47:ILE:HG12	5:Y:47:ILE:H	1.61	0.41
3:C:100:GLN:NE2	3:C:125:GLY:H	2.14	0.41
3:A:1:MSE:HE3	3:A:1:MSE:HB3	2.03	0.41
3:G:307:LYS:HE3	5:L:46:SEP:O3P	2.20	0.41
3:G:193:HIS:CD2	3:G:193:HIS:C	2.93	0.41
3:G:4:THR:O	3:G:7:ASP:HB2	2.20	0.41
3:A:114:GLY:C	3:A:116:GLN:N	2.74	0.41
3:A:295:TYR:CD1	3:A:295:TYR:C	2.94	0.41
4:D:224:ASP:C	4:D:226:GLY:N	2.72	0.41
3:C:258:ALA:CB	3:C:269:LEU:HD21	2.51	0.41
3:G:282:MSE:SE	3:C:249:GLU:HG3	2.70	0.41
3:A:38:LEU:C	3:A:38:LEU:CD2	2.88	0.41
3:C:185:GLY:O	3:C:186:THR:C	2.59	0.41
4:D:8:VAL:HG13	4:D:40:THR:HG22	2.03	0.41
3:G:180:ILE:HD13	3:G:180:ILE:N	2.36	0.41
5:L:73:ALA:O	5:L:77:LEU:N	2.47	0.41
5:Y:74:LEU:O	5:Y:78:GLU:HB2	2.21	0.41
4:D:174:ASP:OD2	4:D:174:ASP:O	2.38	0.41
2:R:703:DT:C7	3:C:15:SER:OG	2.69	0.41
4:D:271:ILE:HG12	4:D:287:LEU:CD1	2.51	0.41
4:D:223:TYR:OH	4:D:256:HIS:HD2	2.03	0.41
3:A:177:HIS:ND1	3:A:241:THR:CB	2.78	0.41
5:T:35:LEU:HD23	5:T:36:GLU:N	2.35	0.41
4:D:39:GLU:C	4:D:41:ILE:N	2.73	0.41
3:C:263:LEU:CD1	3:C:263:LEU:H	2.34	0.41
3:A:38:LEU:O	3:A:41:ILE:CG2	2.69	0.41
3:A:16:MSE:HA	3:A:19:VAL:HG23	2.03	0.41
4:D:78:LEU:CD1	4:D:123:MSE:HE1	2.51	0.41
3:A:118:ASP:O	3:A:309:MSE:HG2	2.20	0.41
3:A:78:LEU:O	3:A:82:ILE:HG13	2.20	0.41
2:R:712:DT:C6	2:R:713:DC:C5	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:295:TYR:CE1	5:Y:16:ALA:HA	2.55	0.41
1:E:709:DC:C6	1:E:709:DC:H5'	2.49	0.41
3:A:324:ARG:HG2	3:A:325:ILE:O	2.21	0.41
5:Y:69:ASP:OD1	5:Y:70:GLU:N	2.54	0.41
3:C:233:LEU:CD2	3:C:240:PRO:HG2	2.47	0.41
4:D:248:ASP:OD1	4:D:275:ASP:HB2	2.21	0.41
3:A:80:ARG:HD3	3:A:80:ARG:HA	1.90	0.41
4:D:80:ARG:O	4:D:80:ARG:HG3	2.20	0.41
3:G:46:TYR:CE1	3:G:48:PRO:HB3	2.56	0.41
3:C:78:LEU:HD12	3:C:298:GLY:HA3	2.02	0.41
1:H:708:DG:H1'	1:H:709:DC:H5''	2.03	0.41
4:D:227:ILE:O	4:D:230:VAL:HG23	2.21	0.41
3:A:285:PRO:O	3:A:286:GLN:C	2.59	0.41
3:C:235:GLU:CD	3:C:235:GLU:N	2.74	0.41
3:C:265:VAL:HB	3:C:285:PRO:HG3	2.02	0.41
4:D:63:VAL:CG2	4:D:305:LEU:HD23	2.51	0.41
3:C:190:PRO:O	3:C:191:ILE:C	2.58	0.41
4:D:67:ILE:HG22	4:D:96:SER:O	2.20	0.41
4:D:161:TYR:CD2	4:D:191:ILE:HG13	2.55	0.41
3:A:305:LEU:CG	3:A:309:MSE:CE	2.97	0.41
3:A:74:PHE:CD2	3:A:294:MSE:CG	3.04	0.41
2:B:707:DC:O5'	2:B:707:DC:H6	2.04	0.41
1:H:711:DA:N1	2:R:704:DT:C4	2.89	0.41
5:S:18:PRO:HB3	5:S:84:GLU:HG2	2.03	0.41
3:G:157:VAL:O	3:G:158:THR:HB	2.20	0.41
3:C:11:GLU:OE2	3:C:40:THR:HG21	2.21	0.41
4:D:65:VAL:HG22	4:D:95:LEU:HD12	2.02	0.41
4:D:4:THR:HG23	4:D:7:ASP:H	1.86	0.40
4:D:252:LEU:CD2	4:D:283:VAL:HG22	2.51	0.40
3:C:324:ARG:HH12	3:C:326:GLU:CD	2.25	0.40
3:A:7:ASP:HB3	3:A:44:LEU:CD2	2.30	0.40
1:E:703:DA:C2'	1:E:704:DA:OP2	2.67	0.40
3:G:247:THR:HG22	3:G:248:ASP:N	2.36	0.40
5:L:20:THR:O	5:L:20:THR:HG22	2.21	0.40
1:H:700:DC:N4	2:R:715:DG:H1	2.18	0.40
3:G:209:LEU:N	3:G:210:PRO:HD3	2.36	0.40
3:A:187:LEU:HG	3:A:218:GLU:HB2	2.03	0.40
2:B:708:DG:C1'	2:B:709:DC:H5''	2.50	0.40
4:D:180:ILE:HD11	4:D:204:LEU:CD1	2.51	0.40
3:G:15:SER:O	3:G:18:THR:N	2.48	0.40
5:Y:69:ASP:OD1	5:Y:73:ALA:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:T:31:SER:HA	5:T:67:GLY:HA3	2.03	0.40
3:G:166:PHE:CE2	3:G:202:ARG:HG2	2.56	0.40
4:D:39:GLU:O	4:D:41:ILE:N	2.55	0.40
3:C:241:THR:O	3:C:269:LEU:HA	2.21	0.40
4:D:303:ARG:HA	4:D:303:ARG:HE	1.86	0.40
3:A:70:ILE:HG22	3:A:97:ASN:HD21	1.85	0.40
3:G:143:VAL:HG22	3:G:144:LEU:O	2.21	0.40
3:G:143:VAL:CG2	3:G:156:SER:HA	2.40	0.40
1:E:709:DC:H2'	1:E:710:DT:C7	2.49	0.40
3:G:43:ARG:HE	3:G:44:LEU:CB	2.33	0.40
5:L:80:THR:O	5:L:84:GLU:HB2	2.21	0.40
5:L:18:PRO:HB3	5:L:86:LEU:HD21	2.02	0.40
3:A:85:ILE:HD11	5:S:20:THR:HG23	2.02	0.40
3:A:307:LYS:HZ2	3:A:314:VAL:HG21	1.86	0.40
3:A:113:LEU:HD22	3:A:139:PRO:HD2	2.02	0.40
4:D:15:SER:O	4:D:16:MSE:C	2.59	0.40
4:D:217:VAL:O	4:D:217:VAL:HG13	2.21	0.40
1:E:700:DC:C5	1:E:701:DT:H72	2.56	0.40
3:G:142:VAL:CG1	3:G:143:VAL:N	2.85	0.40
3:C:182:PHE:CD1	3:C:216:ILE:HG23	2.56	0.40
4:D:35:LYS:HD3	4:D:35:LYS:HA	1.83	0.40
3:G:212:ARG:HG2	3:G:212:ARG:H	1.62	0.40
3:C:120:ILE:HB	3:C:142:VAL:HG22	2.03	0.40
3:G:112:MSE:O	3:G:115:LYS:HB3	2.22	0.40
3:A:173:ILE:CD1	3:A:209:LEU:HD12	2.52	0.40
3:A:182:PHE:CD2	3:A:244:PHE:O	2.75	0.40
3:A:330:SER:OG	3:A:331:THR:N	2.54	0.40
3:C:230:VAL:O	3:C:231:GLU:C	2.59	0.40
4:D:166:PHE:CD2	4:D:202:ARG:CZ	3.04	0.40
4:D:169:VAL:O	4:D:172:LEU:N	2.43	0.40
3:C:168:ALA:HB3	3:C:244:PHE:HE2	1.85	0.40
3:A:193:HIS:C	3:A:193:HIS:ND1	2.75	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:198:LYS:NZ	3:C:133:GLU:OE1[2_556]	2.17	0.03

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	
3	A	330/332 (99%)	259 (78%)	56 (17%)	15 (4%)	3	10
3	C	330/332 (99%)	251 (76%)	62 (19%)	17 (5%)	2	7
3	G	330/332 (99%)	271 (82%)	40 (12%)	19 (6%)	2	5
4	D	330/332 (99%)	246 (74%)	63 (19%)	21 (6%)	2	4
5	L	84/88 (96%)	71 (84%)	12 (14%)	1 (1%)	16	47
5	S	84/88 (96%)	76 (90%)	7 (8%)	1 (1%)	16	47
5	T	84/88 (96%)	72 (86%)	8 (10%)	4 (5%)	3	9
5	Y	84/88 (96%)	73 (87%)	10 (12%)	1 (1%)	16	47
All	All	1656/1680 (99%)	1319 (80%)	258 (16%)	79 (5%)	3	9

All (79) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	G	100	GLN
3	G	102	GLN
3	G	141	PRO
3	G	150	SER
3	G	151	THR
3	G	275	ASP
3	G	311	LYS
3	G	316	SER
3	C	44	LEU
3	C	221	TYR
3	C	236	GLU
3	C	284	ARG
3	A	286	GLN
3	A	316	SER
4	D	150	SER
4	D	151	THR
4	D	210	PRO

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Mol	Chain	Res	Type
4	D	275	ASP
4	D	284	ARG
4	D	316	SER
5	Y	70	GLU
3	G	28	ASN
3	G	29	VAL
3	G	146	ALA
3	G	210	PRO
3	G	284	ARG
3	G	330	SER
3	C	29	VAL
3	C	128	THR
3	C	192	ASN
3	A	210	PRO
3	A	230	VAL
4	D	25	GLY
4	D	45	GLY
4	D	213	ASP
4	D	221	TYR
4	D	268	ASP
4	D	278	ARG
4	D	294	MSE
5	T	70	GLU
5	T	71	ALA
5	S	68	SER
3	G	68	PRO
3	C	45	GLY
3	C	112	MSE
3	C	210	PRO
3	C	215	TYR
3	C	279	LEU
3	A	141	PRO
3	A	186	THR
3	A	213	ASP
3	A	268	ASP
3	A	275	ASP
4	D	17	ALA
4	D	68	PRO
4	D	115	LYS
4	D	190	PRO
3	G	237	ASP
3	G	265	VAL

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Mol	Chain	Res	Type
3	G	276	ASN
3	C	28	ASN
3	C	278	ARG
3	C	315	ASP
3	A	68	PRO
4	D	28	ASN
4	D	188	GLU
5	T	16	ALA
3	C	234	LEU
3	C	240	PRO
3	A	150	SER
4	D	260	ASP
5	L	70	GLU
3	A	28	ASN
4	D	16	MSE
3	G	173	ILE
5	T	55	ILE
3	A	73	ILE
3	A	322	PRO
3	A	29	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	286/279 (102%)	240 (84%)	46 (16%)	3	9
3	C	285/279 (102%)	241 (85%)	44 (15%)	3	10
3	G	287/279 (103%)	235 (82%)	52 (18%)	2	6
4	D	285/280 (102%)	236 (83%)	49 (17%)	2	7
5	L	66/67 (98%)	54 (82%)	12 (18%)	2	6
5	S	66/67 (98%)	53 (80%)	13 (20%)	1	5
5	T	66/67 (98%)	51 (77%)	15 (23%)	1	3
5	Y	66/67 (98%)	52 (79%)	14 (21%)	1	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1407/1385 (102%)	1162 (83%)	245 (17%)	2 7

All (245) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	G	1	MSE
3	G	26	ASN
3	G	42	GLU
3	G	43	ARG
3	G	49	ASN
3	G	55	LEU
3	G	62	THR
3	G	63	VAL
3	G	73	ILE
3	G	77	GLU
3	G	78	LEU
3	G	83	GLU
3	G	84	ASP
3	G	88	MSE
3	G	90	LYS
3	G	101	ASN
3	G	109	LEU
3	G	111	ASN
3	G	112	MSE
3	G	117	VAL
3	G	121	ILE
3	G	131	HIS
3	G	135	LEU
3	G	136	LYS
3	G	143	VAL
3	G	144	LEU
3	G	148	ILE
3	G	150	SER
3	G	154	ILE
3	G	155	PRO
3	G	159	ILE
3	G	162	GLU
3	G	163	GLN
3	G	180	ILE
3	G	191	ILE
3	G	195	LYS
3	G	198	LYS

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Mol	Chain	Res	Type
3	G	211	VAL
3	G	212	ARG
3	G	216	ILE
3	G	220	ASP
3	G	245	VAL
3	G	247	THR
3	G	248	ASP
3	G	252	LEU
3	G	276	ASN
3	G	280	SER
3	G	282	MSE
3	G	303	ARG
3	G	304	LEU
3	G	322	PRO
3	G	324	ARG
3	C	4	THR
3	C	11	GLU
3	C	18	THR
3	C	55	LEU
3	C	62	THR
3	C	65	VAL
3	C	67	ILE
3	C	70	ILE
3	C	74	PHE
3	C	87	THR
3	C	100	GLN
3	C	101	ASN
3	C	102	GLN
3	C	112	MSE
3	C	117	VAL
3	C	129	GLU
3	C	137	LYS
3	C	143	VAL
3	C	144	LEU
3	C	148	ILE
3	C	152	ASN
3	C	170	GLN
3	C	189	GLU
3	C	191	ILE
3	C	193	HIS
3	C	195	LYS
3	C	198	LYS

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Mol	Chain	Res	Type
3	C	202	ARG
3	C	210	PRO
3	C	211	VAL
3	C	218	GLU
3	C	224	ASP
3	C	233	LEU
3	C	235	GLU
3	C	238	GLU
3	C	264	ASN
3	C	269	LEU
3	C	271	ILE
3	C	279	LEU
3	C	294	MSE
3	C	303	ARG
3	C	306	THR
3	C	325	ILE
3	C	327	PHE
3	A	1	MSE
3	A	7	ASP
3	A	24	ASN
3	A	39	GLU
3	A	41	ILE
3	A	55	LEU
3	A	63	VAL
3	A	65	VAL
3	A	78	LEU
3	A	80	ARG
3	A	84	ASP
3	A	93	ILE
3	A	95	LEU
3	A	100	GLN
3	A	102	GLN
3	A	130	GLU
3	A	136	LYS
3	A	143	VAL
3	A	144	LEU
3	A	148	ILE
3	A	149	GLU
3	A	151	THR
3	A	153	GLN
3	A	170	GLN
3	A	180	ILE

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Mol	Chain	Res	Type
3	A	184	SER
3	A	192	ASN
3	A	206	GLU
3	A	207	SER
3	A	210	PRO
3	A	212	ARG
3	A	216	ILE
3	A	217	VAL
3	A	220	ASP
3	A	227	ILE
3	A	236	GLU
3	A	241	THR
3	A	281	THR
3	A	282	MSE
3	A	288	THR
3	A	294	MSE
3	A	304	LEU
3	A	306	THR
3	A	312	GLU
3	A	316	SER
3	A	328	ARG
4	D	2	ASN
4	D	13	SER
4	D	18	THR
4	D	39	GLU
4	D	44	LEU
4	D	53	ARG
4	D	55	LEU
4	D	63	VAL
4	D	65	VAL
4	D	70	ILE
4	D	72	ASN
4	D	73	ILE
4	D	77	GLU
4	D	78	LEU
4	D	90	LYS
4	D	93	ILE
4	D	100	GLN
4	D	102	GLN
4	D	112	MSE
4	D	117	VAL
4	D	142	VAL

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Mol	Chain	Res	Type
4	D	144	LEU
4	D	148	ILE
4	D	149	GLU
4	D	151	THR
4	D	152	ASN
4	D	156	SER
4	D	162	GLU
4	D	170	GLN
4	D	190	PRO
4	D	201	LYS
4	D	210	PRO
4	D	212	ARG
4	D	224	ASP
4	D	230	VAL
4	D	233	LEU
4	D	235	GLU
4	D	239	LYS
4	D	264	ASN
4	D	269	LEU
4	D	271	ILE
4	D	274	PHE
4	D	279	LEU
4	D	292	GLN
4	D	302	MSE
4	D	306	THR
4	D	314	VAL
4	D	324	ARG
4	D	329	GLN
5	T	6	PHE
5	T	8	VAL
5	T	9	THR
5	T	21	THR
5	T	28	LYS
5	T	34	ASN
5	T	35	LEU
5	T	36	GLU
5	T	37	PHE
5	T	44	LEU
5	T	56	GLN
5	T	57	LYS
5	T	63	ILE
5	T	80	THR

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Mol	Chain	Res	Type
5	T	86	LEU
5	L	5	THR
5	L	11	ASP
5	L	14	ILE
5	L	17	ARG
5	L	24	GLN
5	L	32	ASP
5	L	35	LEU
5	L	44	LEU
5	L	47	ILE
5	L	60	THR
5	L	62	THR
5	L	84	GLU
5	Y	6	PHE
5	Y	8	VAL
5	Y	9	THR
5	Y	11	ASP
5	Y	14	ILE
5	Y	24	GLN
5	Y	36	GLU
5	Y	47	ILE
5	Y	56	GLN
5	Y	57	LYS
5	Y	69	ASP
5	Y	74	LEU
5	Y	84	GLU
5	Y	88	GLU
5	S	8	VAL
5	S	9	THR
5	S	20	THR
5	S	22	LEU
5	S	27	SER
5	S	32	ASP
5	S	40	LYS
5	S	44	LEU
5	S	52	SER
5	S	53	LEU
5	S	63	ILE
5	S	68	SER
5	S	79	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (45) such sidechains are listed below:

Mol	Chain	Res	Type
3	G	49	ASN
3	G	116	GLN
3	G	163	GLN
3	G	192	ASN
3	G	193	HIS
3	G	276	ASN
3	G	329	GLN
3	C	2	ASN
3	C	24	ASN
3	C	100	GLN
3	C	102	GLN
3	C	111	ASN
3	C	152	ASN
3	C	153	GLN
3	C	163	GLN
3	C	170	GLN
3	C	259	GLN
3	C	264	ASN
3	C	323	HIS
3	A	24	ASN
3	A	97	ASN
3	A	131	HIS
3	A	152	ASN
3	A	170	GLN
3	A	192	ASN
3	A	193	HIS
3	A	256	HIS
3	A	310	ASN
4	D	72	ASN
4	D	97	ASN
4	D	131	HIS
4	D	152	ASN
4	D	170	GLN
4	D	256	HIS
4	D	264	ASN
4	D	267	ASN
4	D	329	GLN
5	T	3	GLN
5	T	15	HIS
5	L	34	ASN
5	L	38	ASN
5	L	56	GLN
5	Y	56	GLN

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Mol	Chain	Res	Type
5	S	3	GLN
5	S	34	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
5	SEP	L	46	5	8,9,10	1.21	1 (12%)	8,12,14	1.57	1 (12%)
5	SEP	S	46	5	8,9,10	1.18	1 (12%)	8,12,14	1.83	2 (25%)
5	SEP	T	46	5	8,9,10	1.18	1 (12%)	8,12,14	1.73	2 (25%)
5	SEP	Y	46	5	8,9,10	1.24	2 (25%)	8,12,14	1.50	2 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	SEP	L	46	5	-	0/6/8/10	0/0/0/0
5	SEP	S	46	5	-	0/6/8/10	0/0/0/0
5	SEP	T	46	5	-	0/6/8/10	0/0/0/0
5	SEP	Y	46	5	-	0/6/8/10	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	S	46	SEP	P-O3P	-2.62	1.45	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	46	SEP	P-O3P	-2.54	1.45	1.54
5	Y	46	SEP	P-O3P	-2.49	1.45	1.54
5	T	46	SEP	P-O3P	-2.13	1.47	1.54
5	Y	46	SEP	P-O2P	-2.03	1.47	1.54

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	T	46	SEP	OG-CB-CA	-2.90	105.80	108.27
5	Y	46	SEP	O2P-P-O1P	-2.03	104.04	110.58
5	S	46	SEP	OG-CB-CA	2.53	110.43	108.27
5	Y	46	SEP	O3P-P-O1P	2.93	120.02	110.58
5	L	46	SEP	O3P-P-O1P	3.20	120.88	110.58
5	T	46	SEP	O3P-P-O1P	3.32	121.27	110.58
5	S	46	SEP	O3P-P-O1P	3.72	122.57	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	L	46	SEP	3	0
5	S	46	SEP	1	0
5	T	46	SEP	2	0
5	Y	46	SEP	4	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 for Mogul analysis.

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	$\# Z > 2$
6	SO4	A	599	-	4,4,4	0.33	0	6,6,6	0.13	0
6	SO4	A	946	-	4,4,4	0.63	0	6,6,6	0.59	0
6	SO4	C	346	-	4,4,4	0.27	0	6,6,6	0.13	0
6	SO4	C	846	-	4,4,4	0.26	0	6,6,6	0.24	0
6	SO4	C	947	-	4,4,4	0.16	0	6,6,6	0.21	0
6	SO4	G	646	-	4,4,4	0.27	0	6,6,6	0.12	0
6	SO4	G	647	-	4,4,4	0.17	0	6,6,6	0.18	0

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
6	SO4	A	599	-	-	0/0/0/0	0/0/0/0
6	SO4	A	946	-	-	0/0/0/0	0/0/0/0
6	SO4	C	346	-	-	0/0/0/0	0/0/0/0
6	SO4	C	846	-	-	0/0/0/0	0/0/0/0
6	SO4	C	947	-	-	0/0/0/0	0/0/0/0
6	SO4	G	646	-	-	0/0/0/0	0/0/0/0
6	SO4	G	647	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	946	SO4	1	0
6	C	947	SO4	1	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

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, 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	E	16/16 (100%)	-0.24	0 100 100	49, 75, 90, 91	0
1	H	16/16 (100%)	-0.19	0 100 100	52, 78, 93, 111	0
2	B	16/16 (100%)	-0.27	0 100 100	54, 79, 95, 104	0
2	R	16/16 (100%)	-0.16	0 100 100	47, 77, 94, 94	0
3	A	322/332 (96%)	0.37	18 (5%) 28 18	34, 80, 119, 141	0
3	C	322/332 (96%)	0.50	21 (6%) 22 13	33, 86, 119, 135	0
3	G	322/332 (96%)	0.35	9 (2%) 56 44	28, 71, 107, 127	0
4	D	323/332 (97%)	0.46	24 (7%) 17 9	33, 90, 129, 148	0
5	L	86/88 (97%)	0.26	4 (4%) 35 24	43, 79, 102, 127	0
5	S	86/88 (97%)	0.18	2 (2%) 64 52	43, 74, 96, 109	0
5	T	86/88 (97%)	0.25	2 (2%) 64 52	54, 75, 96, 103	0
5	Y	86/88 (97%)	0.10	4 (4%) 35 24	54, 75, 89, 111	0
All	All	1697/1744 (97%)	0.35	84 (4%) 33 22	28, 79, 118, 148	0

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	44	LEU	6.7
4	D	215	TYR	4.5
3	C	210	PRO	4.5
4	D	211	VAL	4.4
3	C	217	VAL	4.2
3	C	215	TYR	4.1
4	D	161	TYR	4.1
4	D	265	VAL	4.0
3	G	265	VAL	3.9
3	C	182	PHE	3.9
3	A	265	VAL	3.8

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Mol	Chain	Res	Type	RSRZ
3	C	211	VAL	3.8
3	G	43	ARG	3.7
3	C	227	ILE	3.7
3	G	211	VAL	3.7
3	A	5	ILE	3.7
3	C	236	GLU	3.6
3	G	210	PRO	3.3
3	A	209	LEU	3.3
4	D	212	ARG	3.2
3	A	43	ARG	3.2
3	A	332	LYS	3.1
5	L	77	LEU	3.1
4	D	191	ILE	3.1
3	A	271	ILE	3.0
3	G	130	GLU	3.0
4	D	269	LEU	2.9
4	D	263	LEU	2.9
4	D	165	ALA	2.9
4	D	287	LEU	2.8
3	C	183	VAL	2.8
4	D	268	ASP	2.7
4	D	234	LEU	2.7
3	C	228	GLU	2.7
4	D	182	PHE	2.7
3	G	209	LEU	2.7
5	T	2	ALA	2.7
3	A	217	VAL	2.6
4	D	239	LYS	2.6
3	C	213	ASP	2.6
3	C	180	ILE	2.5
5	Y	10	ALA	2.5
4	D	254	VAL	2.5
3	A	102	GLN	2.5
4	D	271	ILE	2.5
5	L	86	LEU	2.5
3	A	215	TYR	2.4
3	C	314	VAL	2.4
4	D	190	PRO	2.4
3	G	284	ARG	2.4
4	D	261	ARG	2.4
4	D	44	LEU	2.4
3	A	329	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
3	A	37	VAL	2.4
3	A	29	VAL	2.3
5	L	63	ILE	2.3
4	D	332	LYS	2.3
3	C	235	GLU	2.3
3	G	18	THR	2.3
3	A	7	ASP	2.2
5	Y	35	LEU	2.2
3	G	271	ILE	2.2
4	D	1	MET	2.2
3	C	2	ASN	2.2
3	C	12	ALA	2.2
3	A	32	SER	2.1
3	C	331	THR	2.1
3	C	278	ARG	2.1
3	C	234	LEU	2.1
5	T	35	LEU	2.1
5	S	22	LEU	2.1
5	L	58	GLY	2.1
4	D	33	THR	2.1
5	Y	23	VAL	2.1
3	C	191	ILE	2.0
3	C	187	LEU	2.0
4	D	187	LEU	2.0
3	A	241	THR	2.0
3	C	265	VAL	2.0
5	Y	88	GLU	2.0
3	A	256	HIS	2.0
4	D	243	ILE	2.0
3	A	239	LYS	2.0
5	S	77	LEU	2.0

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

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(\AA^2)	Q<0.9
5	SEP	S	46	10/11	0.96	0.21	-	48,58,66,69	0
5	SEP	L	46	10/11	0.93	0.20	-	49,59,66,72	0
5	SEP	Y	46	10/11	0.94	0.18	-	61,66,80,84	0
5	SEP	T	46	10/11	0.93	0.18	-	54,66,74,75	0

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(\AA^2)	Q<0.9
6	SO4	C	947	5/5	0.70	0.49	6.28	133,136,138,141	0
6	SO4	C	846	5/5	0.93	0.37	4.45	94,98,99,102	0
6	SO4	A	946	5/5	0.91	0.28	2.41	110,111,114,115	0
6	SO4	A	599	5/5	0.91	0.27	1.45	109,114,116,116	0
6	SO4	C	346	5/5	0.93	0.17	-0.84	113,119,120,122	0
7	MG	A	704	1/1	0.74	0.07	-	61,61,61,61	0
6	SO4	G	646	5/5	0.82	0.33	-	139,141,143,146	0
7	MG	D	754	1/1	0.80	0.09	-	74,74,74,74	0
6	SO4	G	647	5/5	0.87	0.14	-	120,123,124,127	0

6.5 Other polymers [i](#)

There are no such residues in this entry.