



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:44 PM UTC

PDB ID : 5EXC / pdb_00005exc
Title : Photoconverted red fluorescent protein DendRFP
Authors : Pletnev, V.Z.; Pletneva, N.V.; Pletnev, S.V.
Deposited on : 2015-11-23
Resolution : 2.14 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

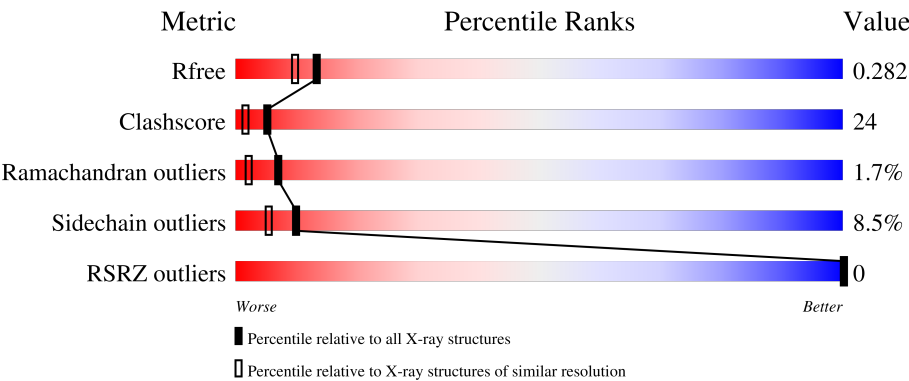
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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.



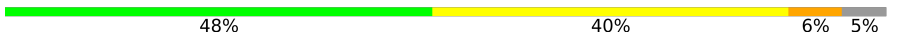
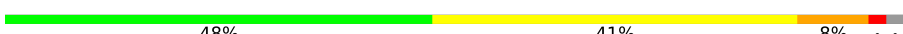
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	62	58% 32% 5% . .
1	B	62	61% 31% 5% .
1	C	62	60% 32% . 5%
1	D	62	45% 42% 8% 5%
1	E	62	45% 40% 8% . 5%

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Mol	Chain	Length	Quality of chain
1	F	62	
1	G	62	
1	H	62	
2	aa	170	
2	bb	170	
2	cc	170	
2	dd	170	
2	ee	170	
2	ff	170	
2	gg	170	
2	hh	170	

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
2	RC7	bb	64	-	-	X	-
2	RC7	ee	64	-	-	X	-
2	RC7	gg	64	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15333 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Green fluorescent protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	60	Total	C	N	O	S	0	1	0
			471	298	79	92	2			
1	B	60	Total	C	N	O	S	0	0	0
			462	293	78	89	2			
1	C	59	Total	C	N	O	S	0	0	0
			454	289	76	87	2			
1	D	59	Total	C	N	O	S	0	0	0
			454	289	76	87	2			
1	E	59	Total	C	N	O	S	0	1	0
			463	295	78	88	2			
1	F	59	Total	C	N	O	S	1	0	0
			454	289	76	87	2			
1	G	59	Total	C	N	O	S	1	0	0
			454	289	76	87	2			
1	H	59	Total	C	N	O	S	0	1	0
			463	297	76	88	2			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP Q8T6U0
A	1	GLY	-	expression tag	UNP Q8T6U0
B	0	MET	-	initiating methionine	UNP Q8T6U0
B	1	GLY	-	expression tag	UNP Q8T6U0
C	0	MET	-	initiating methionine	UNP Q8T6U0
C	1	GLY	-	expression tag	UNP Q8T6U0
D	0	MET	-	initiating methionine	UNP Q8T6U0
D	1	GLY	-	expression tag	UNP Q8T6U0
E	0	MET	-	initiating methionine	UNP Q8T6U0
E	1	GLY	-	expression tag	UNP Q8T6U0
F	0	MET	-	initiating methionine	UNP Q8T6U0
F	1	GLY	-	expression tag	UNP Q8T6U0
G	0	MET	-	initiating methionine	UNP Q8T6U0

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1	GLY	-	expression tag	UNP Q8T6U0
H	0	MET	-	initiating methionine	UNP Q8T6U0
H	1	GLY	-	expression tag	UNP Q8T6U0

- Molecule 2 is a protein called Green fluorescent protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	aa	165	Total	C	N	O	S	0	0	0
			1368	879	231	251	7			
2	bb	167	Total	C	N	O	S	1	1	0
			1399	897	241	254	7			
2	cc	166	Total	C	N	O	S	0	1	0
			1384	888	235	254	7			
2	dd	166	Total	C	N	O	S	1	1	0
			1386	889	236	254	7			
2	ee	162	Total	C	N	O	S	1	2	0
			1367	881	229	250	7			
2	ff	162	Total	C	N	O	S	1	1	0
			1356	872	228	249	7			
2	gg	166	Total	C	N	O	S	0	0	0
			1378	885	234	252	7			
2	hh	162	Total	C	N	O	S	0	0	0
			1348	868	226	247	7			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
aa	64	RC7	HIS	chromophore	UNP Q8T6U0
aa	64	RC7	TYR	chromophore	UNP Q8T6U0
aa	64	RC7	GLY	chromophore	UNP Q8T6U0
aa	226	GLY	-	expression tag	UNP Q8T6U0
aa	227	SER	-	expression tag	UNP Q8T6U0
aa	228	HIS	-	expression tag	UNP Q8T6U0
aa	229	HIS	-	expression tag	UNP Q8T6U0
aa	230	HIS	-	expression tag	UNP Q8T6U0
aa	231	HIS	-	expression tag	UNP Q8T6U0
aa	232	HIS	-	expression tag	UNP Q8T6U0
aa	233	HIS	-	expression tag	UNP Q8T6U0
bb	64	RC7	HIS	chromophore	UNP Q8T6U0
bb	64	RC7	TYR	chromophore	UNP Q8T6U0
bb	64	RC7	GLY	chromophore	UNP Q8T6U0
bb	226	GLY	-	expression tag	UNP Q8T6U0

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Chain	Residue	Modelled	Actual	Comment	Reference
bb	227	SER	-	expression tag	UNP Q8T6U0
bb	228	HIS	-	expression tag	UNP Q8T6U0
bb	229	HIS	-	expression tag	UNP Q8T6U0
bb	230	HIS	-	expression tag	UNP Q8T6U0
bb	231	HIS	-	expression tag	UNP Q8T6U0
bb	232	HIS	-	expression tag	UNP Q8T6U0
bb	233	HIS	-	expression tag	UNP Q8T6U0
cc	64	RC7	HIS	chromophore	UNP Q8T6U0
cc	64	RC7	TYR	chromophore	UNP Q8T6U0
cc	64	RC7	GLY	chromophore	UNP Q8T6U0
cc	226	GLY	-	expression tag	UNP Q8T6U0
cc	227	SER	-	expression tag	UNP Q8T6U0
cc	228	HIS	-	expression tag	UNP Q8T6U0
cc	229	HIS	-	expression tag	UNP Q8T6U0
cc	230	HIS	-	expression tag	UNP Q8T6U0
cc	231	HIS	-	expression tag	UNP Q8T6U0
cc	232	HIS	-	expression tag	UNP Q8T6U0
cc	233	HIS	-	expression tag	UNP Q8T6U0
dd	64	RC7	HIS	chromophore	UNP Q8T6U0
dd	64	RC7	TYR	chromophore	UNP Q8T6U0
dd	64	RC7	GLY	chromophore	UNP Q8T6U0
dd	226	GLY	-	expression tag	UNP Q8T6U0
dd	227	SER	-	expression tag	UNP Q8T6U0
dd	228	HIS	-	expression tag	UNP Q8T6U0
dd	229	HIS	-	expression tag	UNP Q8T6U0
dd	230	HIS	-	expression tag	UNP Q8T6U0
dd	231	HIS	-	expression tag	UNP Q8T6U0
dd	232	HIS	-	expression tag	UNP Q8T6U0
dd	233	HIS	-	expression tag	UNP Q8T6U0
ee	64	RC7	HIS	chromophore	UNP Q8T6U0
ee	64	RC7	TYR	chromophore	UNP Q8T6U0
ee	64	RC7	GLY	chromophore	UNP Q8T6U0
ee	226	GLY	-	expression tag	UNP Q8T6U0
ee	227	SER	-	expression tag	UNP Q8T6U0
ee	228	HIS	-	expression tag	UNP Q8T6U0
ee	229	HIS	-	expression tag	UNP Q8T6U0
ee	230	HIS	-	expression tag	UNP Q8T6U0
ee	231	HIS	-	expression tag	UNP Q8T6U0
ee	232	HIS	-	expression tag	UNP Q8T6U0
ee	233	HIS	-	expression tag	UNP Q8T6U0
ff	64	RC7	HIS	chromophore	UNP Q8T6U0
ff	64	RC7	TYR	chromophore	UNP Q8T6U0

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Chain	Residue	Modelled	Actual	Comment	Reference
ff	64	RC7	GLY	chromophore	UNP Q8T6U0
ff	226	GLY	-	expression tag	UNP Q8T6U0
ff	227	SER	-	expression tag	UNP Q8T6U0
ff	228	HIS	-	expression tag	UNP Q8T6U0
ff	229	HIS	-	expression tag	UNP Q8T6U0
ff	230	HIS	-	expression tag	UNP Q8T6U0
ff	231	HIS	-	expression tag	UNP Q8T6U0
ff	232	HIS	-	expression tag	UNP Q8T6U0
ff	233	HIS	-	expression tag	UNP Q8T6U0
gg	64	RC7	HIS	chromophore	UNP Q8T6U0
gg	64	RC7	TYR	chromophore	UNP Q8T6U0
gg	64	RC7	GLY	chromophore	UNP Q8T6U0
gg	226	GLY	-	expression tag	UNP Q8T6U0
gg	227	SER	-	expression tag	UNP Q8T6U0
gg	228	HIS	-	expression tag	UNP Q8T6U0
gg	229	HIS	-	expression tag	UNP Q8T6U0
gg	230	HIS	-	expression tag	UNP Q8T6U0
gg	231	HIS	-	expression tag	UNP Q8T6U0
gg	232	HIS	-	expression tag	UNP Q8T6U0
gg	233	HIS	-	expression tag	UNP Q8T6U0
hh	64	RC7	HIS	chromophore	UNP Q8T6U0
hh	64	RC7	TYR	chromophore	UNP Q8T6U0
hh	64	RC7	GLY	chromophore	UNP Q8T6U0
hh	226	GLY	-	expression tag	UNP Q8T6U0
hh	227	SER	-	expression tag	UNP Q8T6U0
hh	228	HIS	-	expression tag	UNP Q8T6U0
hh	229	HIS	-	expression tag	UNP Q8T6U0
hh	230	HIS	-	expression tag	UNP Q8T6U0
hh	231	HIS	-	expression tag	UNP Q8T6U0
hh	232	HIS	-	expression tag	UNP Q8T6U0
hh	233	HIS	-	expression tag	UNP Q8T6U0

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	dd	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	G	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	2	Total	Mg	0	0
			2	2		
4	F	1	Total	Mg	0	0
			1	1		
4	ff	1	Total	Mg	0	0
			1	1		
4	G	1	Total	Mg	0	0
			1	1		
4	gg	1	Total	Mg	0	0
			1	1		
4	H	2	Total	Mg	0	0
			2	2		
4	hh	3	Total	Mg	0	0
			3	3		

- Molecule 5 is water.

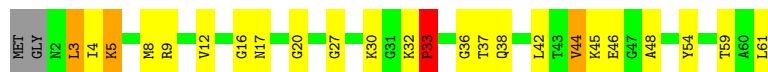
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	18	Total 18	O 18	0	0
5	aa	62	Total 62	O 62	0	0
5	B	21	Total 21	O 21	0	0
5	bb	62	Total 62	O 62	0	0
5	C	16	Total 16	O 16	0	0
5	cc	59	Total 59	O 59	0	0
5	D	17	Total 17	O 17	0	0
5	dd	54	Total 54	O 54	0	0
5	E	22	Total 22	O 22	0	0
5	ee	71	Total 71	O 71	0	0
5	F	19	Total 19	O 19	0	0
5	ff	47	Total 47	O 47	0	0
5	G	20	Total 20	O 20	0	0
5	gg	57	Total 57	O 57	0	0
5	H	19	Total 19	O 19	0	0
5	hh	79	Total 79	O 79	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Green fluorescent protein

Chain A: 



- Molecule 1: Green fluorescent protein

Chain B: 



- Molecule 1: Green fluorescent protein

Chain C: 

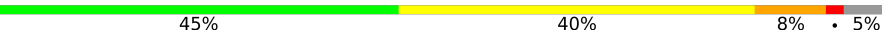


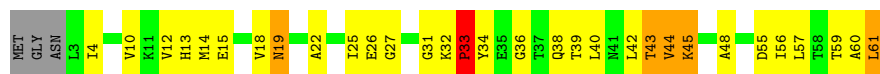
- Molecule 1: Green fluorescent protein

Chain D: 

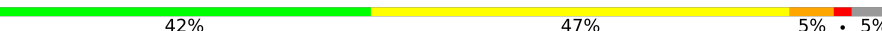


- Molecule 1: Green fluorescent protein

Chain E: 

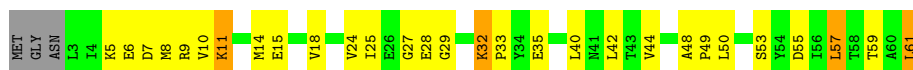


- Molecule 1: Green fluorescent protein

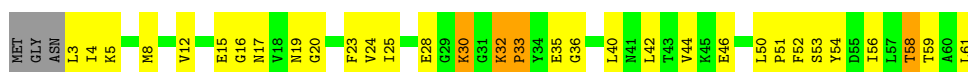
Chain F: 



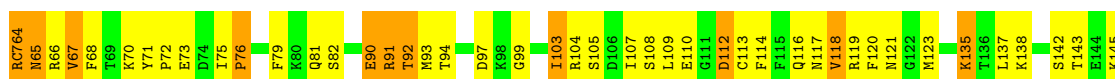
- Molecule 1: Green fluorescent protein



- Molecule 1: Green fluorescent protein



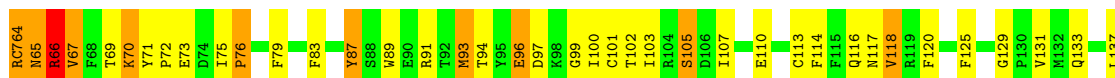
- Molecule 2: Green fluorescent protein



- Molecule 2: Green fluorescent protein



- Molecule 2: Green fluorescent protein





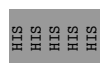
- Molecule 2: Green fluorescent protein

Chain dd: 52% 39% 6% ..



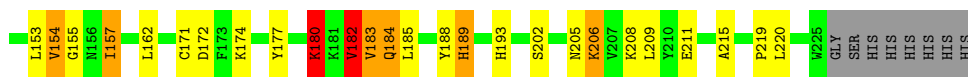
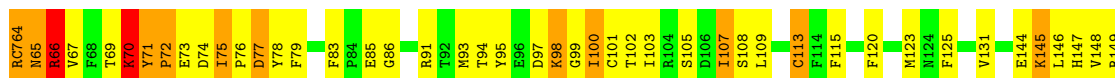
- Molecule 2: Green fluorescent protein

Chain ee: 47% 39% 7% 5%



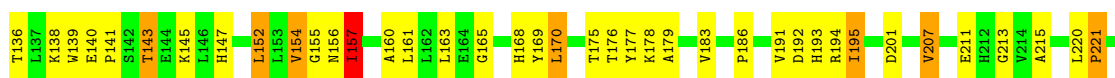
- Molecule 2: Green fluorescent protein

Chain ff: 54% 29% 10% 5%

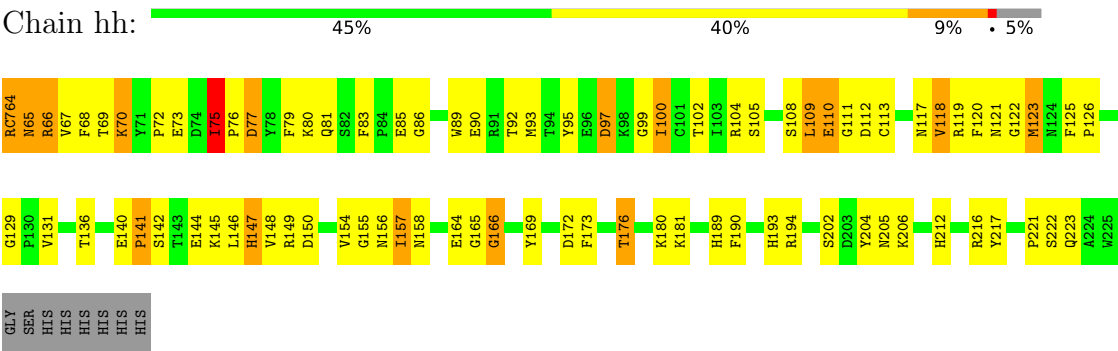


- Molecule 2: Green fluorescent protein

Chain gg: 46% 39% 12% ..



● Molecule 2: Green fluorescent protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.42Å 69.52Å 124.48Å 89.88° 89.94° 65.57°	Depositor
Resolution (Å)	29.87 – 2.14 29.87 – 2.14	Depositor EDS
% Data completeness (in resolution range)	93.2 (29.87-2.14) 93.3 (29.87-2.14)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.195 , 0.279 0.196 , 0.282	Depositor DCC
R_{free} test set	1817 reflections (1.80%)	wwPDB-VP
Wilson B-factor (Å ²)	24.6	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 14.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.470 for h,h-k,-l 0.469 for -h,-k,l 0.467 for -h,-h+k,-l	Xtriage
Reported twinning fraction	0.285 for H, K, L 0.253 for H, H-K, -L 0.218 for -H, -H+K, -L 0.244 for -h,-k,l	Depositor
Outliers	0 of 90214 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15333	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: NLW, MG, RC7, GOL

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	1.14	1/470 (0.2%)	1.13	3/634 (0.5%)
1	B	1.22	1/461 (0.2%)	1.14	0/622
1	C	1.09	2/453 (0.4%)	1.18	0/611
1	D	1.04	1/453 (0.2%)	1.24	5/611 (0.8%)
1	E	1.16	1/462 (0.2%)	1.32	3/622 (0.5%)
1	F	1.23	1/453 (0.2%)	1.21	4/611 (0.7%)
1	G	1.27	3/453 (0.7%)	1.14	5/611 (0.8%)
1	H	1.00	2/466 (0.4%)	1.23	4/629 (0.6%)
2	aa	1.33	14/1384 (1.0%)	1.28	9/1873 (0.5%)
2	bb	1.89	13/1417 (0.9%)	1.25	10/1917 (0.5%)
2	cc	1.42	7/1401 (0.5%)	1.28	12/1896 (0.6%)
2	dd	1.27	9/1403 (0.6%)	1.28	14/1899 (0.7%)
2	ee	1.16	5/1383 (0.4%)	1.27	9/1872 (0.5%)
2	ff	1.08	2/1371 (0.1%)	1.33	14/1856 (0.8%)
2	gg	1.06	6/1395 (0.4%)	1.22	11/1888 (0.6%)
2	hh	1.23	4/1363 (0.3%)	1.27	14/1845 (0.8%)
All	All	1.29	72/14788 (0.5%)	1.25	117/19997 (0.6%)

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	G	0	1
2	bb	0	3
2	cc	0	2
2	ff	0	2
All	All	0	8

All (72) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	bb	110	GLU	CD-OE1	36.22	1.94	1.25
2	bb	110	GLU	CD-OE2	31.87	1.85	1.25
2	bb	66	ARG	C-N	-20.91	1.07	1.34
2	cc	66	ARG	C-N	-20.66	1.08	1.33
2	cc	65	ASN	C-N	-19.61	1.06	1.33
2	hh	65	ASN	C-N	-19.00	1.07	1.33
1	G	11	LYS	CG-CD	12.26	1.89	1.52
2	gg	74	ASP	CA-C	-9.74	1.39	1.52
2	dd	65	ASN	C-N	-9.73	1.08	1.33
2	bb	110	GLU	CG-CD	9.37	1.75	1.52
2	aa	65	ASN	C-N	-8.99	1.21	1.33
1	G	11	LYS	CD-CE	8.61	1.78	1.52
2	dd	119	ARG	C-O	-8.34	1.14	1.24
2	bb	176	THR	CA-C	-7.69	1.43	1.52
2	aa	117	ASN	C-O	-7.61	1.14	1.24
2	aa	103	ILE	C-O	-7.43	1.16	1.23
2	bb	75	ILE	C-O	-7.39	1.15	1.24
2	dd	103	ILE	C-O	-7.26	1.16	1.24
2	aa	175	THR	C-O	-7.16	1.15	1.23
2	dd	117	ASN	C-O	-7.12	1.16	1.24
2	gg	118	VAL	C-O	-6.78	1.17	1.24
2	dd	119	ARG	CZ-NH2	6.73	1.42	1.33
1	C	33	PRO	C-O	-6.62	1.15	1.24
2	aa	92	THR	C-O	-6.29	1.16	1.24
2	bb	103	ILE	N-CA	-6.25	1.39	1.46
2	dd	92	THR	C-O	-6.22	1.16	1.24
2	bb	70	LYS	C-O	-6.15	1.16	1.23
2	cc	93	MET	N-CA	-6.12	1.39	1.46
2	hh	76	PRO	C-O	-6.09	1.19	1.24
2	cc	70	LYS	C-O	-6.09	1.16	1.24
2	bb	102	THR	C-O	-6.00	1.16	1.24
2	cc	118	VAL	C-O	-5.82	1.18	1.24
2	cc	91	ARG	CA-C	-5.77	1.45	1.52
2	gg	75	ILE	C-N	5.77	1.41	1.33
2	bb	76	PRO	N-CD	5.76	1.55	1.47
1	H	33	PRO	C-O	-5.70	1.16	1.24
2	aa	90	GLU	CA-C	-5.64	1.45	1.52
1	F	33	PRO	N-CD	5.64	1.55	1.47
2	bb	77	ASP	CA-C	-5.63	1.46	1.53
2	ee	67	VAL	C-O	-5.62	1.17	1.24
2	aa	73	GLU	C-O	-5.61	1.17	1.24
2	ee	66	ARG	C-O	-5.61	1.17	1.24
2	aa	119	ARG	C-O	-5.58	1.16	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	aa	76	PRO	N-CD	5.56	1.55	1.47
2	dd	76	PRO	N-CD	5.54	1.55	1.47
2	aa	91	ARG	CA-C	-5.51	1.45	1.52
1	B	33	PRO	N-CD	5.49	1.55	1.47
1	D	32	LYS	C-O	-5.47	1.19	1.24
2	cc	131	VAL	C-O	-5.44	1.18	1.24
2	dd	160	ALA	CA-C	-5.41	1.46	1.52
2	ee	70	LYS	C-O	-5.40	1.17	1.24
2	hh	76	PRO	N-CD	5.36	1.55	1.47
2	ee	75	ILE	C-N	5.35	1.40	1.33
1	G	32	LYS	C-N	5.31	1.40	1.34
2	dd	194	ARG	C-O	-5.31	1.18	1.23
2	aa	170	LEU	CA-C	-5.30	1.46	1.52
2	gg	95	TYR	CA-C	-5.29	1.46	1.52
2	aa	194	ARG	C-O	-5.28	1.17	1.23
2	aa	121	ASN	C-O	-5.25	1.18	1.24
2	gg	76	PRO	N-CD	5.24	1.55	1.47
2	ff	71	TYR	C-N	5.23	1.39	1.33
2	gg	67	VAL	C-O	-5.23	1.17	1.24
2	ff	72	PRO	N-CD	5.21	1.55	1.47
1	H	33	PRO	N-CD	5.21	1.55	1.47
1	A	32	LYS	C-O	-5.13	1.18	1.24
2	bb	117	ASN	C-O	-5.13	1.17	1.24
1	C	31	GLY	C-O	-5.12	1.18	1.24
1	E	33	PRO	N-CD	5.11	1.54	1.47
2	aa	118	VAL	N-CA	-5.11	1.40	1.46
2	hh	157	ILE	C-O	-5.07	1.18	1.23
2	bb	121	ASN	N-CA	-5.06	1.39	1.46
2	ee	136	THR	C-O	5.03	1.30	1.23

All (117) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	cc	65	ASN	O-C-N	-12.38	103.20	123.00
2	cc	66	ARG	O-C-N	-10.13	109.12	122.59
2	aa	99	GLY	N-CA-C	-9.09	100.72	111.36
2	bb	118	VAL	O-C-N	-9.01	113.46	123.10
2	hh	99	GLY	N-CA-C	-8.69	100.83	112.82
2	aa	65	ASN	O-C-N	8.52	136.63	123.00
2	hh	118	VAL	N-CA-C	8.51	120.37	108.12
2	gg	125	PHE	N-CA-C	-8.17	97.88	109.24
2	bb	110	GLU	CG-CD-OE1	7.92	136.61	118.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	cc	65	ASN	CA-C-N	7.60	136.05	121.54
2	cc	65	ASN	C-N-CA	7.60	136.05	121.54
1	D	50	LEU	CA-C-N	7.35	129.03	119.84
1	D	50	LEU	C-N-CA	7.35	129.03	119.84
2	bb	216	ARG	N-CA-C	7.33	118.22	107.88
1	F	46	GLU	CB-CG-CD	-7.14	100.46	112.60
1	G	11	LYS	CD-CE-NZ	-7.11	89.16	111.90
2	ee	157	ILE	N-CA-C	7.10	118.95	108.45
1	F	58	THR	N-CA-C	7.09	118.66	111.07
1	G	11	LYS	CB-CG-CD	-7.07	95.04	111.30
2	hh	157	ILE	N-CA-C	6.82	117.61	108.27
2	ff	125	PHE	CA-C-N	-6.79	114.77	119.66
2	ff	125	PHE	C-N-CA	-6.79	114.77	119.66
2	aa	214	VAL	N-CA-C	6.75	117.84	108.12
2	ff	71	TYR	CA-C-N	-6.74	113.36	120.03
2	ff	71	TYR	C-N-CA	-6.74	113.36	120.03
2	hh	129	GLY	CA-C-N	6.74	126.53	119.05
2	hh	129	GLY	C-N-CA	6.74	126.53	119.05
1	E	31	GLY	N-CA-C	6.66	119.55	110.69
2	ee	75	ILE	CA-C-N	-6.61	113.17	119.85
2	ee	75	ILE	C-N-CA	-6.61	113.17	119.85
2	ff	180	LYS	N-CA-C	-6.50	106.30	114.56
2	bb	85	GLU	N-CA-C	6.47	119.15	111.71
1	D	29	GLY	N-CA-C	6.45	119.85	110.63
2	aa	154	VAL	CA-C-N	-6.45	116.65	121.61
2	aa	154	VAL	C-N-CA	-6.45	116.65	121.61
2	bb	110	GLU	CG-CD-OE2	-6.41	103.66	118.40
2	aa	216	ARG	N-CA-C	6.36	116.63	108.24
2	ee	76	PRO	CA-N-CD	-6.33	103.14	112.00
1	H	58	THR	N-CA-C	6.31	119.45	111.69
1	G	57	LEU	N-CA-C	6.20	119.01	111.82
2	ee	123	MET	N-CA-C	6.12	118.15	108.79
1	A	33	PRO	N-CA-C	6.12	125.07	112.47
2	gg	75	ILE	CA-C-N	-6.07	113.70	119.89
2	gg	75	ILE	C-N-CA	-6.07	113.70	119.89
2	bb	138	LYS	N-CA-C	6.03	117.31	108.14
1	G	32	LYS	CA-C-N	-5.95	113.55	119.56
1	G	32	LYS	C-N-CA	-5.95	113.55	119.56
2	hh	75	ILE	CA-C-N	-5.93	113.08	120.79
2	hh	75	ILE	C-N-CA	-5.93	113.08	120.79
2	ff	66	ARG	O-C-N	-5.89	114.76	122.59
2	cc	87	TYR	N-CA-C	5.86	117.15	108.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	33	PRO	CA-N-CD	-5.85	103.82	112.00
2	ff	66	ARG	CA-C-N	5.79	129.61	120.47
2	ff	66	ARG	C-N-CA	5.79	129.61	120.47
2	gg	103	ILE	N-CA-C	5.76	115.95	108.35
2	ee	118	VAL	N-CA-C	5.75	117.71	108.85
2	cc	75	ILE	CA-C-N	-5.71	113.90	119.78
2	cc	75	ILE	C-N-CA	-5.71	113.90	119.78
2	dd	118	VAL	N-CA-C	5.69	116.48	108.17
2	gg	90	GLU	N-CA-C	-5.68	100.92	109.95
1	A	44	VAL	CB-CA-C	-5.66	105.12	111.23
2	ee	69	THR	CB-CA-C	-5.65	99.69	109.86
2	cc	192	ASP	N-CA-C	-5.64	100.52	109.59
2	hh	99	GLY	CA-C-N	-5.58	113.49	122.25
2	hh	99	GLY	C-N-CA	-5.58	113.49	122.25
1	H	30	LYS	N-CA-C	5.55	116.67	107.73
1	E	44	VAL	N-CA-C	5.55	116.36	107.98
2	dd	76	PRO	CA-N-CD	-5.54	104.25	112.00
1	D	53	SER	N-CA-C	5.52	118.36	110.24
2	cc	66	ARG	CA-C-N	5.48	127.47	120.56
2	cc	66	ARG	C-N-CA	5.48	127.47	120.56
2	hh	97	ASP	N-CA-C	-5.46	105.93	112.59
2	aa	76	PRO	CA-N-CD	-5.45	104.38	112.00
2	gg	157	ILE	CB-CA-C	-5.44	102.36	111.29
2	gg	102	THR	CB-CA-C	5.44	119.18	109.38
2	ff	99	GLY	N-CA-C	-5.38	104.84	112.37
2	aa	148	VAL	CB-CA-C	5.37	117.57	110.91
2	ff	72	PRO	N-CA-C	5.35	119.43	111.41
2	ff	113	CYS	N-CA-C	5.34	117.79	108.76
1	H	32	LYS	CA-C-N	-5.34	113.69	119.24
1	H	32	LYS	C-N-CA	-5.34	113.69	119.24
2	dd	75	ILE	CB-CA-C	-5.34	104.71	110.85
2	dd	71	TYR	CA-C-N	5.33	125.33	120.21
2	dd	71	TYR	C-N-CA	5.33	125.33	120.21
2	hh	126	PRO	CA-C-N	5.31	126.48	119.84
2	hh	126	PRO	C-N-CA	5.31	126.48	119.84
2	ff	202	SER	N-CA-C	5.29	120.04	111.37
1	E	45	LYS	N-CA-C	5.25	116.82	111.14
2	ee	192	ASP	N-CA-C	-5.24	101.23	109.25
2	gg	72	PRO	CA-C-N	5.22	131.51	121.54
2	gg	72	PRO	C-N-CA	5.22	131.51	121.54
1	A	33	PRO	CA-N-CD	-5.20	104.72	112.00
2	dd	142	SER	N-CA-C	5.20	115.15	108.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	ff	182	VAL	N-CA-C	5.18	118.32	111.17
2	dd	139	TRP	N-CA-C	-5.17	103.66	110.43
2	cc	76	PRO	CA-N-CD	-5.16	104.78	112.00
2	dd	99	GLY	N-CA-C	-5.16	103.54	111.64
2	dd	125	PHE	CA-C-N	-5.16	115.06	120.38
2	dd	125	PHE	C-N-CA	-5.16	115.06	120.38
2	gg	72	PRO	N-CA-C	5.15	119.18	111.14
2	bb	66	ARG	CA-C-N	5.15	127.79	120.53
2	bb	66	ARG	C-N-CA	5.15	127.79	120.53
2	dd	76	PRO	N-CA-C	5.15	119.40	111.21
2	aa	202	SER	N-CA-C	-5.14	106.51	112.89
2	bb	200	ASN	N-CA-C	5.14	115.13	107.88
2	hh	76	PRO	N-CA-CB	5.12	105.79	102.92
2	dd	114	PHE	N-CA-C	-5.12	101.36	109.96
2	hh	70	LYS	CD-CE-NZ	-5.11	95.55	111.90
2	gg	170	LEU	N-CA-C	5.08	118.02	110.14
2	dd	76	PRO	CA-C-O	-5.08	115.67	121.56
2	bb	170	LEU	N-CA-C	5.07	117.70	109.24
2	ff	70	LYS	N-CA-C	-5.05	103.86	110.53
1	F	32	LYS	CA-C-N	-5.04	113.54	119.84
1	F	32	LYS	C-N-CA	-5.04	113.54	119.84
2	cc	170	LEU	N-CA-C	5.01	117.73	109.72
2	ee	216	ARG	N-CA-C	5.01	116.67	108.55
2	dd	131	VAL	CB-CA-C	-5.00	105.37	111.92

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	29	GLY	Peptide
2	bb	118	VAL	Mainchain
2	bb	66	ARG	Peptide,Mainchain
2	cc	66	ARG	Mainchain
2	cc	83	PHE	Peptide
2	ff	180	LYS	Peptide
2	ff	66	ARG	Mainchain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	471	0	456	20	0
1	B	462	0	451	19	0
1	C	454	0	445	17	0
1	D	454	0	445	28	0
1	E	463	0	457	32	0
1	F	454	0	445	30	0
1	G	454	0	445	33	0
1	H	463	0	454	37	0
2	aa	1368	0	1304	66	0
2	bb	1399	0	1329	64	0
2	cc	1384	0	1313	65	0
2	dd	1386	0	1315	62	0
2	ee	1367	0	1302	95	0
2	ff	1356	0	1294	71	0
2	gg	1378	0	1311	95	0
2	hh	1348	0	1288	98	0
3	E	6	0	8	3	0
3	G	6	0	8	0	0
3	dd	6	0	8	0	0
4	E	2	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	2	0	0	0	0
4	ff	1	0	0	0	0
4	gg	1	0	0	0	0
4	hh	3	0	0	0	0
5	A	18	0	0	0	0
5	B	21	0	0	3	0
5	C	16	0	0	1	0
5	D	17	0	0	5	0
5	E	22	0	0	9	0
5	F	19	0	0	2	0
5	G	20	0	0	4	0
5	H	19	0	0	5	0
5	aa	62	0	0	5	0
5	bb	62	0	0	2	0
5	cc	59	0	0	7	0
5	dd	54	0	0	3	0
5	ee	71	0	0	5	0
5	ff	47	0	0	6	0
5	gg	57	0	0	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	hh	79	0	0	10	0
All	All	15333	0	14078	697	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 24.

All (697) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:ff:66:ARG:HB2	2:ff:79:PHE:CE2	1.67	1.30
2:ff:66:ARG:HB2	2:ff:79:PHE:CD2	1.79	1.16
2:ff:72:PRO:HD2	2:ff:75:ILE:HG21	1.19	1.14
2:bb:90:GLU:OE2	2:bb:104:ARG:NH1	1.84	1.10
2:aa:64:RC7:OH	2:aa:142:SER:OG	1.73	1.07
1:E:57:LEU:HG	5:E:413:HOH:O	1.56	1.06
1:F:7:ASP:OD1	1:F:32:LYS:HE2	1.56	1.06
2:ff:76:PRO:HG2	2:ff:185:LEU:O	1.66	0.95
2:cc:110:GLU:HG2	5:cc:319:HOH:O	1.67	0.93
2:ff:123:MET:SD	2:gg:102:THR:OG1	2.26	0.92
2:ee:64:RC7:OH	2:ee:142:SER:OG	1.87	0.91
1:B:32:LYS:NZ	5:B:301:HOH:O	2.03	0.91
2:hh:65:ASN:O	2:hh:67:VAL:N	2.03	0.90
2:ee:76:PRO:HD3	5:ee:347:HOH:O	1.71	0.90
2:bb:200:ASN:ND2	2:bb:201:ASP:O	2.05	0.89
2:ee:168:HIS:HB3	5:ee:331:HOH:O	1.73	0.89
2:ee:102:THR:HG21	2:hh:123:MET:HG2	1.54	0.88
2:gg:64:RC7:C2	2:gg:66:ARG:HH12	1.86	0.88
2:hh:147:HIS:CE1	2:hh:154:VAL:HB	2.09	0.88
1:F:52:PHE:HE1	1:F:57:LEU:HD11	1.38	0.87
1:G:57:LEU:HG	5:G:404:HOH:O	1.74	0.86
2:aa:105:SER:HB2	2:aa:118:VAL:HG22	1.57	0.85
2:ee:67:VAL:HA	2:ee:79[B]:PHE:CE1	2.12	0.84
2:hh:102:THR:HG22	2:hh:123:MET:HE1	1.58	0.84
2:ff:66:ARG:CB	2:ff:79:PHE:CE2	2.58	0.84
2:gg:194:ARG:HA	5:gg:421:HOH:O	1.77	0.84
2:ee:70:LYS:HE3	2:ee:214:VAL:HG22	1.58	0.83
1:C:61:NLW:NH2	2:cc:64:RC7:HA11	1.94	0.83
2:dd:76:PRO:HG3	5:dd:448:HOH:O	1.78	0.82
1:F:25:ILE:HG12	1:F:44:VAL:HG22	1.59	0.82
2:dd:66:ARG:HH11	2:dd:69:THR:HG22	1.45	0.82
2:gg:64:RC7:OH	2:gg:193:HIS:HB2	1.81	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:34:TYR:CE1	2:ee:80:LYS:HE2	2.16	0.81
2:cc:105:SER:HB2	2:cc:118:VAL:HG22	1.60	0.80
1:G:15:GLU:HG2	1:G:24:VAL:HG22	1.63	0.80
1:G:59:THR:O	2:gg:64:RC7:C2	2.29	0.80
2:gg:101:CYS:SG	2:gg:125:PHE:HZ	2.03	0.80
2:hh:66:ARG:HG2	5:hh:462:HOH:O	1.82	0.80
2:cc:97:ASP:OD2	5:cc:301:HOH:O	2.02	0.78
1:A:9:ARG:NH1	2:aa:112:ASP:OD1	2.16	0.77
2:aa:76:PRO:HG2	2:aa:186:PRO:HA	1.67	0.77
2:bb:123:MET:HE1	2:dd:103:ILE:O	1.85	0.76
1:E:25:ILE:HG12	1:E:44:VAL:HA	1.67	0.76
1:D:6:GLU:O	1:D:32:LYS:HB3	1.86	0.76
2:ff:83:PHE:CE1	2:ff:86:GLY:HA2	2.22	0.75
1:G:40:LEU:HB2	2:gg:64:RC7:HE3	1.66	0.75
1:F:39:THR:HA	2:ff:209:LEU:O	1.87	0.75
1:D:9:ARG:NH2	5:D:401:HOH:O	2.20	0.74
2:ff:72:PRO:HD2	2:ff:75:ILE:CG2	2.11	0.74
2:ff:102:THR:HB	2:gg:123:MET:SD	2.28	0.74
2:gg:126:PRO:O	2:gg:129:GLY:N	2.20	0.74
2:gg:201:ASP:OD1	5:gg:402:HOH:O	2.05	0.73
2:ee:72:PRO:HG2	2:ee:75:ILE:HG13	1.70	0.73
1:F:29:GLY:HA2	5:F:216:HOH:O	1.88	0.73
2:dd:66:ARG:HE	2:dd:69:THR:HG21	1.53	0.72
2:ff:182:VAL:O	2:ff:183:VAL:HG12	1.88	0.72
1:D:32:LYS:HD2	1:D:35:GLU:CD	2.15	0.72
2:dd:66:ARG:HD2	5:dd:414:HOH:O	1.89	0.72
2:ff:72:PRO:CD	2:ff:75:ILE:HG21	2.09	0.72
2:bb:174:LYS:HE2	2:dd:124:ASN:HD21	1.55	0.71
1:E:19:ASN:O	5:E:401:HOH:O	2.08	0.71
2:hh:102:THR:CG2	2:hh:123:MET:HE1	2.21	0.71
2:aa:93:MET:HE2	2:aa:173:PHE:CZ	2.26	0.71
2:dd:105:SER:HB2	2:dd:118:VAL:HG13	1.71	0.71
2:hh:145:LYS:O	2:hh:155:GLY:HA2	1.91	0.71
2:aa:107:ILE:HD12	2:aa:116:GLN:HG2	1.73	0.71
2:ee:123:MET:SD	2:hh:102:THR:OG1	2.47	0.71
2:ee:72:PRO:HD2	2:ee:215:ALA:HB3	1.71	0.70
2:dd:109:LEU:HD12	2:dd:113:CYS:O	1.92	0.70
2:ee:160:ALA:HB1	5:ee:331:HOH:O	1.91	0.70
2:aa:137:LEU:HD11	2:aa:164:GLU:HA	1.72	0.70
2:gg:101:CYS:HG	2:gg:125:PHE:HZ	1.39	0.70
1:D:40:LEU:HB2	2:dd:64:RC7:HE3	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:dd:85:GLU:OE1	2:dd:181:LYS:NZ	2.25	0.69
2:hh:122:GLY:C	2:hh:123:MET:HG3	2.17	0.69
1:H:40:LEU:HD21	1:H:42:LEU:HD21	1.73	0.68
2:hh:100:ILE:HG23	2:hh:123:MET:HB2	1.76	0.68
1:H:30:LYS:HA	5:H:414:HOH:O	1.94	0.68
2:bb:64:RC7:NE1	2:bb:209:LEU:HG	2.09	0.68
1:G:32:LYS:HD2	1:G:35:GLU:OE1	1.93	0.68
2:cc:97:ASP:OD1	2:cc:169:TYR:OH	2.07	0.68
2:ee:67:VAL:HA	2:ee:79[B]:PHE:CD1	2.29	0.67
1:F:7:ASP:OD1	1:F:32:LYS:CE	2.40	0.67
2:ee:65:ASN:OD1	2:ee:87:TYR:OH	2.08	0.67
2:hh:80:LYS:NZ	5:hh:403:HOH:O	2.15	0.67
2:bb:64:RC7:C3	2:bb:65:ASN:CA	2.68	0.67
1:C:16:GLY:HA2	2:cc:120:PHE:O	1.95	0.67
2:aa:113:CYS:N	5:aa:301:HOH:O	2.28	0.67
1:D:61:NLW:NH2	2:dd:64:RC7:HA11	2.11	0.66
1:D:28:GLU:HB2	5:D:412:HOH:O	1.94	0.66
1:F:4:ILE:CG2	1:F:33:PRO:HG2	2.25	0.66
2:hh:81:GLN:O	2:hh:181:LYS:HE3	1.96	0.66
2:ff:71:TYR:CE1	2:ff:215:ALA:CB	2.79	0.66
2:aa:64:RC7:HE1	2:aa:157:ILE:HD13	1.78	0.66
2:hh:221:PRO:HB2	2:hh:223:GLN:HG2	1.77	0.66
1:H:36:GLY:O	2:hh:212:HIS:HD2	1.79	0.65
2:ee:64:RC7:CE1	2:ee:193:HIS:CD2	2.79	0.65
2:ee:90:GLU:OE2	2:ee:104:ARG:NH2	2.29	0.65
2:ff:69:THR:HG22	2:ff:70:LYS:O	1.96	0.65
1:D:40:LEU:HD23	1:D:42:LEU:HD21	1.79	0.65
2:ff:67:VAL:HA	5:ff:419:HOH:O	1.95	0.65
1:G:44:VAL:HG11	1:G:48:ALA:HB2	1.78	0.65
2:aa:64:RC7:HD3	2:aa:211:GLU:HB2	1.79	0.65
2:aa:200:ASN:ND2	2:aa:201:ASP:O	2.30	0.65
1:E:14:MET:HE2	1:E:61:NLW:CD2	2.27	0.64
2:dd:128[A]:ASN:HA	2:dd:133:GLN:HE21	1.62	0.64
2:ee:67:VAL:CA	2:ee:79[B]:PHE:CE1	2.80	0.64
2:ff:79:PHE:HZ	2:ff:177:TYR:CD1	2.16	0.64
2:hh:109:LEU:C	2:hh:109:LEU:HD23	2.23	0.63
1:B:6:GLU:O	1:B:32:LYS:HG2	1.98	0.63
1:C:39:THR:OG1	2:cc:208:LYS:HE2	1.98	0.63
1:E:14:MET:HE1	1:E:57:LEU:HD13	1.80	0.63
1:H:44:VAL:HG22	2:hh:205:ASN:HA	1.78	0.63
1:F:45:LYS:HE2	5:F:219:HOH:O	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:19:ASN:HD21	2:cc:125:PHE:HB2	1.63	0.63
2:bb:64:RC7:CD3	2:bb:209:LEU:HG	2.29	0.62
2:gg:89:TRP:O	2:gg:104:ARG:HA	1.99	0.62
1:G:14:MET:HB2	2:gg:118:VAL:HG13	1.82	0.62
1:B:36:GLY:O	2:bb:212:HIS:HA	1.99	0.62
2:bb:72:PRO:HB2	2:bb:74:ASP:OD1	2.00	0.62
1:C:12:VAL:HG22	2:cc:116:GLN:HB2	1.81	0.62
1:G:59:THR:O	2:gg:64:RC7:O2	2.18	0.62
2:bb:64:RC7:HE2	2:bb:195:ILE:HB	1.80	0.62
1:C:9:ARG:HD3	5:cc:324:HOH:O	1.98	0.62
2:ee:66:ARG:NH1	2:ee:211:GLU:OE1	2.29	0.62
1:F:52:PHE:CE1	1:F:57:LEU:HD11	2.28	0.62
2:gg:152:LEU:HD21	2:gg:178:LYS:HB2	1.81	0.62
2:ee:66:ARG:O	2:ee:67:VAL:HG22	2.00	0.62
2:hh:89:TRP:CE2	2:hh:105:SER:HB3	2.35	0.62
2:hh:121:ASN:HB3	2:hh:123:MET:HE3	1.81	0.62
2:bb:86:GLY:HA3	5:bb:320:HOH:O	2.00	0.62
2:cc:96:GLU:N	2:cc:170:LEU:O	2.32	0.61
2:aa:105:SER:CB	2:aa:118:VAL:HG22	2.27	0.61
2:ff:75:ILE:HD11	2:ff:189:HIS:CD2	2.36	0.61
2:gg:147:HIS:HA	5:gg:440:HOH:O	2.00	0.61
2:gg:131:VAL:HG12	2:gg:132:MET:HE2	1.83	0.61
2:hh:92:THR:HG23	5:hh:457:HOH:O	2.00	0.61
1:A:17:ASN:ND2	1:A:20:GLY:O	2.34	0.61
2:dd:72:PRO:HB2	2:dd:74:ASP:OD1	2.00	0.61
2:gg:143:THR:O	2:gg:157:ILE:HG23	2.01	0.61
2:ee:145:LYS:O	2:ee:155:GLY:HA2	2.00	0.60
1:G:18:VAL:CG1	2:gg:132:MET:HE1	2.30	0.60
2:gg:65:ASN:OD1	2:gg:67:VAL:HB	2.02	0.60
1:D:32:LYS:HD2	1:D:35:GLU:OE2	2.02	0.60
2:aa:210:TYR:CE2	2:ee:223:GLN:HG2	2.36	0.60
2:bb:200:ASN:HA	2:bb:206:LYS:O	2.02	0.60
2:hh:154:VAL:HG22	2:hh:176:THR:HG23	1.84	0.60
2:bb:137:LEU:HD23	2:bb:138:LYS:HB3	1.84	0.60
1:D:26:GLU:HG3	1:D:45:LYS:HG3	1.83	0.60
1:D:49:PRO:HG2	5:D:408:HOH:O	2.01	0.60
2:ee:64:RC7:HB12	2:ee:195:ILE:HD11	1.83	0.60
5:B:318:HOH:O	2:bb:132:MET:HE1	2.02	0.60
2:cc:65:ASN:O	2:cc:67:VAL:N	2.35	0.60
1:H:51:PRO:HB2	5:H:403:HOH:O	2.01	0.60
1:D:58:THR:HG21	5:D:410:HOH:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:27:GLY:HA3	1:G:40:LEU:HD11	1.84	0.59
1:A:45:LYS:O	1:A:46:GLU:HG3	2.01	0.59
2:gg:95:TYR:CE2	2:gg:125:PHE:HE2	2.21	0.59
1:H:44:VAL:HG23	1:H:44:VAL:O	2.03	0.59
2:hh:164:GLU:O	2:hh:166:GLY:N	2.35	0.59
1:D:16:GLY:HA2	2:dd:120:PHE:O	2.02	0.59
2:hh:144:GLU:CD	2:hh:157:ILE:HD11	2.28	0.59
2:gg:139:TRP:CE2	2:gg:161:LEU:HD21	2.38	0.59
2:bb:66:ARG:NH1	2:bb:211:GLU:OE2	2.26	0.59
1:C:13:HIS:ND1	1:C:26:GLU:OE2	2.33	0.59
1:H:50:LEU:HB2	1:H:54[B]:TYR:CE2	2.37	0.58
2:hh:66:ARG:HB2	2:hh:79:PHE:CD1	2.38	0.58
2:gg:72:PRO:HG2	2:gg:74:ASP:OD1	2.03	0.58
2:cc:143:THR:OG1	2:cc:192:ASP:OD1	2.16	0.58
1:D:4:ILE:HG22	1:D:33:PRO:HG3	1.84	0.58
2:ee:79[A]:PHE:O	2:ee:82:SER:OG	2.13	0.58
2:ee:139:TRP:CD2	2:ee:161:LEU:HD21	2.38	0.58
2:hh:147:HIS:ND1	2:hh:154:VAL:HB	2.18	0.58
1:B:9:ARG:O	2:bb:114:PHE:N	2.30	0.58
1:D:42:LEU:O	2:dd:206:LYS:HA	2.03	0.58
2:aa:109:LEU:HD12	5:aa:301:HOH:O	2.03	0.58
2:bb:70:LYS:HD3	2:bb:214:VAL:HG13	1.85	0.58
1:C:26:GLU:HG3	1:C:45:LYS:HD3	1.86	0.58
1:B:16:GLY:HA2	2:bb:120:PHE:O	2.03	0.58
2:bb:130:PRO:HA	2:bb:135:LYS:HG3	1.85	0.58
1:G:61:NLW:NH2	2:gg:64:RC7:CA1	2.67	0.58
2:gg:145:LYS:O	2:gg:156:ASN:N	2.30	0.57
2:bb:92:THR:HG21	2:dd:100:ILE:HG21	1.85	0.57
2:cc:146:LEU:CD1	2:cc:191:VAL:HG23	2.33	0.57
2:bb:174:LYS:CE	2:dd:124:ASN:HD21	2.17	0.57
2:bb:64:RC7:N2	2:bb:64:RC7:HD2	2.18	0.57
2:dd:68:PHE:C	2:dd:69:THR:HG23	2.27	0.57
2:dd:93:MET:HE2	2:dd:101:CYS:HB2	1.86	0.57
1:F:56:ILE:HG13	1:F:57:LEU:HD12	1.87	0.57
2:bb:144:GLU:HG3	2:bb:157:ILE:HG12	1.85	0.57
2:hh:140:GLU:C	2:hh:141:PRO:O	2.47	0.57
2:gg:145:LYS:N	2:gg:156:ASN:O	2.25	0.57
2:dd:68:PHE:C	2:dd:69:THR:CG2	2.77	0.57
2:dd:71:TYR:HB2	2:dd:77:ASP:OD2	2.04	0.57
2:ff:97:ASP:C	2:ff:98:LYS:HG2	2.30	0.56
1:A:36:GLY:O	2:aa:212:HIS:HA	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:bb:119[A]:ARG:NH2	5:bb:303:HOH:O	2.37	0.56
2:gg:83:PHE:HZ	2:gg:107:ILE:HG22	1.69	0.56
2:aa:76:PRO:HG2	2:aa:186:PRO:CA	2.34	0.56
1:C:40:LEU:HB2	2:cc:64:RC7:HE3	1.87	0.56
2:cc:159:MET:HE2	2:cc:173:PHE:CE2	2.39	0.56
2:hh:66:ARG:O	2:hh:69:THR:OG1	2.19	0.56
2:cc:96:GLU:CD	2:hh:149:ARG:HH22	2.14	0.56
1:D:4:ILE:CG2	1:D:33:PRO:HG3	2.35	0.56
2:ee:223:GLN:O	2:ee:225:TRP:CD1	2.58	0.56
2:gg:107:ILE:HG12	2:gg:116:GLN:HG2	1.87	0.56
1:D:43:THR:HA	2:dd:205:ASN:O	2.06	0.56
2:ee:79[A]:PHE:HE1	2:ee:177:TYR:CD2	2.24	0.56
2:bb:96:GLU:OE2	2:bb:170:LEU:HB2	2.06	0.56
2:hh:147:HIS:HE1	2:hh:154:VAL:HB	1.66	0.56
2:gg:87:TYR:HB2	2:gg:178:LYS:O	2.06	0.56
2:hh:147:HIS:ND1	2:hh:147:HIS:O	2.39	0.56
2:ee:71:TYR:CE1	2:ee:79[B]:PHE:CZ	2.94	0.56
2:ff:79:PHE:HB2	5:ff:419:HOH:O	2.06	0.56
2:hh:64:RC7:OH	2:hh:142:SER:OG	2.23	0.56
1:F:25:ILE:CG1	1:F:44:VAL:HG22	2.33	0.55
2:hh:90:GLU:HG2	2:hh:104:ARG:HG2	1.87	0.55
2:ee:67:VAL:N	2:ee:79[B]:PHE:CE1	2.75	0.55
1:F:9:ARG:HG3	2:ff:113:CYS:SG	2.46	0.55
1:G:49:PRO:HA	5:gg:419:HOH:O	2.06	0.55
1:A:12:VAL:HG22	2:aa:116:GLN:HB2	1.88	0.55
2:ee:64:RC7:OH	2:ee:193:HIS:HB2	2.06	0.55
2:ee:67:VAL:CA	2:ee:79[B]:PHE:CD1	2.89	0.55
2:bb:103:ILE:N	2:dd:123:MET:HE1	2.21	0.55
2:gg:140:GLU:OE2	2:gg:168:HIS:NE2	2.37	0.55
2:aa:222:SER:CB	5:aa:318:HOH:O	2.55	0.55
2:cc:66:ARG:HG2	5:cc:341:HOH:O	2.06	0.55
2:ff:148:VAL:HG23	5:ff:433:HOH:O	2.07	0.55
2:gg:78:TYR:CD1	2:gg:183:VAL:HG21	2.42	0.55
2:aa:145:LYS:HE2	2:ee:158:ASN:O	2.06	0.54
2:hh:66:ARG:HB3	2:hh:79:PHE:CE2	2.42	0.54
2:aa:81:GLN:OE1	2:aa:183:VAL:HB	2.06	0.54
2:bb:115:PHE:CE2	2:bb:117:ASN:HB2	2.42	0.54
2:ff:98:LYS:HA	5:ff:442:HOH:O	2.07	0.54
2:aa:192:ASP:OD2	2:ee:216:ARG:NH1	2.39	0.54
2:ff:71:TYR:CD1	2:ff:215:ALA:HB3	2.41	0.54
2:aa:123:MET:SD	2:cc:102:THR:HB	2.48	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:bb:97:ASP:OD2	2:bb:169:TYR:OH	2.23	0.54
1:C:21:HIS:NE2	1:C:47:GLY:O	2.40	0.54
2:aa:145:LYS:O	2:aa:155:GLY:HA2	2.08	0.54
2:ff:71:TYR:CD2	2:ff:77:ASP:HA	2.42	0.54
1:A:27:GLY:HA3	1:A:42:LEU:HD23	1.89	0.54
2:aa:168:HIS:O	2:ee:149:ARG:NH2	2.40	0.54
2:bb:150:ASP:OD2	2:dd:128[B]:ASN:ND2	2.41	0.54
2:ff:66:ARG:CB	2:ff:79:PHE:CD2	2.72	0.54
2:ff:74:ASP:C	2:ff:75:ILE:HG22	2.33	0.54
2:bb:143:THR:OG1	2:bb:192:ASP:OD1	2.25	0.54
2:ee:102:THR:HG21	2:hh:123:MET:CG	2.32	0.54
2:gg:101:CYS:SG	2:gg:125:PHE:CZ	2.93	0.54
2:hh:172:ASP:O	2:hh:173:PHE:HD1	1.91	0.54
2:ee:64:RC7:CZ	2:ee:193:HIS:CB	2.86	0.53
2:gg:66:ARG:NH1	5:gg:406:HOH:O	2.40	0.53
2:hh:83:PHE:CE1	2:hh:86:GLY:HA2	2.42	0.53
2:cc:70:LYS:HB3	2:cc:214:VAL:HG22	1.91	0.53
2:cc:229:HIS:CE1	2:hh:136:THR:O	2.62	0.53
1:D:9:ARG:NH1	5:D:403:HOH:O	2.42	0.53
2:ff:153:LEU:O	2:ff:177:TYR:N	2.42	0.53
2:gg:72:PRO:HB2	2:gg:74:ASP:OD1	2.09	0.53
2:gg:124:ASN:HB3	5:gg:442:HOH:O	2.07	0.53
2:hh:189:HIS:HB2	2:hh:216:ARG:O	2.08	0.53
2:bb:64:RC7:HB11	2:bb:211:GLU:OE1	2.09	0.53
1:E:4:ILE:CG2	1:E:33:PRO:HG2	2.39	0.53
2:ee:67:VAL:N	2:ee:79[B]:PHE:CD1	2.77	0.53
2:aa:176:THR:HG22	5:aa:311:HOH:O	2.08	0.53
2:gg:64:RC7:OH	2:gg:193:HIS:CB	2.55	0.53
2:gg:83:PHE:CZ	2:gg:107:ILE:HG22	2.44	0.53
1:H:32:LYS:HB2	1:H:35:GLU:HB2	1.89	0.53
1:B:55:ASP:OD2	2:bb:136:THR:OG1	2.25	0.53
1:E:44:VAL:CG1	1:E:48:ALA:HB2	2.40	0.53
2:ee:66:ARG:HH12	2:ee:211:GLU:CD	2.16	0.53
2:cc:64:RC7:CD3	2:cc:209:LEU:HG	2.39	0.52
2:cc:93:MET:HE2	2:cc:101:CYS:SG	2.49	0.52
2:cc:143:THR:HB	2:hh:145:LYS:HZ1	1.74	0.52
1:G:33:PRO:HA	2:gg:68:PHE:CD1	2.44	0.52
1:G:40:LEU:HD21	1:G:42:LEU:HD21	1.91	0.52
1:A:9:ARG:O	2:aa:113:CYS:HA	2.09	0.52
2:ee:89:TRP:HE1	2:ee:107:ILE:HD11	1.75	0.52
2:ee:139:TRP:CE2	2:ee:161:LEU:HD21	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:gg:78:TYR:CE1	2:gg:183:VAL:HG21	2.44	0.52
2:hh:65:ASN:O	2:hh:66:ARG:C	2.47	0.52
2:cc:64:RC7:CE1	2:cc:159:MET:HE1	2.39	0.52
2:dd:97:ASP:CG	2:dd:169:TYR:HH	2.16	0.52
2:dd:105:SER:HA	2:dd:117:ASN:O	2.09	0.52
2:dd:196:GLU:O	2:dd:209:LEU:HD12	2.09	0.52
2:cc:198:LEU:HB2	5:cc:338:HOH:O	2.08	0.52
2:gg:83:PHE:CD1	2:gg:86:GLY:HA2	2.45	0.52
2:gg:96:GLU:OE2	2:gg:169:TYR:HA	2.09	0.52
2:aa:92:THR:CG2	2:aa:174:LYS:HB3	2.40	0.52
1:G:40:LEU:CB	2:gg:64:RC7:HE3	2.36	0.52
1:B:12:VAL:HG22	2:bb:116:GLN:HB2	1.91	0.52
1:B:49:PRO:HB2	2:bb:203:ASP:HB3	1.91	0.52
1:D:36:GLY:HA2	2:dd:69:THR:HA	1.91	0.52
2:gg:96:GLU:OE2	2:gg:170:LEU:N	2.39	0.52
1:H:25:ILE:CD1	1:H:44:VAL:HG12	2.40	0.52
1:H:25:ILE:HG12	1:H:44:VAL:HA	1.91	0.52
2:cc:160:ALA:HA	2:cc:170:LEU:HD12	1.92	0.52
2:aa:70:LYS:HB3	2:aa:214:VAL:HG13	1.92	0.52
2:hh:66:ARG:HB2	2:hh:79:PHE:CE1	2.45	0.52
1:D:12:VAL:HG22	2:dd:116:GLN:HB2	1.92	0.51
2:dd:200:ASN:ND2	2:dd:201:ASP:O	2.43	0.51
2:ff:71:TYR:CD2	2:ff:77:ASP:CG	2.88	0.51
2:gg:76:PRO:HD2	2:gg:186:PRO:HB3	1.91	0.51
1:D:54:TYR:CZ	2:dd:207:VAL:HG21	2.45	0.51
1:A:16:GLY:HA2	2:aa:120:PHE:O	2.11	0.51
2:ff:78:TYR:CG	2:ff:153:LEU:HD12	2.46	0.51
2:ee:140:GLU:OE1	2:ee:141:PRO:HD2	2.10	0.51
2:hh:140:GLU:O	2:hh:141:PRO:C	2.51	0.51
2:cc:129:GLY:O	2:cc:133:GLN:HB2	2.11	0.51
1:E:13:HIS:ND1	1:E:26:GLU:OE2	2.43	0.51
2:ff:79:PHE:HZ	2:ff:177:TYR:CG	2.28	0.51
2:ff:206:LYS:HG3	5:ff:440:HOH:O	2.09	0.51
2:bb:108:SER:HB3	2:bb:115:PHE:HB3	1.93	0.51
2:dd:133:GLN:O	2:dd:134:LYS:C	2.53	0.51
1:H:3:LEU:HD21	2:hh:109:LEU:HD13	1.92	0.51
1:B:9:ARG:O	2:bb:113:CYS:HA	2.11	0.51
1:E:59:THR:HG22	5:E:412:HOH:O	2.11	0.51
1:F:25:ILE:HD11	1:F:50:LEU:HD21	1.93	0.50
2:aa:192:ASP:N	2:aa:192:ASP:OD1	2.44	0.50
1:D:44:VAL:CG1	1:D:48:ALA:HB2	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:44:VAL:CG1	1:G:48:ALA:HB2	2.41	0.50
2:aa:137:LEU:HD11	2:aa:164:GLU:CA	2.41	0.50
2:aa:223:GLN:HG3	2:ee:210:TYR:CE2	2.47	0.50
2:hh:77:ASP:OD2	2:hh:80:LYS:NZ	2.45	0.50
1:B:48:ALA:HB1	2:bb:205:ASN:OD1	2.11	0.50
1:F:4:ILE:HG23	1:F:33:PRO:HG2	1.92	0.50
1:G:5:LYS:HB3	1:G:8:MET:SD	2.52	0.50
2:hh:85:GLU:OE1	2:hh:181:LYS:HB3	2.12	0.50
2:ff:147:HIS:HB3	2:ff:188:TYR:CE1	2.47	0.50
2:gg:88:SER:HA	2:gg:105:SER:O	2.12	0.50
2:hh:105:SER:HA	2:hh:117:ASN:O	2.11	0.50
1:F:59:THR:O	2:ff:64:RC7:C2	2.59	0.50
1:H:59:THR:HG22	2:hh:64:RC7:CD2	2.42	0.50
2:ee:73:GLU:HG2	2:ee:73:GLU:O	2.11	0.50
1:G:40:LEU:HD13	5:G:411:HOH:O	2.11	0.50
2:gg:90:GLU:O	2:gg:176:THR:N	2.44	0.50
2:gg:126:PRO:O	2:gg:128:ASN:N	2.45	0.50
2:hh:145:LYS:HE3	2:hh:190:PHE:HD2	1.75	0.50
2:aa:146:LEU:HA	2:aa:154:VAL:O	2.12	0.49
1:G:44:VAL:HG21	5:gg:419:HOH:O	2.11	0.49
2:hh:148:VAL:O	5:hh:404:HOH:O	2.20	0.49
2:cc:96:GLU:OE2	2:cc:170:LEU:N	2.45	0.49
1:G:55:ASP:OD2	2:gg:136:THR:OG1	2.29	0.49
2:gg:72:PRO:HB2	2:gg:74:ASP:CG	2.38	0.49
1:D:59:THR:O	2:dd:91:ARG:NH1	2.45	0.49
2:dd:97:ASP:OD1	2:dd:169:TYR:OH	2.29	0.49
2:dd:146:LEU:O	2:dd:188:TYR:HA	2.12	0.49
2:bb:83:PHE:HA	2:bb:84:PRO:C	2.36	0.49
2:cc:218:SER:HB3	2:hh:194:ARG:NH2	2.27	0.49
2:hh:119:ARG:NH2	5:hh:414:HOH:O	2.46	0.49
1:A:33:PRO:HD3	2:aa:68:PHE:HE1	1.77	0.49
2:ee:102:THR:OG1	2:hh:123:MET:SD	2.67	0.49
2:ff:95:TYR:HA	2:ff:171:CYS:HA	1.94	0.49
1:H:42:LEU:O	2:hh:206:LYS:HA	2.13	0.49
2:aa:137:LEU:HD12	2:aa:162:LEU:O	2.12	0.49
2:dd:68:PHE:O	2:dd:69:THR:HG22	2.13	0.49
2:ee:66:ARG:C	2:ee:68:PHE:H	2.19	0.49
2:gg:66:ARG:HG3	2:gg:69:THR:HG21	1.94	0.49
1:G:7:ASP:OD1	1:G:32:LYS:HE2	2.12	0.49
2:bb:140:GLU:OE2	2:bb:168:HIS:NE2	2.27	0.49
2:dd:128[B]:ASN:HA	2:dd:133:GLN:HE21	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:28:GLU:CG	5:H:419:HOH:O	2.61	0.49
1:H:54[B]:TYR:CE2	2:hh:204:TYR:HB2	2.46	0.49
2:cc:137:LEU:HD11	2:cc:164:GLU:HA	1.95	0.48
2:cc:65:ASN:CG	2:cc:107:ILE:HD13	2.38	0.48
2:hh:145:LYS:HE3	2:hh:190:PHE:CD2	2.48	0.48
1:A:9:ARG:N	2:aa:112:ASP:O	2.37	0.48
2:bb:146:LEU:CD1	2:bb:191:VAL:HG23	2.43	0.48
2:bb:161:LEU:O	2:bb:168:HIS:HA	2.14	0.48
2:cc:67:VAL:HG23	2:cc:87:TYR:HE1	1.78	0.48
2:ee:140:GLU:C	2:ee:141:PRO:O	2.52	0.48
2:ff:83:PHE:CD1	2:ff:86:GLY:HA2	2.47	0.48
2:bb:64:RC7:CD3	2:bb:211:GLU:HB3	2.43	0.48
2:bb:135:LYS:O	2:bb:163:LEU:HD23	2.14	0.48
1:H:36:GLY:N	2:hh:70:LYS:HG2	2.28	0.48
2:hh:104:ARG:NH1	5:hh:413:HOH:O	2.45	0.48
2:bb:97:ASP:C	2:bb:97:ASP:OD1	2.56	0.48
2:cc:66:ARG:HB2	2:cc:79:PHE:CD2	2.49	0.48
2:cc:168:HIS:C	2:hh:149:ARG:HH21	2.22	0.48
2:ff:108:SER:HB2	2:ff:115:PHE:HB3	1.96	0.48
2:gg:82:SER:HB2	2:gg:87:TYR:HB3	1.95	0.48
2:hh:125:PHE:CD2	2:hh:131:VAL:HG21	2.49	0.48
2:cc:99:GLY:HA3	2:cc:125:PHE:CD1	2.48	0.48
2:ff:182:VAL:O	2:ff:183:VAL:CG1	2.61	0.48
1:C:59:THR:O	2:cc:64:RC7:C2	2.61	0.48
2:ee:64:RC7:CZ	2:ee:159:MET:HE1	2.43	0.48
2:ff:95:TYR:CD2	2:ff:171:CYS:HB2	2.49	0.48
1:G:10:VAL:HB	5:G:411:HOH:O	2.14	0.48
2:hh:140:GLU:O	2:hh:141:PRO:O	2.31	0.47
2:ff:79:PHE:CZ	2:ff:177:TYR:CD1	2.99	0.47
2:hh:180:LYS:HD2	2:hh:180:LYS:HA	1.76	0.47
2:aa:90:GLU:OE2	2:aa:104:ARG:NH1	2.46	0.47
2:ff:123:MET:HE1	2:gg:91:ARG:H	1.79	0.47
2:gg:64:RC7:HE2	2:gg:195:ILE:HB	1.95	0.47
2:aa:137:LEU:O	2:aa:138:LYS:HB3	2.12	0.47
1:D:8:MET:HE2	2:dd:114:PHE:CE2	2.49	0.47
1:E:33:PRO:HD3	2:ee:68:PHE:HE1	1.80	0.47
2:hh:93:MET:HE3	2:hh:95:TYR:OH	2.15	0.47
2:bb:107:ILE:HD13	2:bb:116:GLN:HG2	1.96	0.47
2:ff:123:MET:HE3	2:gg:90:GLU:HB3	1.97	0.47
2:gg:66:ARG:O	2:gg:69:THR:OG1	2.23	0.47
2:aa:91:ARG:HB3	2:aa:103:ILE:HB	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:bb:130:PRO:HB3	2:bb:163:LEU:HD21	1.95	0.47
1:E:34:TYR:CZ	2:ee:80:LYS:HE2	2.50	0.47
1:F:16:GLY:HA2	2:ff:120:PHE:O	2.15	0.47
1:F:21:HIS:NE2	1:F:47:GLY:O	2.40	0.47
2:ff:149:ARG:HB3	2:ff:154:VAL:HG21	1.95	0.47
2:aa:64:RC7:HD3	2:aa:211:GLU:CB	2.44	0.47
1:B:58:THR:HG21	5:B:308:HOH:O	2.15	0.47
2:ee:79[B]:PHE:O	2:ee:82:SER:OG	2.25	0.47
2:ee:149:ARG:HB3	2:ee:154:VAL:CG2	2.45	0.47
1:F:50:LEU:HD12	1:F:50:LEU:N	2.30	0.47
2:gg:160:ALA:HB1	2:gg:168:HIS:HB3	1.96	0.47
2:gg:72:PRO:HB2	2:gg:74:ASP:OD2	2.14	0.47
1:A:33:PRO:HD3	2:aa:68:PHE:CE1	2.49	0.47
2:aa:65:ASN:OD1	2:aa:67:VAL:HB	2.14	0.47
2:cc:144:GLU:HB2	2:cc:193:HIS:NE2	2.30	0.47
2:ee:77:ASP:OD1	2:ee:79[B]:PHE:CE1	2.67	0.47
2:aa:222:SER:HB3	5:aa:318:HOH:O	2.14	0.46
1:C:13:HIS:HD1	1:C:26:GLU:CD	2.23	0.46
2:ee:162:LEU:HD12	2:ee:163:LEU:N	2.30	0.46
2:ee:148:VAL:HA	2:ee:152:LEU:O	2.14	0.46
2:ee:149:ARG:HB3	2:ee:154:VAL:HG21	1.97	0.46
2:aa:97:ASP:OD1	2:aa:169:TYR:OH	2.32	0.46
2:gg:163:LEU:HD11	2:gg:169:TYR:HB2	1.97	0.46
1:F:44:VAL:HG11	1:F:50:LEU:HD11	1.96	0.46
2:ff:144:GLU:HG3	2:ff:157:ILE:HG12	1.97	0.46
2:gg:69:THR:HG22	2:gg:213:GLY:HA3	1.96	0.46
1:H:17:ASN:ND2	1:H:20:GLY:O	2.48	0.46
2:bb:93:MET:HE3	2:bb:95:TYR:OH	2.16	0.46
1:C:54:TYR:CZ	2:cc:207:VAL:HG21	2.51	0.46
2:cc:105:SER:HA	2:cc:117:ASN:O	2.15	0.46
1:E:59:THR:CG2	5:E:412:HOH:O	2.63	0.46
2:hh:204:TYR:OH	5:hh:402:HOH:O	2.11	0.46
2:cc:66:ARG:HB2	2:cc:79:PHE:CE2	2.51	0.46
2:cc:89:TRP:HA	2:cc:176:THR:O	2.15	0.46
2:cc:93:MET:O	2:cc:100:ILE:HD12	2.15	0.46
2:cc:144:GLU:HG3	2:cc:157:ILE:HG12	1.98	0.46
2:ff:66:ARG:HB3	5:ff:423:HOH:O	2.15	0.46
2:ff:71:TYR:HD2	2:ff:77:ASP:CG	2.23	0.46
2:ff:146:LEU:HB2	2:ff:189:HIS:ND1	2.31	0.46
2:bb:100:ILE:HG12	2:bb:101:CYS:N	2.31	0.46
2:cc:71:TYR:CE2	2:cc:76:PRO:O	2.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:cc:146:LEU:HD11	2:cc:191:VAL:HG23	1.98	0.46
2:dd:68:PHE:O	2:dd:69:THR:CG2	2.63	0.46
2:dd:85:GLU:OE2	5:dd:401:HOH:O	2.21	0.46
1:E:56:ILE:HG12	5:E:413:HOH:O	2.14	0.46
1:F:40:LEU:O	2:ff:208:LYS:HA	2.16	0.46
2:dd:66:ARG:HH11	2:dd:69:THR:CG2	2.22	0.46
1:E:22:ALA:HB3	5:E:406:HOH:O	2.15	0.46
1:E:59:THR:HB	5:E:412:HOH:O	2.16	0.46
2:ee:64:RC7:HB12	2:ee:195:ILE:CD1	2.45	0.46
2:bb:65:ASN:ND2	2:bb:107:ILE:HD12	2.31	0.45
2:dd:110:GLU:O	2:dd:112:ASP:N	2.48	0.45
1:E:4:ILE:HB	2:ee:80:LYS:NZ	2.31	0.45
2:ff:71:TYR:CE1	2:ff:215:ALA:HB1	2.50	0.45
2:ff:75:ILE:CD1	2:ff:189:HIS:CD2	2.99	0.45
2:gg:64:RC7:HD3	2:gg:211:GLU:HB2	1.98	0.45
2:cc:103:ILE:HG12	2:cc:120:PHE:CD2	2.51	0.45
2:gg:78:TYR:OH	2:gg:179:ALA:N	2.47	0.45
2:gg:123:MET:O	2:gg:124:ASN:C	2.59	0.45
2:hh:120:PHE:CD1	2:hh:120:PHE:C	2.94	0.45
2:cc:64:RC7:OH	2:cc:193:HIS:HB2	2.17	0.45
2:ee:70:LYS:HE3	2:ee:214:VAL:CG2	2.37	0.45
2:ee:123:MET:HG2	2:ee:124:ASN:N	2.31	0.45
1:F:56:ILE:HD13	2:ff:131:VAL:CG1	2.47	0.45
2:gg:64:RC7:CZ	2:gg:193:HIS:CB	2.94	0.45
1:H:3:LEU:HD21	2:hh:109:LEU:CD1	2.47	0.45
2:hh:147:HIS:HE1	2:hh:154:VAL:CB	2.29	0.45
2:aa:81:GLN:HE22	2:aa:184:GLN:HB3	1.80	0.45
1:B:34:TYR:CD1	2:bb:80:LYS:HE3	2.52	0.45
2:cc:107:ILE:HG12	2:cc:116:GLN:HG2	1.99	0.45
2:cc:143:THR:HB	2:hh:145:LYS:NZ	2.32	0.45
2:hh:102:THR:HG22	2:hh:123:MET:CE	2.39	0.45
1:E:15:GLU:O	2:ee:119:ARG:HA	2.17	0.45
2:gg:64:RC7:C3	2:gg:65:ASN:CA	2.83	0.45
2:hh:97:ASP:HB3	5:hh:445:HOH:O	2.16	0.45
2:aa:145:LYS:HE3	2:aa:190:PHE:HE1	1.81	0.45
2:dd:79:PHE:O	2:dd:82:SER:OG	2.34	0.45
1:E:55:ASP:OD2	2:ee:136:THR:OG1	2.32	0.45
2:ee:66:ARG:C	2:ee:68:PHE:N	2.73	0.45
2:ff:65:ASN:OD1	2:ff:67:VAL:HG23	2.17	0.45
2:ff:102:THR:C	2:ff:103:ILE:HG13	2.42	0.45
1:A:38:GLN:O	2:aa:210:TYR:HD1	2.00	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:MET:HE1	2:bb:112:ASP:HA	1.99	0.45
2:ff:183:VAL:HG22	2:ff:184:GLN:N	2.32	0.45
1:D:26:GLU:CG	1:D:45:LYS:HG3	2.47	0.45
2:dd:97:ASP:CG	2:dd:169:TYR:OH	2.60	0.45
1:G:25:ILE:HD11	1:G:50:LEU:HD11	1.99	0.45
2:hh:105:SER:OG	2:hh:118:VAL:HG22	2.17	0.45
1:A:54:TYR:CZ	2:aa:207:VAL:HG21	2.51	0.44
2:ee:139:TRP:CE3	2:ee:161:LEU:HG	2.52	0.44
2:ee:139:TRP:HA	2:ee:161:LEU:HD23	1.99	0.44
1:G:14:MET:HB2	2:gg:118:VAL:CG1	2.46	0.44
2:hh:147:HIS:CE1	2:hh:154:VAL:CB	2.92	0.44
2:aa:208:LYS:NZ	2:ee:225:TRP:HH2	2.15	0.44
2:cc:164:GLU:HB3	5:cc:348:HOH:O	2.17	0.44
1:F:38:GLN:HG3	2:ff:64:RC7:NE1	2.32	0.44
2:gg:143:THR:OG1	2:gg:192:ASP:OD1	2.34	0.44
1:B:40:LEU:HB2	2:bb:64:RC7:HE3	1.99	0.44
1:G:33:PRO:HG3	2:gg:68:PHE:CE1	2.53	0.44
2:ee:148:VAL:HG11	2:ee:185:LEU:HD13	1.99	0.44
2:ff:64:RC7:OH	2:ff:193:HIS:HB2	2.18	0.44
2:ff:65:ASN:HB2	2:ff:107:ILE:HD13	1.99	0.44
2:gg:66:ARG:HG3	2:gg:69:THR:CG2	2.48	0.44
2:gg:165:GLY:N	5:gg:413:HOH:O	2.49	0.44
2:hh:66:ARG:NE	2:hh:66:ARG:HA	2.33	0.44
2:hh:110:GLU:O	2:hh:113:CYS:N	2.47	0.44
2:ee:171:CYS:SG	2:ee:173:PHE:HE1	2.41	0.44
1:F:56:ILE:HD13	2:ff:131:VAL:HG11	1.99	0.44
2:ff:219:PRO:C	2:ff:220:LEU:HD23	2.42	0.44
2:gg:66:ARG:HB3	2:gg:79:PHE:CD2	2.52	0.44
2:hh:156:ASN:O	2:hh:157:ILE:HG13	2.17	0.44
2:bb:118:VAL:C	2:bb:119[B]:ARG:HD2	2.43	0.44
2:dd:70:LYS:HB3	2:dd:214:VAL:HG22	2.00	0.44
1:E:34:TYR:O	2:ee:70:LYS:HG2	2.18	0.44
3:E:301:GOL:H12	2:ee:123:MET:CG	2.47	0.44
5:G:401:HOH:O	2:gg:207:VAL:HB	2.18	0.44
2:gg:95:TYR:CD2	2:gg:125:PHE:HE2	2.35	0.44
2:gg:175:THR:CG2	2:gg:177:TYR:CE1	3.01	0.44
1:A:12:VAL:HG22	2:aa:116:GLN:NE2	2.32	0.44
1:E:18:VAL:HG12	1:E:19:ASN:HB2	1.99	0.44
1:G:18:VAL:HG12	2:gg:132:MET:HE1	2.00	0.44
2:gg:141:PRO:HA	5:gg:421:HOH:O	2.18	0.44
2:hh:65:ASN:OD1	2:hh:67:VAL:HB	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:hh:112:ASP:HB3	5:hh:439:HOH:O	2.18	0.44
2:gg:103:ILE:HG12	2:gg:120:PHE:CD2	2.53	0.44
1:B:27:GLY:HA3	1:B:42:LEU:HD23	1.98	0.44
2:cc:139:TRP:CE3	2:cc:159:MET:HG2	2.53	0.44
2:ee:104:ARG:NH1	1:H:19:ASN:HA	2.33	0.44
1:F:48:ALA:CB	2:ff:205:ASN:ND2	2.81	0.44
2:ee:200:ASN:O	2:ee:200:ASN:CG	2.61	0.43
1:H:33:PRO:HA	2:hh:68:PHE:HA	2.00	0.43
1:A:54:TYR:CE2	2:aa:207:VAL:HG21	2.52	0.43
2:aa:66:ARG:HB2	2:aa:79:PHE:CE1	2.53	0.43
2:ff:100:ILE:HG13	2:ff:101:CYS:N	2.33	0.43
1:H:36:GLY:HA3	2:hh:70:LYS:HG3	2.01	0.43
2:hh:95:TYR:HD2	2:hh:169:TYR:CE2	2.35	0.43
2:aa:79:PHE:O	2:aa:82:SER:OG	2.37	0.43
2:aa:148:VAL:HA	2:aa:152:LEU:O	2.19	0.43
2:ee:66:ARG:O	2:ee:67:VAL:HG13	2.18	0.43
2:ee:102:THR:CG2	2:hh:123:MET:HG2	2.38	0.43
2:gg:102:THR:C	2:gg:103:ILE:HD12	2.43	0.43
2:cc:200:ASN:ND2	5:cc:310:HOH:O	2.51	0.43
1:F:34:TYR:O	2:ff:70:LYS:CE	2.67	0.43
1:F:34:TYR:O	2:ff:70:LYS:HE2	2.17	0.43
2:gg:147:HIS:NE2	2:gg:154:VAL:HB	2.33	0.43
1:H:3:LEU:HD23	1:H:4:ILE:HG13	1.99	0.43
1:A:59:THR:O	2:aa:64:RC7:C2	2.67	0.43
2:cc:190:PHE:CD1	2:cc:190:PHE:N	2.87	0.43
2:dd:64:RC7:OH	2:dd:142:SER:OG	2.32	0.43
2:ee:180:LYS:NZ	5:ee:306:HOH:O	2.50	0.43
1:H:28:GLU:HG2	5:H:419:HOH:O	2.18	0.43
2:aa:103:ILE:HG22	2:aa:104:ARG:N	2.34	0.43
2:bb:145:LYS:O	2:bb:155:GLY:HA2	2.18	0.43
1:C:16:GLY:CA	2:cc:120:PHE:O	2.65	0.43
2:dd:89:TRP:HA	2:dd:176:THR:O	2.18	0.43
2:ee:102:THR:C	2:ee:103:ILE:CG2	2.90	0.43
2:gg:65:ASN:HA	5:gg:406:HOH:O	2.19	0.43
2:gg:138:LYS:O	2:gg:161:LEU:HA	2.19	0.43
1:H:24:VAL:O	1:H:25:ILE:HG13	2.18	0.43
2:hh:66:ARG:HB3	2:hh:79:PHE:CD2	2.53	0.43
2:hh:144:GLU:HA	2:hh:157:ILE:HG13	2.01	0.43
2:aa:135:LYS:HD3	2:aa:164:GLU:HB2	2.00	0.43
2:cc:67:VAL:HG11	2:cc:114:PHE:CZ	2.54	0.43
2:cc:93:MET:HE2	2:cc:101:CYS:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:cc:96:GLU:OE2	2:cc:170:LEU:HB2	2.18	0.43
1:D:36:GLY:O	2:dd:212:HIS:HA	2.19	0.43
2:dd:215:ALA:O	2:dd:216:ARG:HB3	2.19	0.43
1:E:60:ALA:C	5:E:407:HOH:O	2.61	0.43
1:G:5:LYS:HG3	1:G:6:GLU:H	1.84	0.43
1:B:59:THR:O	2:bb:64:RC7:C2	2.66	0.43
2:bb:66:ARG:HB3	2:bb:79:PHE:CE2	2.54	0.43
2:bb:136:THR:HG21	2:bb:161:LEU:HD13	2.00	0.43
2:ff:94:THR:O	2:ff:172:ASP:N	2.43	0.43
1:G:40:LEU:HG	1:G:42:LEU:HG	2.00	0.43
2:gg:220:LEU:HA	2:gg:221:PRO:HD3	1.81	0.43
2:bb:89:TRP:CE2	2:bb:105:SER:HB3	2.54	0.43
1:H:5:LYS:O	1:H:8:MET:HG2	2.18	0.43
2:bb:139:TRP:CZ3	2:bb:159:MET:HB3	2.54	0.43
2:bb:201:ASP:OD2	2:bb:205:ASN:HB2	2.18	0.43
2:hh:64:RC7:OH	2:hh:193:HIS:HB2	2.19	0.43
2:ff:71:TYR:CD1	2:ff:215:ALA:CB	3.01	0.42
2:gg:120:PHE:CD1	2:gg:120:PHE:C	2.96	0.42
1:A:37:THR:HG23	2:aa:210:TYR:HE1	1.83	0.42
2:dd:97:ASP:OD2	2:dd:169:TYR:OH	2.37	0.42
2:ee:146:LEU:HB3	2:ee:153:LEU:HD11	2.01	0.42
1:E:4:ILE:HD11	2:ee:83:PHE:HB2	2.01	0.42
1:E:25:ILE:HG23	1:E:43:THR:O	2.20	0.42
1:E:27:GLY:HA3	1:E:42:LEU:HD23	2.02	0.42
2:ee:126:PRO:O	2:ee:129:GLY:N	2.50	0.42
1:H:24:VAL:C	1:H:25:ILE:HG13	2.44	0.42
1:H:52:PHE:HB2	2:hh:131:VAL:HG12	2.00	0.42
2:dd:69:THR:HA	2:dd:213:GLY:O	2.20	0.42
2:dd:93:MET:HE3	2:dd:95:TYR:OH	2.20	0.42
1:E:36:GLY:O	2:ee:212:HIS:HD2	2.02	0.42
2:ee:166:GLY:HA2	5:ee:356:HOH:O	2.18	0.42
1:H:59:THR:O	2:hh:64:RC7:C2	2.68	0.42
1:A:12:VAL:CG2	2:aa:116:GLN:NE2	2.82	0.42
2:bb:85:GLU:HB2	2:bb:181:LYS:HE3	2.01	0.42
2:bb:144:GLU:O	2:bb:190:PHE:HA	2.19	0.42
1:F:31:GLY:HA2	1:F:38:GLN:HA	2.01	0.42
1:H:23:PHE:CD1	1:H:23:PHE:C	2.97	0.42
2:ff:71:TYR:CE2	2:ff:77:ASP:HA	2.55	0.42
2:ff:91:ARG:HA	2:ff:174:LYS:O	2.19	0.42
2:hh:172:ASP:O	2:hh:173:PHE:CD1	2.72	0.42
2:hh:216:ARG:HD2	2:hh:217:TYR:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:9:ARG:NH2	1:G:49:PRO:HD3	2.35	0.42
2:dd:96:GLU:CD	2:dd:170:LEU:HB2	2.45	0.42
2:ee:118:VAL:HG12	2:ee:119:ARG:N	2.35	0.42
2:gg:154:VAL:HG12	2:gg:155:GLY:H	1.85	0.42
2:ff:93:MET:O	2:ff:100:ILE:HD12	2.19	0.42
1:G:48:ALA:HA	5:gg:419:HOH:O	2.18	0.42
2:gg:64:RC7:O2	2:gg:66:ARG:NH1	2.52	0.42
1:H:50:LEU:HB2	1:H:54[B]:TYR:HE2	1.83	0.42
2:hh:158:ASN:HB3	5:hh:448:HOH:O	2.19	0.42
2:dd:84:PRO:HD2	2:dd:85:GLU:OE1	2.20	0.42
2:dd:125:PHE:CE1	2:dd:131:VAL:HG21	2.55	0.42
3:E:301:GOL:H12	2:ee:123:MET:HG2	2.02	0.42
1:F:14:MET:SD	1:F:23:PHE:HE2	2.43	0.42
1:F:56:ILE:HG13	1:F:57:LEU:CD1	2.48	0.42
2:gg:83:PHE:HA	2:gg:84:PRO:C	2.45	0.42
2:hh:147:HIS:HD1	2:hh:154:VAL:HB	1.85	0.42
1:B:59:THR:O	2:bb:64:RC7:N3	2.53	0.42
2:bb:106:ASP:OD1	2:bb:180:LYS:HE3	2.19	0.42
2:cc:137:LEU:HD21	2:cc:164:GLU:HG3	2.02	0.42
1:D:36:GLY:HA2	2:dd:69:THR:CA	2.49	0.42
2:dd:158:ASN:OD1	2:dd:172:ASP:OD1	2.38	0.42
2:dd:201:ASP:OD1	2:dd:201:ASP:N	2.49	0.42
1:E:19:ASN:ND2	3:E:301:GOL:H31	2.34	0.42
2:ff:145:LYS:O	2:ff:155:GLY:HA2	2.20	0.42
1:A:5:LYS:HG3	1:A:8:MET:SD	2.60	0.41
2:aa:64:RC7:HE1	2:aa:157:ILE:CD1	2.48	0.41
2:aa:71:TYR:HA	2:aa:72:PRO:HD2	1.86	0.41
2:aa:223:GLN:HG3	2:ee:210:TYR:CZ	2.55	0.41
1:C:5:LYS:O	1:C:7:ASP:N	2.53	0.41
2:cc:168:HIS:O	2:hh:149:ARG:NH2	2.53	0.41
2:dd:64:RC7:N2	2:dd:64:RC7:HD2	2.35	0.41
2:ee:152:LEU:HD13	2:ee:176:THR:CG2	2.50	0.41
2:gg:191:VAL:HG22	2:gg:215:ALA:HA	2.02	0.41
1:C:50:LEU:HG	5:C:108:HOH:O	2.20	0.41
2:dd:64:RC7:HD3	2:dd:209:LEU:HG	2.01	0.41
2:gg:70:LYS:HB3	5:gg:448:HOH:O	2.19	0.41
1:H:25:ILE:HG12	1:H:44:VAL:HG12	2.02	0.41
2:gg:78:TYR:CE2	2:gg:177:TYR:O	2.73	0.41
1:B:12:VAL:O	1:B:26:GLU:HA	2.21	0.41
2:ee:89:TRP:CE2	2:ee:105:SER:HB3	2.55	0.41
2:ee:181:LYS:O	2:ee:181:LYS:HG3	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:ff:93:MET:HE3	2:ff:95:TYR:OH	2.19	0.41
1:G:9:ARG:HH12	1:G:11:LYS:HE2	1.85	0.41
2:gg:67:VAL:O	2:gg:80:LYS:NZ	2.45	0.41
2:gg:95:TYR:HE2	2:gg:125:PHE:HE2	1.66	0.41
1:E:38:GLN:NE2	5:E:404:HOH:O	2.53	0.41
1:F:52:PHE:CD1	1:F:56:ILE:HD11	2.56	0.41
2:aa:72:PRO:HG2	2:aa:75:ILE:HD12	2.02	0.41
2:dd:67:VAL:O	2:dd:80:LYS:NZ	2.41	0.41
1:G:14:MET:CB	2:gg:118:VAL:HG13	2.50	0.41
2:gg:186:PRO:HD2	5:gg:456:HOH:O	2.21	0.41
2:cc:87:TYR:HE2	2:cc:89:TRP:HD1	1.69	0.41
2:gg:65:ASN:HD21	2:gg:67:VAL:HB	1.85	0.41
1:C:9:ARG:HG2	2:cc:113:CYS:SG	2.61	0.41
2:cc:66:ARG:O	2:cc:67:VAL:C	2.57	0.41
1:E:40:LEU:CD2	1:E:42:LEU:HD21	2.51	0.41
2:ee:64:RC7:CE1	2:ee:193:HIS:CG	3.03	0.41
2:hh:89:TRP:CZ2	2:hh:105:SER:CB	3.04	0.41
2:hh:109:LEU:C	2:hh:109:LEU:CD2	2.91	0.41
2:cc:71:TYR:HA	2:cc:72:PRO:HD2	1.92	0.41
1:E:4:ILE:HG12	2:ee:114:PHE:HZ	1.86	0.41
1:E:40:LEU:HD21	1:E:42:LEU:HD21	2.02	0.41
2:ee:85:GLU:OE1	2:ee:181:LYS:CE	2.69	0.41
2:ee:146:LEU:HD13	2:ee:189:HIS:NE2	2.36	0.41
2:ee:163:LEU:HA	2:ee:163:LEU:HD23	1.87	0.41
1:H:28:GLU:HB2	5:H:415:HOH:O	2.21	0.41
1:H:35:GLU:C	2:hh:70:LYS:HG2	2.46	0.41
2:hh:144:GLU:HG2	2:hh:146:LEU:HD21	2.02	0.41
1:B:27:GLY:HA2	1:B:41:ASN:O	2.20	0.41
2:ee:102:THR:HG1	2:hh:123:MET:CG	2.34	0.41
1:G:40:LEU:CD2	1:G:42:LEU:HD21	2.51	0.41
1:D:40:LEU:HD23	1:D:42:LEU:CD2	2.50	0.40
2:ee:85:GLU:OE1	2:ee:181:LYS:HE2	2.21	0.40
2:ff:85:GLU:OE2	2:ff:180:LYS:HE2	2.22	0.40
1:H:36:GLY:O	2:hh:212:HIS:CD2	2.66	0.40
1:A:44:VAL:HG11	1:A:48:ALA:HB2	2.03	0.40
2:aa:94:THR:O	2:aa:171:CYS:HA	2.21	0.40
2:aa:145:LYS:HZ1	2:ee:143:THR:N	2.20	0.40
2:ee:66:ARG:O	2:ee:67:VAL:CB	2.69	0.40
2:gg:71:TYR:HA	2:gg:72:PRO:HD3	1.92	0.40
2:gg:123:MET:HE2	2:gg:123:MET:HB3	1.84	0.40
2:cc:220:LEU:HD12	2:hh:193:HIS:C	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:ee:65:ASN:C	2:ee:66:ARG:O	2.65	0.40
2:aa:108:SER:O	2:aa:114:PHE:HA	2.21	0.40
1:E:4:ILE:HB	2:ee:80:LYS:HZ2	1.86	0.40
1:H:16:GLY:HA2	2:hh:120:PHE:O	2.21	0.40
2:hh:72:PRO:HG2	2:hh:75:ILE:HG13	2.03	0.40
2:cc:195:ILE:HG13	2:cc:211:GLU:HB2	2.03	0.40
2:dd:93:MET:HE2	2:dd:101:CYS:CB	2.50	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	59/62 (95%)	51 (86%)	7 (12%)	1 (2%)	7	2
1	B	58/62 (94%)	52 (90%)	6 (10%)	0	100	100
1	C	57/62 (92%)	51 (90%)	5 (9%)	1 (2%)	6	2
1	D	57/62 (92%)	53 (93%)	4 (7%)	0	100	100
1	E	58/62 (94%)	55 (95%)	3 (5%)	0	100	100
1	F	57/62 (92%)	53 (93%)	4 (7%)	0	100	100
1	G	57/62 (92%)	53 (93%)	4 (7%)	0	100	100
1	H	58/62 (94%)	54 (93%)	4 (7%)	0	100	100
2	aa	162/170 (95%)	151 (93%)	10 (6%)	1 (1%)	21	15
2	bb	165/170 (97%)	150 (91%)	15 (9%)	0	100	100
2	cc	164/170 (96%)	151 (92%)	10 (6%)	3 (2%)	6	2
2	dd	164/170 (96%)	148 (90%)	13 (8%)	3 (2%)	6	2
2	ee	161/170 (95%)	142 (88%)	16 (10%)	3 (2%)	6	2
2	ff	160/170 (94%)	137 (86%)	19 (12%)	4 (2%)	4	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	gg	163/170 (96%)	141 (86%)	16 (10%)	6 (4%)	2	0
2	hh	159/170 (94%)	145 (91%)	7 (4%)	7 (4%)	2	0
All	All	1759/1856 (95%)	1587 (90%)	143 (8%)	29 (2%)	7	2

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	aa	201	ASP
1	C	6	GLU
2	cc	66	ARG
2	dd	111	GLY
2	dd	134	LYS
2	ee	66	ARG
2	ff	183	VAL
2	ff	184	GLN
2	hh	66	ARG
2	hh	77	ASP
2	hh	165	GLY
2	ee	81	GLN
2	ff	75	ILE
2	ff	77	ASP
2	gg	73	GLU
2	gg	74	ASP
2	gg	225	TRP
2	hh	141	PRO
2	hh	222	SER
2	hh	111	GLY
2	gg	84	PRO
2	gg	221	PRO
1	A	3	LEU
2	cc	181	LYS
2	dd	141	PRO
2	gg	127	PRO
2	cc	166	GLY
2	ee	67	VAL
2	hh	166	GLY

5.3.2 Protein sidechains ⓘ

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

resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	50/50 (100%)	45 (90%)	5 (10%)	7	3
1	B	49/50 (98%)	44 (90%)	5 (10%)	7	3
1	C	48/50 (96%)	44 (92%)	4 (8%)	10	6
1	D	48/50 (96%)	41 (85%)	7 (15%)	3	1
1	E	49/50 (98%)	41 (84%)	8 (16%)	2	1
1	F	48/50 (96%)	40 (83%)	8 (17%)	2	1
1	G	48/50 (96%)	46 (96%)	2 (4%)	26	23
1	H	49/50 (98%)	44 (90%)	5 (10%)	7	3
2	aa	148/153 (97%)	142 (96%)	6 (4%)	27	24
2	bb	151/153 (99%)	140 (93%)	11 (7%)	13	8
2	cc	150/153 (98%)	137 (91%)	13 (9%)	9	5
2	dd	150/153 (98%)	142 (95%)	8 (5%)	20	16
2	ee	148/153 (97%)	136 (92%)	12 (8%)	11	6
2	ff	147/153 (96%)	131 (89%)	16 (11%)	6	2
2	gg	149/153 (97%)	137 (92%)	12 (8%)	11	6
2	hh	146/153 (95%)	135 (92%)	11 (8%)	12	7
All	All	1578/1624 (97%)	1445 (92%)	133 (8%)	10	6

All (133) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	4	ILE
1	A	5	LYS
1	A	30	LYS
1	A	33	PRO
2	aa	67	VAL
2	aa	110	GLU
2	aa	112	ASP
2	aa	135	LYS
2	aa	143	THR
2	aa	222	SER
1	B	2	ASN

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Mol	Chain	Res	Type
1	B	6	GLU
1	B	28	GLU
1	B	32	LYS
1	B	33	PRO
2	bb	70	LYS
2	bb	82	SER
2	bb	92	THR
2	bb	100	ILE
2	bb	102	THR
2	bb	123	MET
2	bb	127	PRO
2	bb	164	GLU
2	bb	182	VAL
2	bb	201	ASP
2	bb	211	GLU
1	C	4	ILE
1	C	5	LYS
1	C	6	GLU
1	C	14	MET
2	cc	67	VAL
2	cc	69	THR
2	cc	73	GLU
2	cc	94	THR
2	cc	96	GLU
2	cc	105	SER
2	cc	148	VAL
2	cc	157	ILE
2	cc	159	MET
2	cc	176	THR
2	cc	199	SER
2	cc	202	SER
2	cc	211	GLU
1	D	15	GLU
1	D	28	GLU
1	D	30	LYS
1	D	39	THR
1	D	42	LEU
1	D	51	PRO
1	D	56	ILE
2	dd	76	PRO
2	dd	80	LYS
2	dd	102	THR

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Mol	Chain	Res	Type
2	dd	107	ILE
2	dd	118	VAL
2	dd	126	PRO
2	dd	157	ILE
2	dd	174	LYS
1	E	10	VAL
1	E	12	VAL
1	E	19	ASN
1	E	32	LYS
1	E	33	PRO
1	E	39	THR
1	E	43	THR
1	E	45	LYS
2	ee	67	VAL
2	ee	75	ILE
2	ee	98	LYS
2	ee	104	ARG
2	ee	108	SER
2	ee	134	LYS
2	ee	149	ARG
2	ee	150	ASP
2	ee	153	LEU
2	ee	157	ILE
2	ee	170	LEU
2	ee	211	GLU
1	F	6	GLU
1	F	10	VAL
1	F	28	GLU
1	F	30	LYS
1	F	33	PRO
1	F	35	GLU
1	F	39	THR
1	F	57	LEU
2	ff	65	ASN
2	ff	70	LYS
2	ff	73	GLU
2	ff	98	LYS
2	ff	100	ILE
2	ff	105	SER
2	ff	107	ILE
2	ff	109	LEU
2	ff	145	LYS

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Mol	Chain	Res	Type
2	ff	154	VAL
2	ff	157	ILE
2	ff	162	LEU
2	ff	182	VAL
2	ff	189	HIS
2	ff	206	LYS
2	ff	211	GLU
1	G	28	GLU
1	G	53	SER
2	gg	66	ARG
2	gg	74	ASP
2	gg	92	THR
2	gg	104	ARG
2	gg	109	LEU
2	gg	143	THR
2	gg	152	LEU
2	gg	154	VAL
2	gg	157	ILE
2	gg	195	ILE
2	gg	207	VAL
2	gg	227	SER
1	H	12	VAL
1	H	15	GLU
1	H	46	GLU
1	H	53	SER
1	H	56	ILE
2	hh	73	GLU
2	hh	75	ILE
2	hh	100	ILE
2	hh	108	SER
2	hh	109	LEU
2	hh	110	GLU
2	hh	123	MET
2	hh	147	HIS
2	hh	150	ASP
2	hh	176	THR
2	hh	202	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN

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Mol	Chain	Res	Type
2	aa	116	GLN
2	aa	128	ASN
2	aa	156	ASN
2	aa	158	ASN
1	B	38	GLN
2	bb	65	ASN
2	bb	193	HIS
2	bb	205	ASN
1	C	19	ASN
2	cc	116	GLN
2	cc	121	ASN
2	cc	124	ASN
2	cc	158	ASN
2	cc	212	HIS
1	D	19	ASN
1	D	38	GLN
2	dd	81	GLN
2	dd	124	ASN
2	dd	133	GLN
1	E	19	ASN
2	ee	147	HIS
2	ee	156	ASN
1	F	13	HIS
2	ff	81	GLN
2	ff	116	GLN
2	ff	158	ASN
2	ff	205	ASN
2	ff	212	HIS
1	G	13	HIS
2	gg	223	GLN
1	H	13	HIS
2	hh	156	ASN
2	hh	158	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

16 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	$\# Z > 2$
2	RC7	gg	64	2	26,26,27	3.39	7 (26%)	33,35,37	3.32	13 (39%)
1	NLW	D	61	1	7,8,8	0.66	0	7,10,10	1.33	1 (14%)
1	NLW	E	61	1	7,8,8	1.03	1 (14%)	7,10,10	1.29	1 (14%)
2	RC7	bb	64	2	26,26,27	1.99	8 (30%)	33,35,37	2.44	12 (36%)
1	NLW	F	61	1	7,8,8	0.40	0	7,10,10	1.03	1 (14%)
2	RC7	hh	64	2	26,26,27	3.25	8 (30%)	33,35,37	2.45	8 (24%)
2	RC7	ff	64	2	26,26,27	3.34	9 (34%)	33,35,37	3.07	18 (54%)
1	NLW	B	61	1	7,8,8	0.45	0	7,10,10	1.22	1 (14%)
1	NLW	C	61	1	7,8,8	0.82	0	7,10,10	1.09	0
1	NLW	G	61	1	7,8,8	0.35	0	7,10,10	1.17	1 (14%)
2	RC7	ee	64	2	26,26,27	2.96	6 (23%)	33,35,37	2.98	12 (36%)
1	NLW	H	61	1	7,8,8	0.24	0	7,10,10	1.28	1 (14%)
2	RC7	aa	64	2	26,26,27	3.17	13 (50%)	33,35,37	2.21	9 (27%)
1	NLW	A	61	1	7,8,8	0.44	0	7,10,10	0.98	1 (14%)
2	RC7	dd	64	2	26,26,27	1.95	9 (34%)	33,35,37	2.35	8 (24%)
2	RC7	cc	64	2	26,26,27	1.69	5 (19%)	33,35,37	2.34	11 (33%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	RC7	gg	64	2	-	0/11/28/29	0/3/3/3
1	NLW	D	61	1	-	2/8/8/8	-
1	NLW	E	61	1	-	6/8/8/8	-
2	RC7	bb	64	2	-	2/11/28/29	0/3/3/3
1	NLW	F	61	1	-	0/8/8/8	-
2	RC7	hh	64	2	-	0/11/28/29	0/3/3/3
2	RC7	ff	64	2	-	0/11/28/29	0/3/3/3
1	NLW	B	61	1	-	1/8/8/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	NLW	C	61	1	-	4/8/8/8	-
1	NLW	G	61	1	-	2/8/8/8	-
2	RC7	ee	64	2	-	1/11/28/29	0/3/3/3
1	NLW	H	61	1	-	3/8/8/8	-
2	RC7	aa	64	2	-	1/11/28/29	0/3/3/3
1	NLW	A	61	1	-	3/8/8/8	-
2	RC7	dd	64	2	-	1/11/28/29	0/3/3/3
2	RC7	cc	64	2	-	0/11/28/29	0/3/3/3

All (66) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	hh	64	RC7	CA1-C1	-14.75	1.26	1.45
2	gg	64	RC7	CA1-C1	-13.98	1.27	1.45
2	ff	64	RC7	CA1-C1	-12.70	1.29	1.45
2	ee	64	RC7	CA1-C1	-12.40	1.29	1.45
2	aa	64	RC7	CA1-C1	9.57	1.58	1.45
2	ff	64	RC7	CB1-CG1	6.42	1.65	1.45
2	aa	64	RC7	C1-N2	-5.76	1.24	1.33
2	dd	64	RC7	O2-C2	-5.34	1.12	1.23
2	bb	64	RC7	C1-N2	-5.00	1.25	1.33
2	aa	64	RC7	CD3-CG1	-5.00	1.33	1.37
2	gg	64	RC7	O2-C2	-4.93	1.13	1.23
2	ff	64	RC7	CD3-CG1	-4.43	1.33	1.37
2	aa	64	RC7	O2-C2	-4.36	1.14	1.23
2	cc	64	RC7	CD3-CG1	-4.24	1.33	1.37
2	ee	64	RC7	O2-C2	-4.14	1.14	1.23
2	gg	64	RC7	CD3-CG1	-4.13	1.33	1.37
2	ff	64	RC7	O2-C2	-4.12	1.14	1.23
2	bb	64	RC7	CB2-CA2	-4.05	1.31	1.35
2	aa	64	RC7	CG1-ND1	-3.85	1.32	1.39
2	bb	64	RC7	O2-C2	-3.72	1.15	1.23
2	aa	64	RC7	CB1-CG1	-3.59	1.34	1.45
2	aa	64	RC7	CE3-ND1	-3.53	1.25	1.33
2	gg	64	RC7	CE3-ND1	-3.40	1.25	1.33
2	aa	64	RC7	C1-N3	-3.39	1.33	1.38
2	cc	64	RC7	O2-C2	-3.38	1.16	1.23
2	gg	64	RC7	OH-CZ	-3.30	1.29	1.37
2	ee	64	RC7	C1-N2	-3.10	1.28	1.33
2	ee	64	RC7	CA2-C2	3.05	1.51	1.48
2	dd	64	RC7	CD3-CG1	-3.03	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	aa	64	RC7	CA2-N2	-3.00	1.32	1.38
2	dd	64	RC7	CB1-CG1	2.99	1.54	1.45
2	ff	64	RC7	CE3-ND1	-2.99	1.26	1.33
2	ee	64	RC7	CB2-CA2	2.93	1.38	1.35
2	hh	64	RC7	OH-CZ	-2.90	1.30	1.37
2	aa	64	RC7	CD3-NE1	-2.83	1.29	1.36
2	hh	64	RC7	O2-C2	-2.83	1.17	1.23
2	cc	64	RC7	C1-N2	-2.80	1.29	1.33
2	bb	64	RC7	CA2-N2	-2.76	1.32	1.38
2	dd	64	RC7	CG1-ND1	-2.70	1.34	1.39
2	hh	64	RC7	CD3-CG1	-2.70	1.35	1.37
2	hh	64	RC7	CE3-ND1	-2.67	1.27	1.33
2	bb	64	RC7	OH-CZ	-2.65	1.31	1.37
2	dd	64	RC7	C2-N3	-2.59	1.34	1.40
2	dd	64	RC7	C1-N2	-2.58	1.29	1.33
2	hh	64	RC7	C1-N2	-2.57	1.29	1.33
2	gg	64	RC7	C1-N2	-2.55	1.29	1.33
2	ff	64	RC7	CE2-CZ	-2.51	1.34	1.39
2	ff	64	RC7	OH-CZ	-2.50	1.31	1.37
2	cc	64	RC7	CB2-CA2	-2.48	1.32	1.35
2	ff	64	RC7	CE2-CD2	-2.44	1.34	1.38
2	ee	64	RC7	CE3-ND1	-2.41	1.27	1.33
2	dd	64	RC7	CE3-NE1	-2.27	1.25	1.34
2	hh	64	RC7	CA2-C2	2.19	1.50	1.48
2	gg	64	RC7	CB2-CA2	2.13	1.37	1.35
2	aa	64	RC7	CE3-NE1	-2.11	1.26	1.34
2	bb	64	RC7	CA3-N3	-2.09	1.43	1.47
2	bb	64	RC7	CE1-CD1	-2.09	1.35	1.38
2	dd	64	RC7	CA1-C1	2.09	1.48	1.45
2	cc	64	RC7	C1-N3	2.09	1.41	1.38
1	E	61	NLW	C-NH2	2.08	1.37	1.32
2	dd	64	RC7	CB2-CA2	-2.04	1.33	1.35
2	ff	64	RC7	CG1-ND1	-2.04	1.35	1.39
2	bb	64	RC7	CD3-CG1	-2.04	1.35	1.37
2	aa	64	RC7	C2-N3	-2.03	1.35	1.40
2	aa	64	RC7	CA2-C2	-2.03	1.46	1.48
2	hh	64	RC7	CG1-ND1	-2.00	1.35	1.39

All (98) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	gg	64	RC7	C2-CA2-N2	-11.64	100.61	108.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	ee	64	RC7	C2-CA2-N2	-9.01	102.50	108.95
2	ff	64	RC7	C2-CA2-N2	-8.12	103.13	108.95
2	cc	64	RC7	N3-C1-N2	7.35	116.47	112.87
2	gg	64	RC7	CG2-CB2-CA2	7.25	138.48	129.87
2	bb	64	RC7	N3-C1-N2	6.89	116.25	112.87
2	ee	64	RC7	CG2-CB2-CA2	6.73	137.86	129.87
2	ff	64	RC7	CA2-N2-C1	6.71	111.90	105.57
2	dd	64	RC7	N3-C1-N2	6.67	116.14	112.87
2	hh	64	RC7	C2-CA2-N2	-6.63	104.20	108.95
2	gg	64	RC7	CA2-N2-C1	6.62	111.81	105.57
2	gg	64	RC7	CA2-C2-N3	6.35	108.83	103.50
2	aa	64	RC7	CG2-CB2-CA2	5.89	136.87	129.87
2	bb	64	RC7	O2-C2-CA2	-5.78	127.33	131.02
2	dd	64	RC7	CA1-C1-N3	-5.74	116.64	122.76
2	hh	64	RC7	CA2-N2-C1	5.69	110.94	105.57
2	dd	64	RC7	CD3-CG1-ND1	-5.65	102.88	109.30
2	ee	64	RC7	CA2-C2-N3	5.62	108.22	103.50
2	ee	64	RC7	CA2-N2-C1	5.41	110.67	105.57
2	ff	64	RC7	CG2-CB2-CA2	5.34	136.22	129.87
2	hh	64	RC7	CD3-CG1-ND1	-5.15	103.45	109.30
2	hh	64	RC7	CG2-CB2-CA2	5.05	135.87	129.87
2	bb	64	RC7	CD3-CG1-ND1	-4.67	103.99	109.30
2	aa	64	RC7	CA2-N2-C1	4.48	109.80	105.57
2	ff	64	RC7	CA2-C2-N3	4.45	107.24	103.50
2	bb	64	RC7	CA3-N3-C2	4.33	133.19	123.67
2	ff	64	RC7	CA1-C1-N3	-4.23	118.25	122.76
2	hh	64	RC7	CE3-ND1-CG1	4.18	111.94	104.97
2	cc	64	RC7	CA1-C1-N3	-4.07	118.42	122.76
2	aa	64	RC7	O3-C3-CA3	-4.05	107.25	125.47
2	cc	64	RC7	CD3-CG1-ND1	-3.99	104.76	109.30
2	dd	64	RC7	CE3-ND1-CG1	3.85	111.38	104.97
2	ee	64	RC7	CA1-C1-N3	-3.84	118.66	122.76
2	ee	64	RC7	CD3-CG1-ND1	-3.79	104.98	109.30
2	aa	64	RC7	CA3-N3-C2	3.76	131.93	123.67
2	dd	64	RC7	O3-C3-CA3	-3.73	108.70	125.47
2	ff	64	RC7	CD3-CG1-ND1	-3.72	105.07	109.30
2	ff	64	RC7	CB2-CA2-C2	3.71	126.86	122.36
2	ff	64	RC7	CA1-C1-N2	3.69	129.42	125.03
2	aa	64	RC7	C2-CA2-N2	-3.64	106.34	108.95
2	gg	64	RC7	CB2-CA2-C2	3.60	126.72	122.36
2	ff	64	RC7	CE3-ND1-CG1	3.58	110.93	104.97
2	ee	64	RC7	CB2-CA2-C2	3.56	126.67	122.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	aa	64	RC7	CD3-CG1-ND1	-3.53	105.28	109.30
2	ff	64	RC7	O3-C3-CA3	-3.52	109.63	125.47
2	cc	64	RC7	CE3-ND1-CG1	3.47	110.76	104.97
2	cc	64	RC7	CA2-C2-N3	3.38	106.34	103.50
2	bb	64	RC7	CD2-CG2-CD1	3.33	122.59	117.65
2	ee	64	RC7	CA3-N3-C2	3.28	130.87	123.67
2	cc	64	RC7	C2-N3-C1	-3.23	102.94	110.95
2	cc	64	RC7	O2-C2-CA2	-3.22	128.96	131.02
2	bb	64	RC7	CE2-CD2-CG2	-3.18	117.11	121.22
2	ff	64	RC7	CA1-CB1-CG1	-3.09	115.95	129.21
2	cc	64	RC7	CG2-CB2-CA2	3.02	133.46	129.87
2	ee	64	RC7	CE3-ND1-CG1	3.02	110.00	104.97
2	bb	64	RC7	CE3-ND1-CG1	3.00	109.97	104.97
2	gg	64	RC7	CD2-CE2-CZ	-2.95	116.75	119.88
2	gg	64	RC7	CB2-CA2-N2	2.87	132.65	128.76
1	D	61	NLW	O-C-NH2	-2.79	118.11	123.04
2	ee	64	RC7	C2-N3-C1	-2.78	104.08	110.95
2	aa	64	RC7	CE3-ND1-CG1	2.76	109.58	104.97
2	ee	64	RC7	N3-C1-N2	2.76	114.22	112.87
2	hh	64	RC7	CA1-C1-N3	-2.76	119.82	122.76
2	aa	64	RC7	CE2-CD2-CG2	-2.71	117.72	121.22
2	ff	64	RC7	OH-CZ-CE1	2.70	127.52	120.00
2	dd	64	RC7	CA3-N3-C2	2.69	129.59	123.67
2	cc	64	RC7	O3-C3-CA3	-2.64	113.58	125.47
2	ff	64	RC7	CA3-N3-C2	2.57	129.33	123.67
2	gg	64	RC7	O3-C3-CA3	-2.56	113.95	125.47
1	H	61	NLW	O-C-NH2	-2.56	118.53	123.04
2	ff	64	RC7	O2-C2-CA2	-2.50	129.43	131.02
2	bb	64	RC7	C2-N3-C1	-2.50	104.77	110.95
2	gg	64	RC7	CD3-CG1-ND1	-2.48	106.48	109.30
2	hh	64	RC7	O3-C3-CA3	-2.46	114.38	125.47
2	hh	64	RC7	CB2-CA2-C2	2.45	125.33	122.36
1	G	61	NLW	O-C-NH2	-2.43	118.75	123.04
1	E	61	NLW	O-C-CA	-2.42	116.65	120.25
2	ff	64	RC7	OH-CZ-CE2	-2.42	113.27	120.00
2	gg	64	RC7	CE3-ND1-CG1	2.41	108.98	104.97
1	A	61	NLW	O-C-NH2	-2.39	118.82	123.04
2	ff	64	RC7	N3-C1-N2	-2.35	111.72	112.87
2	bb	64	RC7	O2-C2-N3	2.34	129.19	124.31
1	F	61	NLW	O-C-NH2	-2.33	118.93	123.04
2	bb	64	RC7	O3-C3-CA3	-2.33	114.99	125.47
2	aa	64	RC7	CB2-CA2-C2	2.31	125.16	122.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	cc	64	RC7	CB2-CA2-N2	2.30	131.89	128.76
2	ff	64	RC7	CD2-CE2-CZ	2.28	122.30	119.88
2	gg	64	RC7	CA1-C1-N3	-2.26	120.35	122.76
2	dd	64	RC7	C2-N3-C1	-2.25	105.39	110.95
2	bb	64	RC7	CD1-CE1-CZ	-2.20	117.55	119.88
2	gg	64	RC7	CD3-CG1-CB1	-2.19	123.24	129.18
2	ff	64	RC7	C2-N3-C1	-2.18	105.55	110.95
2	gg	64	RC7	O2-C2-N3	-2.16	119.82	124.31
1	B	61	NLW	O-C-NH2	-2.13	119.28	123.04
2	bb	64	RC7	CA1-C1-N3	-2.12	120.50	122.76
2	dd	64	RC7	CD2-CG2-CD1	2.11	120.78	117.65
2	cc	64	RC7	C2-CA2-N2	-2.09	107.45	108.95
2	ee	64	RC7	O3-C3-CA3	-2.04	116.31	125.47

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	61	NLW	NH2-C-CA-N
1	C	61	NLW	NH2-C-CA-N
2	dd	64	RC7	C3-CA3-N3-C2
1	A	61	NLW	NH2-C-CA-CB
1	D	61	NLW	O-C-CA-N
1	G	61	NLW	O-C-CA-N
2	aa	64	RC7	C3-CA3-N3-C2
2	bb	64	RC7	C3-CA3-N3-C2
1	D	61	NLW	O-C-CA-CB
1	G	61	NLW	O-C-CA-CB
1	E	61	NLW	CA-CB-CG-CD1
1	E	61	NLW	C-CA-CB-CG
2	ee	64	RC7	C3-CA3-N3-C2
1	E	61	NLW	O-C-CA-N
1	H	61	NLW	O-C-CA-N
1	E	61	NLW	CA-CB-CG-CD2
2	bb	64	RC7	C3-CA3-N3-C1
1	E	61	NLW	O-C-CA-CB
1	H	61	NLW	O-C-CA-CB
1	B	61	NLW	O-C-CA-N
1	C	61	NLW	N-CA-CB-CG
1	E	61	NLW	N-CA-CB-CG
1	C	61	NLW	C-CA-CB-CG
1	H	61	NLW	C-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
1	A	61	NLW	O-C-CA-N
1	C	61	NLW	O-C-CA-N

There are no ring outliers.

12 monomers are involved in 56 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	gg	64	RC7	13	0
1	D	61	NLW	1	0
1	E	61	NLW	1	0
2	bb	64	RC7	10	0
2	hh	64	RC7	4	0
2	ff	64	RC7	3	0
1	C	61	NLW	1	0
1	G	61	NLW	1	0
2	ee	64	RC7	8	0
2	aa	64	RC7	6	0
2	dd	64	RC7	5	0
2	cc	64	RC7	6	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 11 are monoatomic - leaving 3 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	$\# Z > 2$
3	GOL	dd	301	-	5,5,5	0.64	0	5,5,5	0.40	0
3	GOL	G	301	-	5,5,5	0.48	0	5,5,5	0.77	0
3	GOL	E	301	-	5,5,5	0.36	0	5,5,5	0.83	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
3	GOL	dd	301	-	-	4/4/4/4	-
3	GOL	G	301	-	-	4/4/4/4	-
3	GOL	E	301	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	dd	301	GOL	O1-C1-C2-C3
3	E	301	GOL	O1-C1-C2-O2
3	E	301	GOL	O1-C1-C2-C3
3	G	301	GOL	O1-C1-C2-C3
3	dd	301	GOL	O1-C1-C2-O2
3	G	301	GOL	O2-C2-C3-O3
3	dd	301	GOL	C1-C2-C3-O3
3	G	301	GOL	C1-C2-C3-O3
3	G	301	GOL	O1-C1-C2-O2
3	dd	301	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	301	GOL	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	hh	2
2	bb	2
2	dd	2
2	cc	2
2	gg	1
2	ee	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	hh	64:RC7	C3	65:ASN	N	1.87
1	gg	64:RC7	C3	65:ASN	N	1.77
1	bb	64:RC7	C3	65:ASN	N	1.68
1	ee	64:RC7	C3	65:ASN	N	1.68
1	dd	64:RC7	C3	65:ASN	N	1.10
1	cc	66:ARG	C	67:VAL	N	1.08
1	dd	65:ASN	C	66:ARG	N	1.08
1	bb	66:ARG	C	67:VAL	N	1.07
1	hh	65:ASN	C	66:ARG	N	1.07
1	cc	65:ASN	C	66:ARG	N	1.06

6 Fit of model and data [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	59/62 (95%)	-1.19	0 100 100	10, 27, 37, 49	1 (1%)
1	B	59/62 (95%)	-1.19	0 100 100	9, 24, 44, 46	0
1	C	58/62 (93%)	-1.20	0 100 100	11, 28, 40, 47	1 (1%)
1	D	58/62 (93%)	-1.18	0 100 100	16, 26, 41, 44	0
1	E	58/62 (93%)	-1.11	0 100 100	12, 26, 37, 40	2 (3%)
1	F	58/62 (93%)	-1.08	0 100 100	14, 26, 48, 53	1 (1%)
1	G	58/62 (93%)	-1.14	0 100 100	16, 27, 40, 44	3 (5%)
1	H	58/62 (93%)	-1.06	0 100 100	8, 29, 50, 53	3 (5%)
2	aa	164/170 (96%)	-1.18	0 100 100	8, 24, 43, 60	2 (1%)
2	bb	166/170 (97%)	-1.20	0 100 100	8, 26, 41, 57	2 (1%)
2	cc	165/170 (97%)	-1.18	0 100 100	10, 25, 40, 48	3 (1%)
2	dd	165/170 (97%)	-1.15	0 100 100	10, 26, 42, 71	4 (2%)
2	ee	161/170 (94%)	-1.12	0 100 100	10, 26, 42, 65	4 (2%)
2	ff	161/170 (94%)	-1.02	0 100 100	13, 29, 52, 96	4 (2%)
2	gg	165/170 (97%)	-1.03	0 100 100	16, 30, 48, 73	2 (1%)
2	hh	161/170 (94%)	-1.05	0 100 100	13, 30, 46, 75	2 (1%)
All	All	1774/1856 (95%)	-1.12	0 100 100	8, 27, 45, 96	34 (1%)

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [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. 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	B-factors($\text{\AA}^2$)	Q<0.9
1	NLW	B	61	9/9	0.97	0.06	16,19,20,21	0
1	NLW	F	61	9/9	0.97	0.06	21,22,24,24	0
2	RC7	bb	64	24/25	0.98	0.04	12,17,19,21	0
1	NLW	C	61	9/9	0.98	0.05	13,15,17,20	0
2	RC7	cc	64	24/25	0.98	0.04	15,18,21,24	0
1	NLW	D	61	9/9	0.98	0.05	18,18,19,21	0
2	RC7	dd	64	24/25	0.98	0.04	18,21,24,28	0
2	RC7	ee	64	24/25	0.98	0.04	14,18,20,25	0
1	NLW	A	61	9/9	0.98	0.06	18,19,20,22	0
1	NLW	G	61	9/9	0.98	0.06	21,22,26,33	0
2	RC7	gg	64	24/25	0.98	0.04	21,26,33,37	0
2	RC7	hh	64	24/25	0.98	0.04	16,23,25,27	0
2	RC7	aa	64	24/25	0.99	0.03	13,15,17,18	0
1	NLW	E	61	9/9	0.99	0.05	17,21,27,29	0
1	NLW	H	61	9/9	0.99	0.05	17,18,20,24	0
2	RC7	ff	64	24/25	0.99	0.04	17,21,24,29	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	E	301	6/6	0.97	0.06	20,21,22,24	0
3	GOL	dd	301	6/6	0.98	0.05	18,19,20,20	0
3	GOL	G	301	6/6	0.98	0.04	21,26,26,26	0
4	MG	hh	303	1/1	0.98	0.03	25,25,25,25	0
4	MG	E	303	1/1	0.99	0.02	28,28,28,28	0
4	MG	F	101	1/1	0.99	0.03	19,19,19,19	0
4	MG	ff	301	1/1	0.99	0.03	19,19,19,19	0
4	MG	G	302	1/1	0.99	0.02	21,21,21,21	0
4	MG	H	301	1/1	0.99	0.02	20,20,20,20	0
4	MG	H	302	1/1	0.99	0.02	19,19,19,19	0
4	MG	hh	301	1/1	0.99	0.02	19,19,19,19	0
4	MG	hh	302	1/1	0.99	0.02	18,18,18,18	0
4	MG	E	302	1/1	0.99	0.02	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MG	gg	301	1/1	1.00	0.04	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.