Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 09:51 PM GMT

PDB ID	:	4V96
Title	:	The structure of a 1.8 MDa viral genome injection device suggests alternative infection mechanisms
Authors	:	Veesler, D.; Spinelli, S.; Mahony, J.; Lichiere, J.; Blangy, S.; Bricogne, G.; Legrand, P.; Ortiz-Lombardia, M.; Campanacci, V.; van Sinderen, D.; Cambillau, C.
Deposited on	:	2012-02-01
Resolution	:	3.80 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

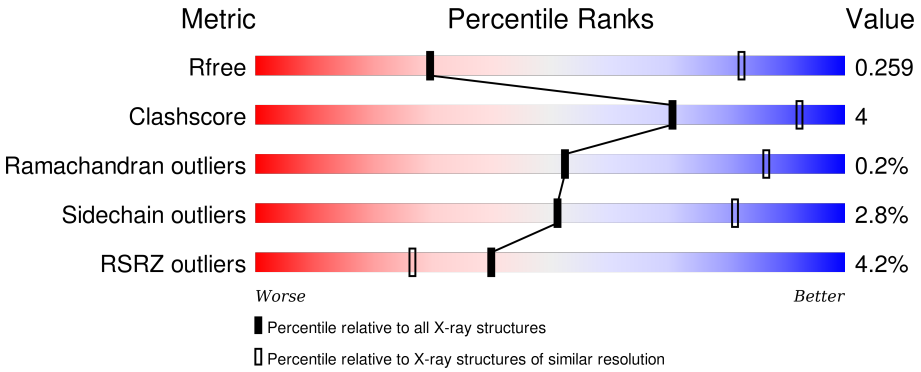
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.80 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	1317 (4.10-3.50)
Clashscore	102246	1458 (4.10-3.50)
Ramachandran outliers	100387	1397 (4.10-3.50)
Sidechain outliers	100360	1392 (4.10-3.50)
RSRZ outliers	91569	1325 (4.10-3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	AA	299	76% 21% •
1	AB	299	3% 81% 16% • •
1	AC	299	79% 20% •
1	AD	299	84% 14% •
1	AE	299	2% 85% 12% • •

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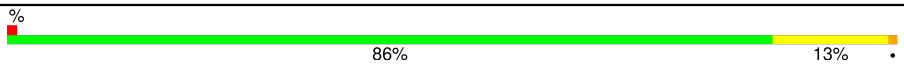
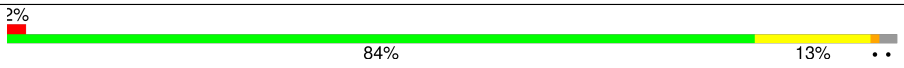
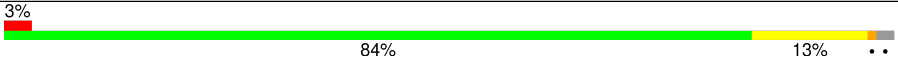
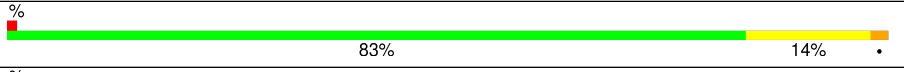
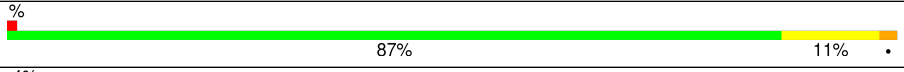
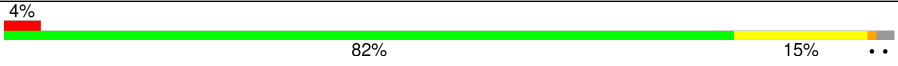
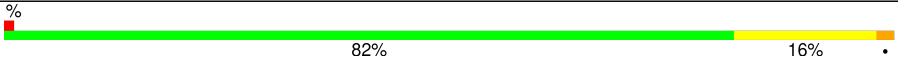
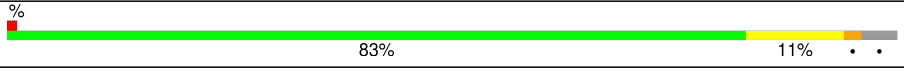
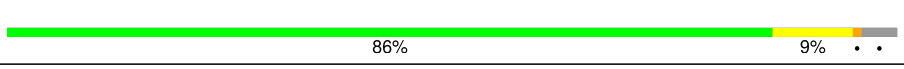
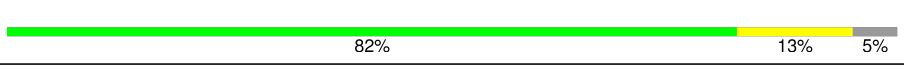
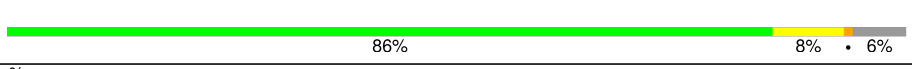
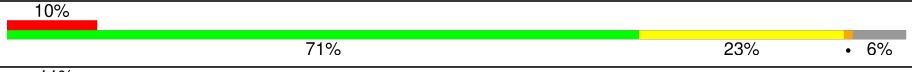
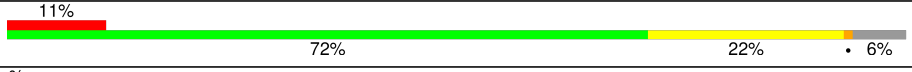
Mol	Chain	Length	Quality of chain
1	AF	299	
1	AG	299	
1	AH	299	
1	AI	299	
1	AJ	299	
1	AK	299	
1	AL	299	
1	AM	299	
1	AN	299	
1	AO	299	
1	AP	299	
1	AQ	299	
1	AR	299	
2	AS	253	
2	AT	253	
2	AU	253	
2	AV	253	
2	AW	253	
2	AX	253	
3	B1	173	
3	B2	173	
3	BA	173	
3	BB	173	
3	BC	173	
3	BD	173	

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Mol	Chain	Length	Quality of chain
3	BE	173	79% 15% • 5%
3	BF	173	3% 80% 14% 6%
3	BG	173	3% 79% 16% 5%
3	BH	173	2% 81% 13% • 5%
3	BI	173	3% 79% 16% 6%
3	BJ	173	% 79% 16% 5%
3	BK	173	2% 82% 12% • 6%
3	BL	173	2% 82% 13% 6%
3	BM	173	20% 80% 14% 6%
3	BN	173	20% 82% 10% • 6%
3	BO	173	20% 77% 16% 6%
3	BP	173	17% 76% 18% 6%
3	BQ	173	16% 79% 14% • 6%
3	BR	173	18% 81% 13% 6%
3	BS	173	% 78% 16% 6%
3	BT	173	% 82% 12% • 5%
3	BU	173	5% 82% 13% • 5%
3	BV	173	% 78% 16% • 6%
3	BW	173	% 81% 13% • 5%
3	BX	173	% 78% 15% • 6%
3	BY	173	79% 16% 6%
3	BZ	173	% 81% 13% • 6%
3	Ba	173	93% • 6%
3	Bb	173	2% 93% • 6%
3	Bc	173	% 94% • 5%

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Mol	Chain	Length	Quality of chain
3	Bd	173	2% 94% 5%
3	Be	173	13% 93% 6%
3	Bf	173	12% 94% 5%
3	Bg	173	7% 94% 6%
3	Bh	173	22% 92% 7%
3	Bi	173	12% 93% 6%
3	Bj	173	19% 92% 6%
3	Bk	173	3% 93% 6%
3	Bl	173	% 94% 6%
3	Bm	173	93% 6%
3	Bn	173	5% 92% 6%
3	Bo	173	9% 93% 6%
3	Bp	173	7% 94% 5%
3	Bq	173	2% 93% 6%
3	Br	173	% 94% 6%
3	Bs	173	% 94% 6%
3	Bt	173	5% 92% 6%
3	Bu	173	16% 93% 6%
3	Bv	173	9% 94% 5%
3	Bw	173	6% 93% 6%
3	Bx	173	12% 93% 6%
3	By	173	17% 92% 6%
3	Bz	173	2% 92% 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 118740 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 ORF48.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	299	Total	C	N	O	S	0	0	0
			2389	1537	386	460	6			
1	AB	294	Total	C	N	O	S	0	0	0
			2345	1511	379	449	6			
1	AC	299	Total	C	N	O	S	0	0	0
			2389	1538	387	458	6			
1	AD	299	Total	C	N	O	S	0	0	0
			2393	1540	387	460	6			
1	AE	291	Total	C	N	O	S	0	0	0
			2336	1509	376	445	6			
1	AF	299	Total	C	N	O	S	0	0	0
			2389	1537	386	460	6			
1	AG	299	Total	C	N	O	S	0	0	0
			2386	1537	387	456	6			
1	AH	294	Total	C	N	O	S	0	0	0
			2343	1508	379	450	6			
1	AI	299	Total	C	N	O	S	0	0	0
			2389	1537	386	460	6			
1	AJ	299	Total	C	N	O	S	0	0	0
			2393	1540	387	460	6			
1	AK	293	Total	C	N	O	S	0	0	0
			2320	1495	373	446	6			
1	AL	298	Total	C	N	O	S	0	0	0
			2382	1535	385	456	6			
1	AM	299	Total	C	N	O	S	0	0	0
			2389	1537	386	460	6			
1	AN	294	Total	C	N	O	S	0	0	0
			2328	1498	377	447	6			
1	AO	299	Total	C	N	O	S	0	0	0
			2393	1540	387	460	6			
1	AP	299	Total	C	N	O	S	0	0	0
			2382	1534	386	456	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AQ	295	Total	C	N	O	S	0	0	0
			2347	1514	377	451	5			
1	AR	299	Total	C	N	O	S	0	0	0
			2390	1537	387	460	6			

- Molecule 2 is a protein called ORF46.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AS	242	Total	C	N	O	S	0	0	0
			1932	1237	313	378	4			
2	AT	242	Total	C	N	O	S	0	0	0
			1931	1238	315	374	4			
2	AU	242	Total	C	N	O	S	0	0	0
			1924	1236	315	369	4			
2	AV	241	Total	C	N	O	S	0	0	0
			1899	1215	311	369	4			
2	AW	241	Total	C	N	O	S	0	0	0
			1917	1228	312	373	4			
2	AX	241	Total	C	N	O	S	0	0	0
			1913	1224	313	372	4			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS	1	GLY	-	EXPRESSION TAG	UNP Q9AZ58
AT	1	GLY	-	EXPRESSION TAG	UNP Q9AZ58
AU	1	GLY	-	EXPRESSION TAG	UNP Q9AZ58
AV	1	GLY	-	EXPRESSION TAG	UNP Q9AZ58
AW	1	GLY	-	EXPRESSION TAG	UNP Q9AZ58
AX	1	GLY	-	EXPRESSION TAG	UNP Q9AZ58

- Molecule 3 is a protein called BPP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	BA	164	Total	C	N	O	S	0	0	0
			1199	743	210	241	5			
3	BB	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	BC	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	BD	164	Total	C	N	O	S	0	0	0
			1199	743	210	241	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	BE	164	Total	C	N	O	S	0	0	0
			1199	743	210	241	5			
3	BF	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	BG	164	Total	C	N	O	S	0	0	0
			1199	743	210	241	5			
3	BH	164	Total	C	N	O	S	0	0	0
			1205	746	213	241	5			
3	BI	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	BJ	164	Total	C	N	O	S	0	0	0
			1199	743	210	241	5			
3	BK	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	BL	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	BM	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	BN	162	Total	C	N	O	S	0	0	0
			1188	737	208	238	5			
3	BO	162	Total	C	N	O	S	0	0	0
			1188	737	208	238	5			
3	BP	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	BQ	162	Total	C	N	O	S	0	0	0
			1194	740	211	238	5			
3	BR	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	BS	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	BT	164	Total	C	N	O	S	0	0	0
			1199	743	210	241	5			
3	BU	164	Total	C	N	O	S	0	0	0
			1199	743	210	241	5			
3	BV	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	BW	164	Total	C	N	O	S	0	0	0
			1199	743	210	241	5			
3	BX	162	Total	C	N	O	S	0	0	0
			1188	737	208	238	5			
3	BY	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	BZ	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	Ba	162	Total	C	N	O	S	0	0	0
			1194	740	211	238	5			
3	Bb	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	Bc	164	Total	C	N	O	S	0	0	0
			1198	743	210	240	5			
3	Bd	165	Total	C	N	O	S	0	0	0
			1209	749	214	241	5			
3	Be	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	Bf	164	Total	C	N	O	S	0	0	0
			1199	743	210	241	5			
3	Bg	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	Bh	161	Total	C	N	O	S	0	0	0
			1186	736	210	235	5			
3	Bi	162	Total	C	N	O	S	0	0	0
			1188	737	208	238	5			
3	Bj	162	Total	C	N	O	S	0	0	0
			1194	740	211	238	5			
3	Bk	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	Bl	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	Bm	162	Total	C	N	O	S	0	0	0
			1188	737	208	238	5			
3	Bn	162	Total	C	N	O	S	0	0	0
			1194	740	211	238	5			
3	Bo	162	Total	C	N	O	S	0	0	0
			1194	740	211	238	5			
3	Bp	164	Total	C	N	O	S	0	0	0
			1205	746	213	241	5			
3	Bq	163	Total	C	N	O	S	0	0	0
			1200	743	212	240	5			
3	Br	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	Bs	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	Bt	162	Total	C	N	O	S	0	0	0
			1188	737	208	238	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	Bu	162	Total	C	N	O	S	0	0	0
			1194	740	211	238	5			
3	Bv	164	Total	C	N	O	S	0	0	0
			1199	743	210	241	5			
3	Bw	163	Total	C	N	O	S	0	0	0
			1194	740	209	240	5			
3	Bx	162	Total	C	N	O	S	0	0	0
			1194	740	211	238	5			
3	By	162	Total	C	N	O	S	0	0	0
			1194	740	211	238	5			
3	Bz	163	Total	C	N	O	S	0	0	0
			1200	743	212	240	5			
3	B1	163	Total	C	N	O	S	0	0	0
			1200	743	212	240	5			
3	B2	162	Total	C	N	O	S	0	0	0
			1194	740	211	238	5			

There are 540 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BA	164	SER	-	EXPRESSION TAG	UNP Q9G096
BA	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BA	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BA	167	SER	-	EXPRESSION TAG	UNP Q9G096
BA	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BA	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BA	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BA	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BA	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BA	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BB	164	SER	-	EXPRESSION TAG	UNP Q9G096
BB	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BB	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BB	167	SER	-	EXPRESSION TAG	UNP Q9G096
BB	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BB	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BB	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BB	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BB	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BB	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BC	164	SER	-	EXPRESSION TAG	UNP Q9G096
BC	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BC	166	TRP	-	EXPRESSION TAG	UNP Q9G096

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Chain	Residue	Modelled	Actual	Comment	Reference
BC	167	SER	-	EXPRESSION TAG	UNP Q9G096
BC	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BC	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BC	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BC	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BC	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BC	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BD	164	SER	-	EXPRESSION TAG	UNP Q9G096
BD	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BD	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BD	167	SER	-	EXPRESSION TAG	UNP Q9G096
BD	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BD	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BD	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BD	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BD	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BD	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BE	164	SER	-	EXPRESSION TAG	UNP Q9G096
BE	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BE	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BE	167	SER	-	EXPRESSION TAG	UNP Q9G096
BE	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BE	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BE	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BE	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BE	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BE	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BF	164	SER	-	EXPRESSION TAG	UNP Q9G096
BF	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BF	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BF	167	SER	-	EXPRESSION TAG	UNP Q9G096
BF	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BF	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BF	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BF	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BF	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BF	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BG	164	SER	-	EXPRESSION TAG	UNP Q9G096
BG	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BG	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BG	167	SER	-	EXPRESSION TAG	UNP Q9G096
BG	168	HIS	-	EXPRESSION TAG	UNP Q9G096

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Chain	Residue	Modelled	Actual	Comment	Reference
BG	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BG	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BG	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BG	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BG	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BH	164	SER	-	EXPRESSION TAG	UNP Q9G096
BH	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BH	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BH	167	SER	-	EXPRESSION TAG	UNP Q9G096
BH	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BH	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BH	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BH	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BH	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BH	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BI	164	SER	-	EXPRESSION TAG	UNP Q9G096
BI	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BI	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BI	167	SER	-	EXPRESSION TAG	UNP Q9G096
BI	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BI	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BI	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BI	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BI	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BI	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BJ	164	SER	-	EXPRESSION TAG	UNP Q9G096
BJ	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BJ	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BJ	167	SER	-	EXPRESSION TAG	UNP Q9G096
BJ	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BJ	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BJ	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BJ	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BJ	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BJ	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BK	164	SER	-	EXPRESSION TAG	UNP Q9G096
BK	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BK	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BK	167	SER	-	EXPRESSION TAG	UNP Q9G096
BK	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BK	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BK	170	GLN	-	EXPRESSION TAG	UNP Q9G096

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Chain	Residue	Modelled	Actual	Comment	Reference
BK	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BK	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BK	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BL	164	SER	-	EXPRESSION TAG	UNP Q9G096
BL	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BL	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BL	167	SER	-	EXPRESSION TAG	UNP Q9G096
BL	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BL	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BL	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BL	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BL	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BL	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BM	164	SER	-	EXPRESSION TAG	UNP Q9G096
BM	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BM	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BM	167	SER	-	EXPRESSION TAG	UNP Q9G096
BM	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BM	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BM	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BM	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BM	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BM	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BN	164	SER	-	EXPRESSION TAG	UNP Q9G096
BN	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BN	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BN	167	SER	-	EXPRESSION TAG	UNP Q9G096
BN	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BN	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BN	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BN	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BN	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BN	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BO	164	SER	-	EXPRESSION TAG	UNP Q9G096
BO	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BO	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BO	167	SER	-	EXPRESSION TAG	UNP Q9G096
BO	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BO	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BO	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BO	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BO	172	GLU	-	EXPRESSION TAG	UNP Q9G096

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Chain	Residue	Modelled	Actual	Comment	Reference
BO	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BP	164	SER	-	EXPRESSION TAG	UNP Q9G096
BP	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BP	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BP	167	SER	-	EXPRESSION TAG	UNP Q9G096
BP	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BP	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BP	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BP	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BP	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BP	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BQ	164	SER	-	EXPRESSION TAG	UNP Q9G096
BQ	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BQ	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BQ	167	SER	-	EXPRESSION TAG	UNP Q9G096
BQ	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BQ	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BQ	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BQ	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BQ	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BQ	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BR	164	SER	-	EXPRESSION TAG	UNP Q9G096
BR	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BR	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BR	167	SER	-	EXPRESSION TAG	UNP Q9G096
BR	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BR	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BR	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BR	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BR	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BR	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BS	164	SER	-	EXPRESSION TAG	UNP Q9G096
BS	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BS	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BS	167	SER	-	EXPRESSION TAG	UNP Q9G096
BS	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BS	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BS	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BS	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BS	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BS	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BT	164	SER	-	EXPRESSION TAG	UNP Q9G096

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Chain	Residue	Modelled	Actual	Comment	Reference
BT	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BT	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BT	167	SER	-	EXPRESSION TAG	UNP Q9G096
BT	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BT	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BT	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BT	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BT	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BT	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BU	164	SER	-	EXPRESSION TAG	UNP Q9G096
BU	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BU	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BU	167	SER	-	EXPRESSION TAG	UNP Q9G096
BU	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BU	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BU	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BU	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BU	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BU	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BV	164	SER	-	EXPRESSION TAG	UNP Q9G096
BV	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BV	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BV	167	SER	-	EXPRESSION TAG	UNP Q9G096
BV	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BV	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BV	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BV	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BV	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BV	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BW	164	SER	-	EXPRESSION TAG	UNP Q9G096
BW	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BW	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BW	167	SER	-	EXPRESSION TAG	UNP Q9G096
BW	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BW	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BW	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BW	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BW	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BW	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BX	164	SER	-	EXPRESSION TAG	UNP Q9G096
BX	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BX	166	TRP	-	EXPRESSION TAG	UNP Q9G096

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Chain	Residue	Modelled	Actual	Comment	Reference
BX	167	SER	-	EXPRESSION TAG	UNP Q9G096
BX	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BX	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BX	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BX	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BX	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BX	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BY	164	SER	-	EXPRESSION TAG	UNP Q9G096
BY	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BY	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BY	167	SER	-	EXPRESSION TAG	UNP Q9G096
BY	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BY	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BY	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BY	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BY	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BY	173	LYS	-	EXPRESSION TAG	UNP Q9G096
BZ	164	SER	-	EXPRESSION TAG	UNP Q9G096
BZ	165	ALA	-	EXPRESSION TAG	UNP Q9G096
BZ	166	TRP	-	EXPRESSION TAG	UNP Q9G096
BZ	167	SER	-	EXPRESSION TAG	UNP Q9G096
BZ	168	HIS	-	EXPRESSION TAG	UNP Q9G096
BZ	169	PRO	-	EXPRESSION TAG	UNP Q9G096
BZ	170	GLN	-	EXPRESSION TAG	UNP Q9G096
BZ	171	PHE	-	EXPRESSION TAG	UNP Q9G096
BZ	172	GLU	-	EXPRESSION TAG	UNP Q9G096
BZ	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Ba	164	SER	-	EXPRESSION TAG	UNP Q9G096
Ba	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Ba	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Ba	167	SER	-	EXPRESSION TAG	UNP Q9G096
Ba	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Ba	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Ba	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Ba	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Ba	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Ba	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bb	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bb	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bb	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bb	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bb	168	HIS	-	EXPRESSION TAG	UNP Q9G096

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Chain	Residue	Modelled	Actual	Comment	Reference
Bb	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bb	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bb	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bb	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bb	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bc	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bc	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bc	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bc	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bc	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bc	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bc	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bc	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bc	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bc	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bd	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bd	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bd	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bd	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bd	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bd	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bd	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bd	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bd	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bd	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Be	164	SER	-	EXPRESSION TAG	UNP Q9G096
Be	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Be	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Be	167	SER	-	EXPRESSION TAG	UNP Q9G096
Be	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Be	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Be	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Be	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Be	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Be	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bf	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bf	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bf	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bf	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bf	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bf	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bf	170	GLN	-	EXPRESSION TAG	UNP Q9G096

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Chain	Residue	Modelled	Actual	Comment	Reference
Bf	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bf	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bf	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bg	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bg	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bg	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bg	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bg	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bg	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bg	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bg	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bg	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bg	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bh	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bh	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bh	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bh	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bh	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bh	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bh	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bh	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bh	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bh	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bi	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bi	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bi	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bi	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bi	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bi	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bi	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bi	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bi	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bi	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bj	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bj	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bj	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bj	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bj	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bj	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bj	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bj	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bj	172	GLU	-	EXPRESSION TAG	UNP Q9G096

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Chain	Residue	Modelled	Actual	Comment	Reference
Bj	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bk	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bk	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bk	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bk	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bk	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bk	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bk	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bk	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bk	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bk	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bl	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bl	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bl	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bl	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bl	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bl	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bl	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bl	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bl	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bl	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bm	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bm	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bm	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bm	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bm	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bm	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bm	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bm	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bm	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bm	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bn	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bn	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bn	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bn	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bn	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bn	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bn	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bn	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bn	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bn	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bo	164	SER	-	EXPRESSION TAG	UNP Q9G096

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Chain	Residue	Modelled	Actual	Comment	Reference
Bo	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bo	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bo	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bo	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bo	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bo	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bo	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bo	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bo	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bp	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bp	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bp	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bp	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bp	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bp	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bp	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bp	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bp	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bp	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bq	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bq	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bq	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bq	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bq	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bq	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bq	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bq	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bq	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bq	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Br	164	SER	-	EXPRESSION TAG	UNP Q9G096
Br	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Br	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Br	167	SER	-	EXPRESSION TAG	UNP Q9G096
Br	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Br	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Br	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Br	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Br	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Br	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bs	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bs	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bs	166	TRP	-	EXPRESSION TAG	UNP Q9G096

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Chain	Residue	Modelled	Actual	Comment	Reference
Bs	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bs	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bs	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bs	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bs	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bs	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bs	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bt	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bt	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bt	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bt	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bt	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bt	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bt	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bt	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bt	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bt	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bu	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bu	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bu	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bu	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bu	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bu	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bu	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bu	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bu	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bu	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bv	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bv	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bv	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bv	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bv	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bv	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bv	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bv	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bv	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bv	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bw	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bw	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bw	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bw	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bw	168	HIS	-	EXPRESSION TAG	UNP Q9G096

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Chain	Residue	Modelled	Actual	Comment	Reference
Bw	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bw	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bw	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bw	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bw	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bx	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bx	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bx	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bx	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bx	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bx	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bx	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bx	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bx	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bx	173	LYS	-	EXPRESSION TAG	UNP Q9G096
By	164	SER	-	EXPRESSION TAG	UNP Q9G096
By	165	ALA	-	EXPRESSION TAG	UNP Q9G096
By	166	TRP	-	EXPRESSION TAG	UNP Q9G096
By	167	SER	-	EXPRESSION TAG	UNP Q9G096
By	168	HIS	-	EXPRESSION TAG	UNP Q9G096
By	169	PRO	-	EXPRESSION TAG	UNP Q9G096
By	170	GLN	-	EXPRESSION TAG	UNP Q9G096
By	171	PHE	-	EXPRESSION TAG	UNP Q9G096
By	172	GLU	-	EXPRESSION TAG	UNP Q9G096
By	173	LYS	-	EXPRESSION TAG	UNP Q9G096
Bz	164	SER	-	EXPRESSION TAG	UNP Q9G096
Bz	165	ALA	-	EXPRESSION TAG	UNP Q9G096
Bz	166	TRP	-	EXPRESSION TAG	UNP Q9G096
Bz	167	SER	-	EXPRESSION TAG	UNP Q9G096
Bz	168	HIS	-	EXPRESSION TAG	UNP Q9G096
Bz	169	PRO	-	EXPRESSION TAG	UNP Q9G096
Bz	170	GLN	-	EXPRESSION TAG	UNP Q9G096
Bz	171	PHE	-	EXPRESSION TAG	UNP Q9G096
Bz	172	GLU	-	EXPRESSION TAG	UNP Q9G096
Bz	173	LYS	-	EXPRESSION TAG	UNP Q9G096
B1	164	SER	-	EXPRESSION TAG	UNP Q9G096
B1	165	ALA	-	EXPRESSION TAG	UNP Q9G096
B1	166	TRP	-	EXPRESSION TAG	UNP Q9G096
B1	167	SER	-	EXPRESSION TAG	UNP Q9G096
B1	168	HIS	-	EXPRESSION TAG	UNP Q9G096
B1	169	PRO	-	EXPRESSION TAG	UNP Q9G096
B1	170	GLN	-	EXPRESSION TAG	UNP Q9G096

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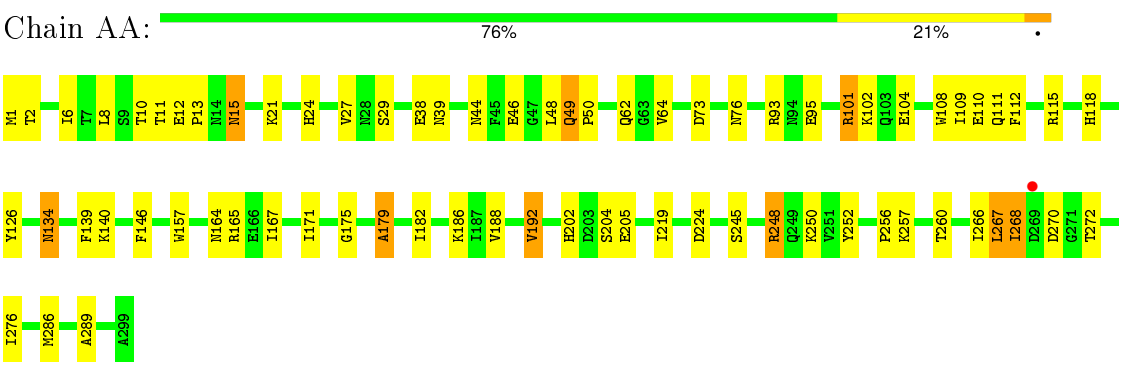
Chain	Residue	Modelled	Actual	Comment	Reference
B1	171	PHE	-	EXPRESSION TAG	UNP Q9G096
B1	172	GLU	-	EXPRESSION TAG	UNP Q9G096
B1	173	LYS	-	EXPRESSION TAG	UNP Q9G096
B2	164	SER	-	EXPRESSION TAG	UNP Q9G096
B2	165	ALA	-	EXPRESSION TAG	UNP Q9G096
B2	166	TRP	-	EXPRESSION TAG	UNP Q9G096
B2	167	SER	-	EXPRESSION TAG	UNP Q9G096
B2	168	HIS	-	EXPRESSION TAG	UNP Q9G096
B2	169	PRO	-	EXPRESSION TAG	UNP Q9G096
B2	170	GLN	-	EXPRESSION TAG	UNP Q9G096
B2	171	PHE	-	EXPRESSION TAG	UNP Q9G096
B2	172	GLU	-	EXPRESSION TAG	UNP Q9G096
B2	173	LYS	-	EXPRESSION TAG	UNP Q9G096

3 Residue-property plots (i)

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.

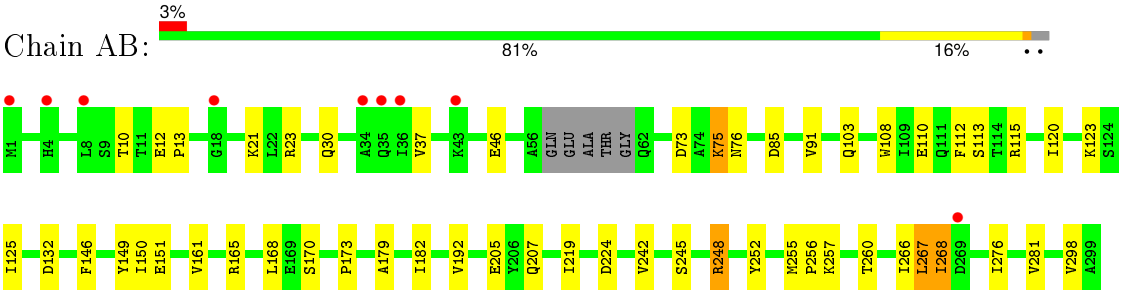
- Molecule 1: ORF48

Chain AA:



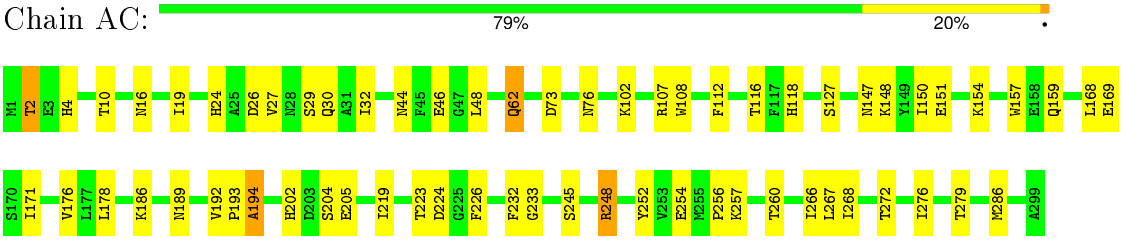
- Molecule 1: ORF48

Chain AB:



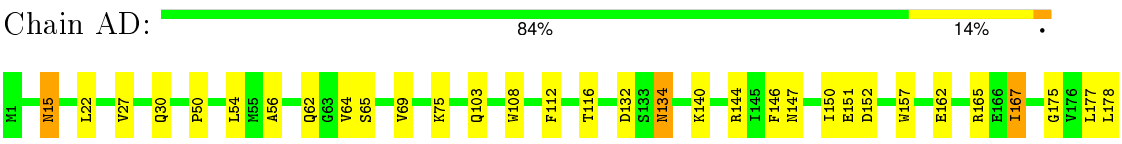
- Molecule 1: ORF48

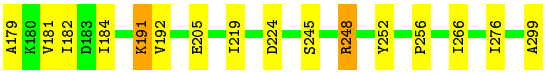
Chain AC:



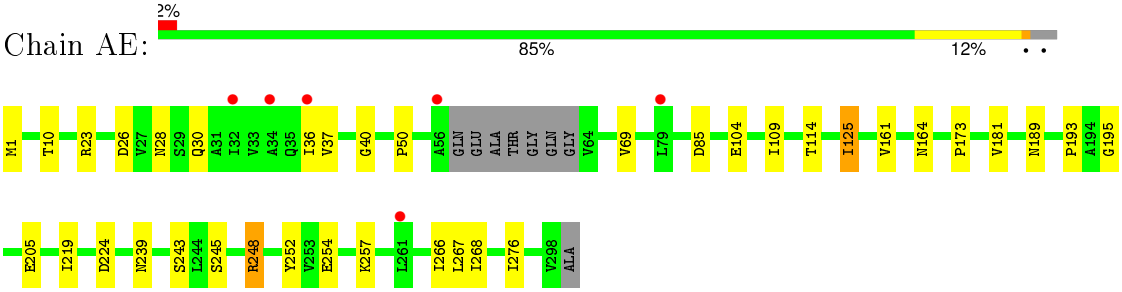
- Molecule 1: ORF48

Chain AD:

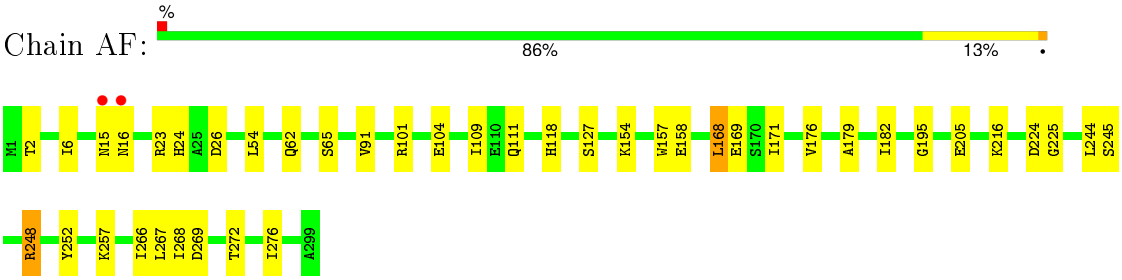




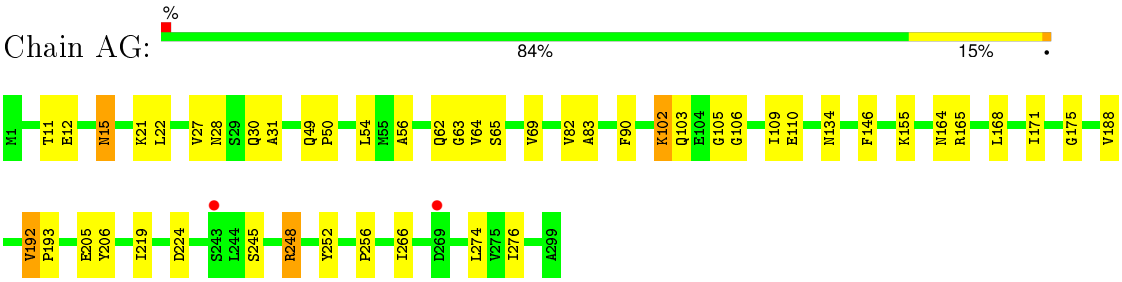
• Molecule 1: ORF48



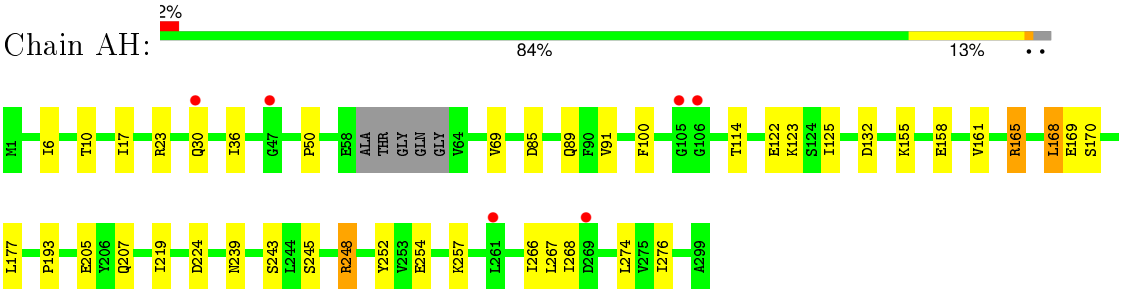
• Molecule 1: ORF48



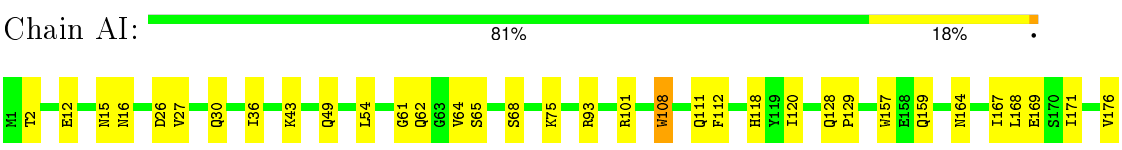
• Molecule 1: ORF48



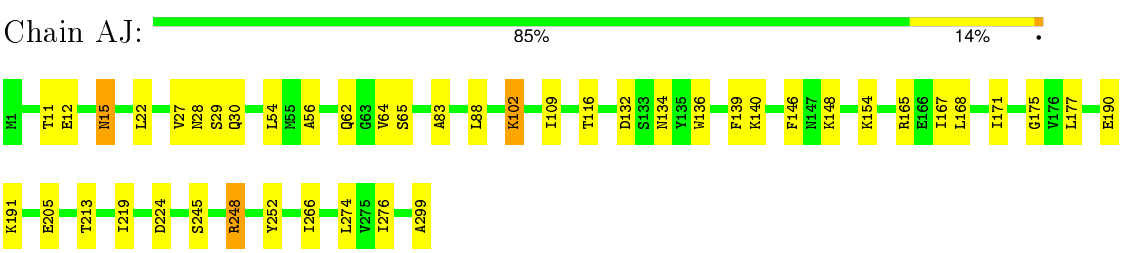
• Molecule 1: ORF48



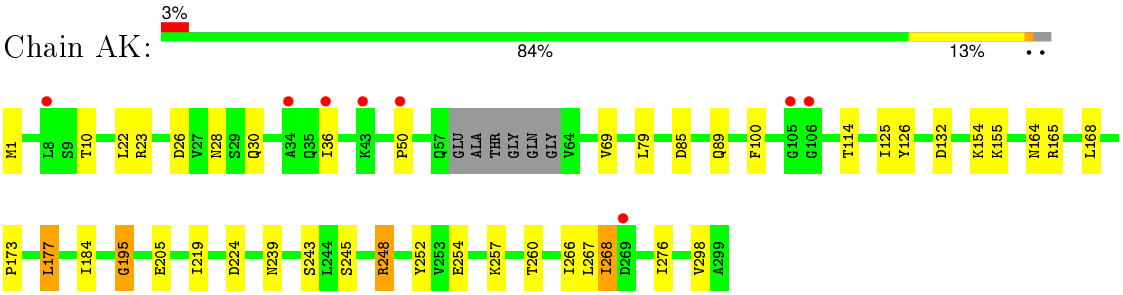
• Molecule 1: ORF48



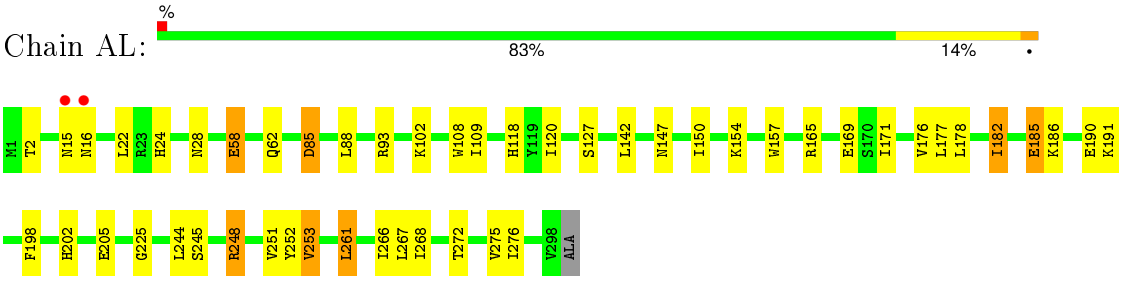
• Molecule 1: ORF48



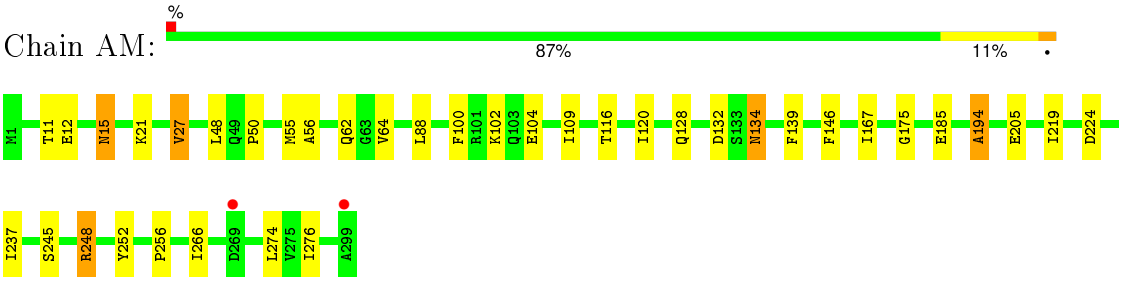
• Molecule 1: ORF48



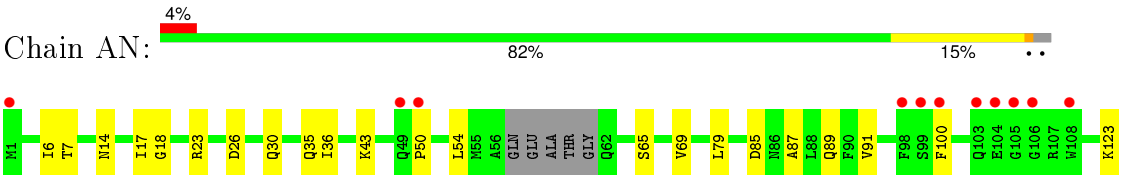
• Molecule 1: ORF48

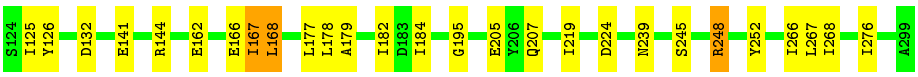


• Molecule 1: ORF48



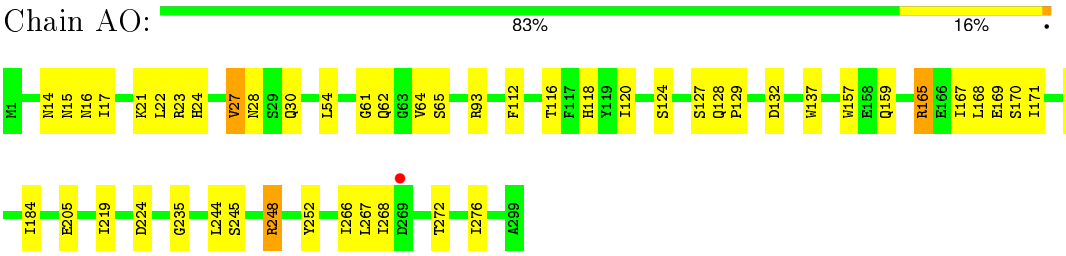
• Molecule 1: ORF48





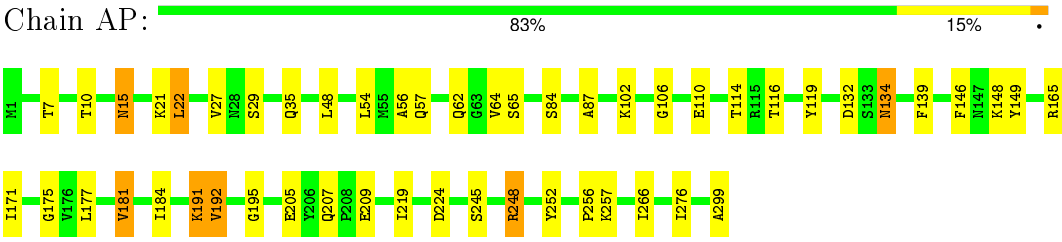
• Molecule 1: ORF48

Chain AO:



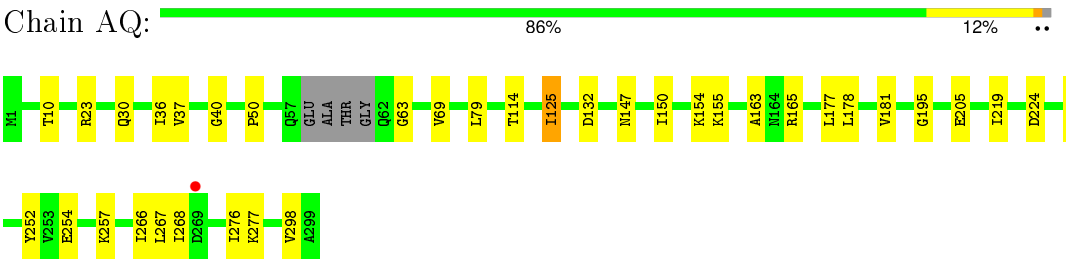
• Molecule 1: ORF48

Chain AP:



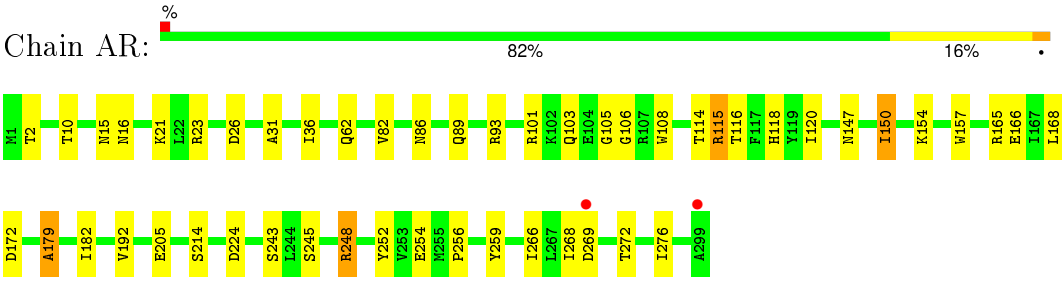
• Molecule 1: ORF48

Chain AQ:



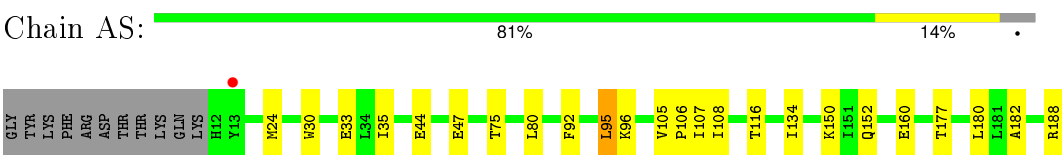
• Molecule 1: ORF48

Chain AR:



• Molecule 2: ORF46

Chain AS:



• Molecule 2: ORF46

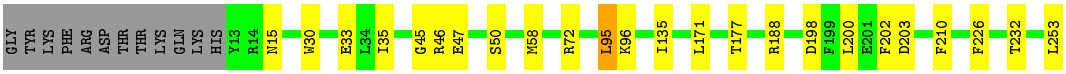
Chain AT:

• Molecule 2: ORF46

Chain AU:

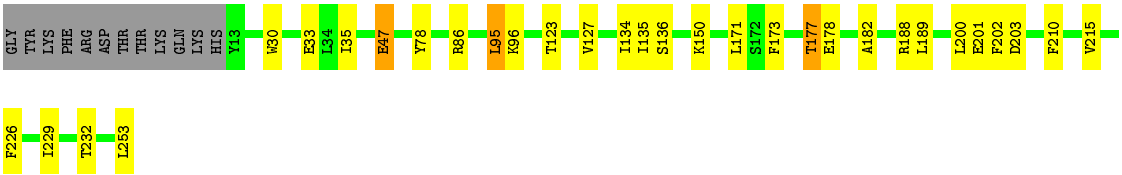
• Molecule 2: ORF46

Chain AV:



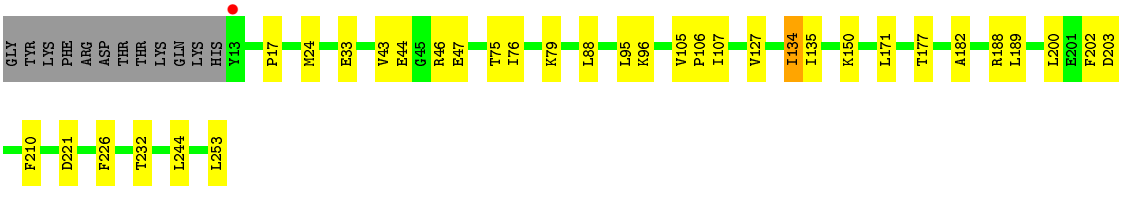
• Molecule 2: ORF46

Chain AW:



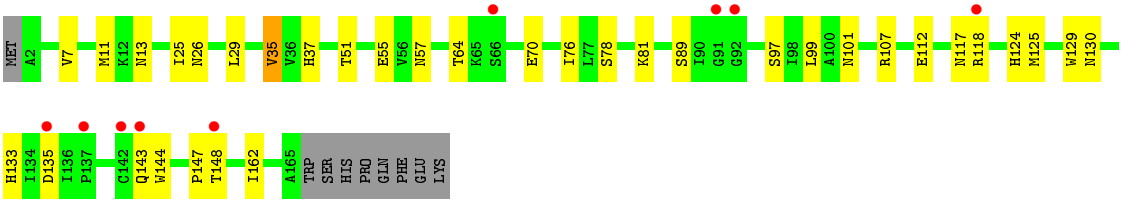
• Molecule 2: ORF46

Chain AX:



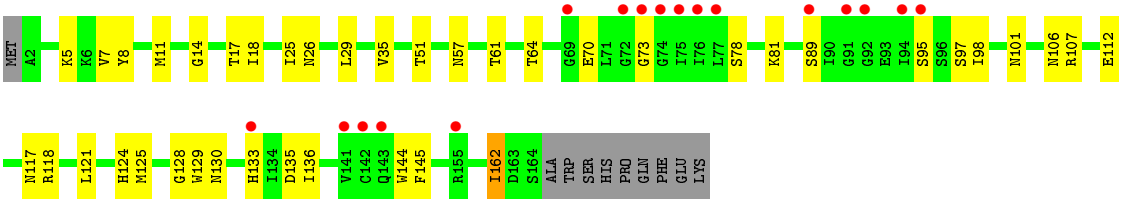
• Molecule 3: BPP

Chain BA:



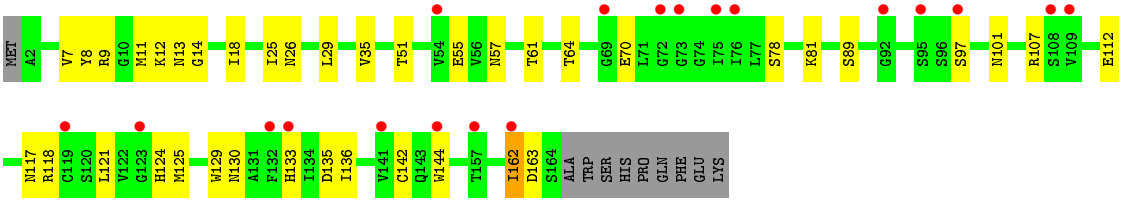
• Molecule 3: BPP

Chain BB:



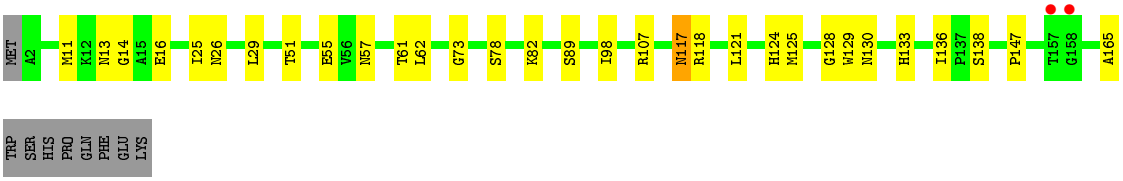
• Molecule 3: BPP

Chain BC:



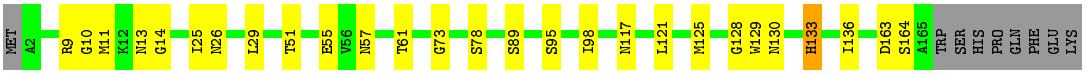
• Molecule 3: BPP

Chain BD:



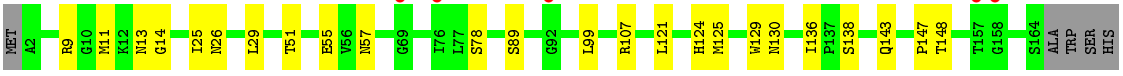
• Molecule 3: BPP

Chain BE:



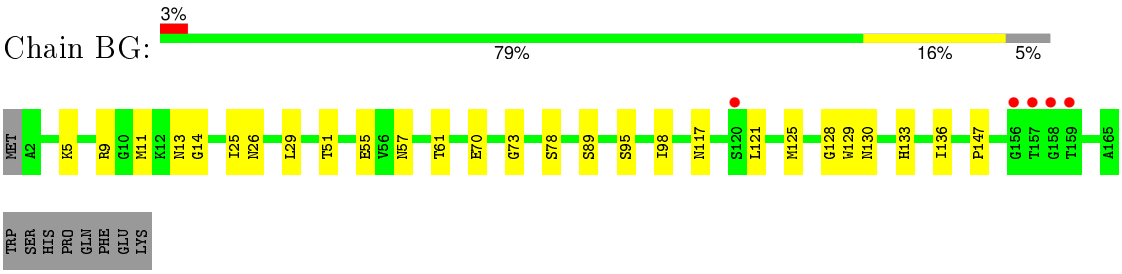
• Molecule 3: BPP

Chain BF:



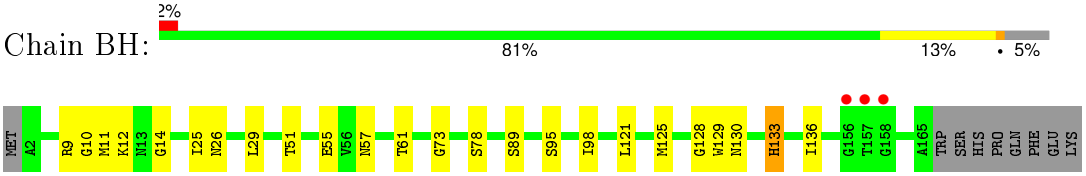
- Molecule 3: BPP

Chain BG:



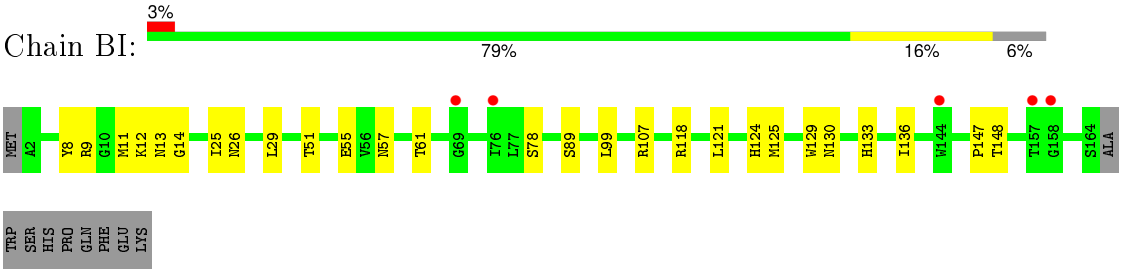
- Molecule 3: BPP

Chain BH:



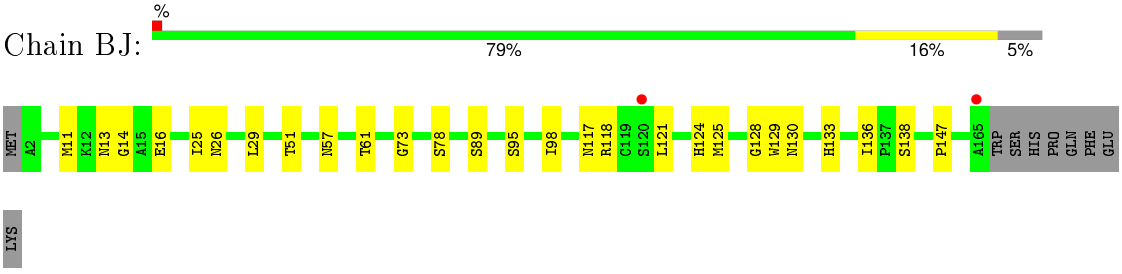
- Molecule 3: BPP

Chain BI:



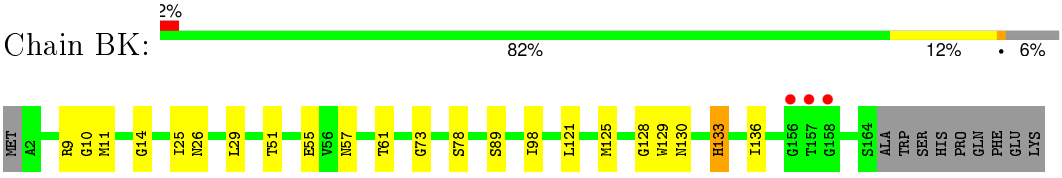
- Molecule 3: BPP

Chain BJ:



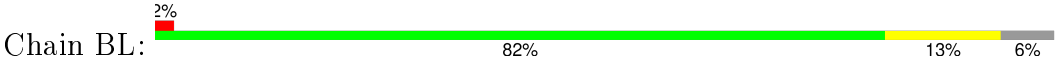
- Molecule 3: BPP

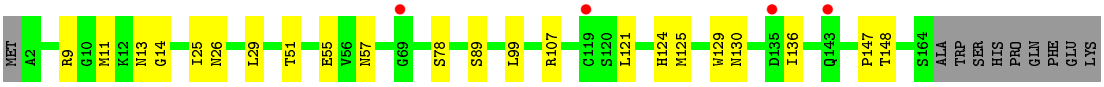
Chain BK:



- Molecule 3: BPP

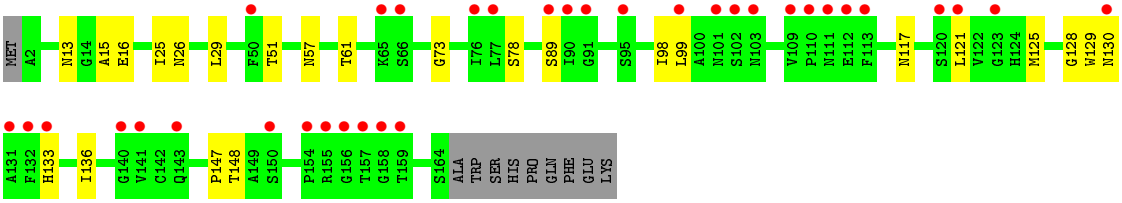
Chain BL:





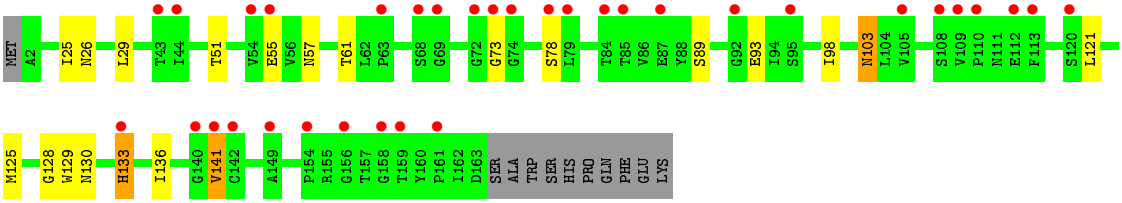
• Molecule 3: BPP

Chain BM:



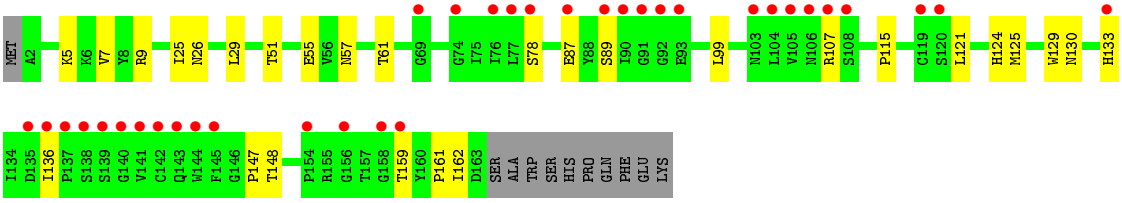
• Molecule 3: BPP

Chain BN:



• Molecule 3: BPP

Chain BO:



• Molecule 3: BPP

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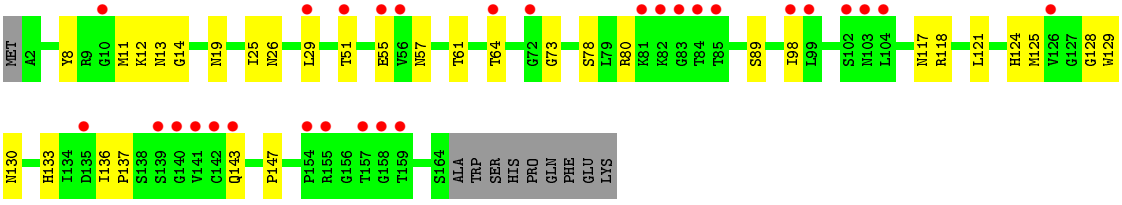
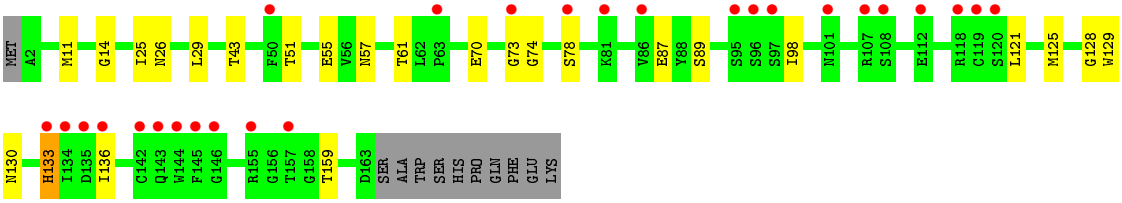


• Molecule 3: BPP

Chain BQ:



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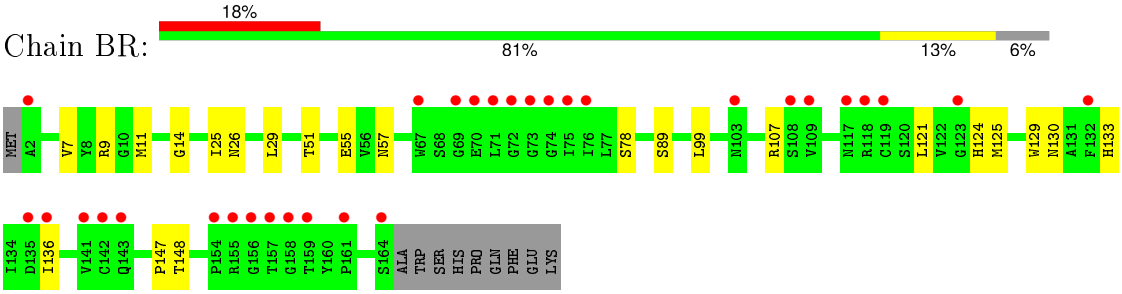

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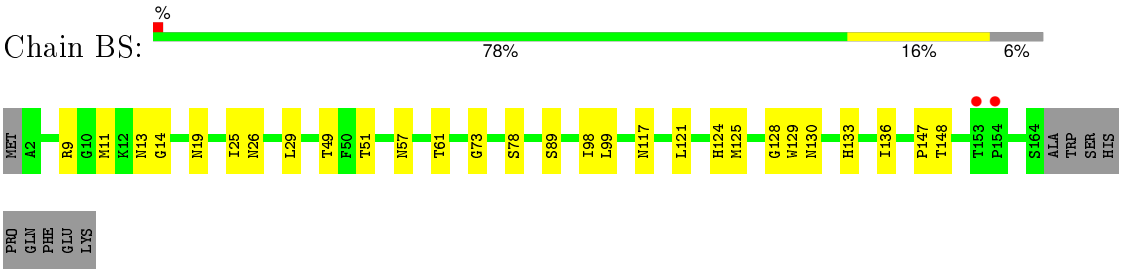

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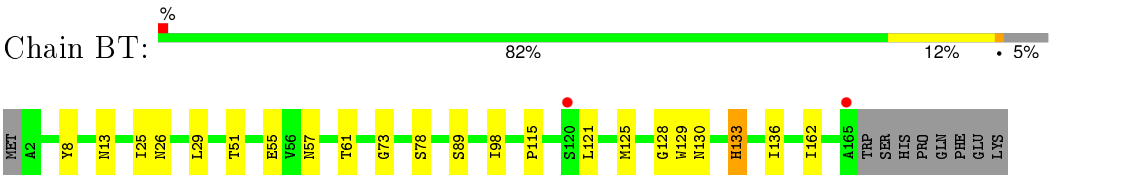

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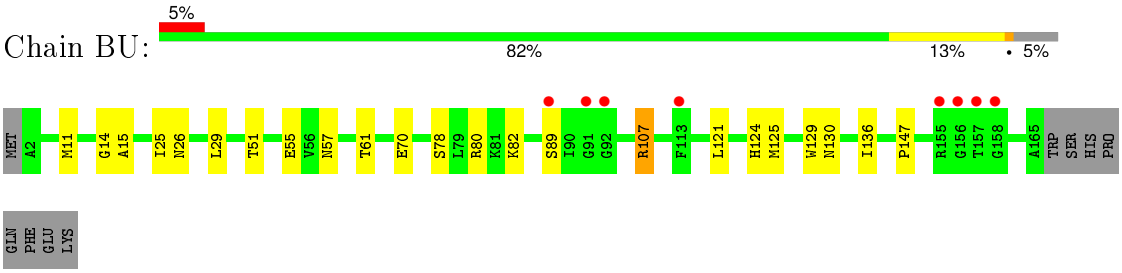

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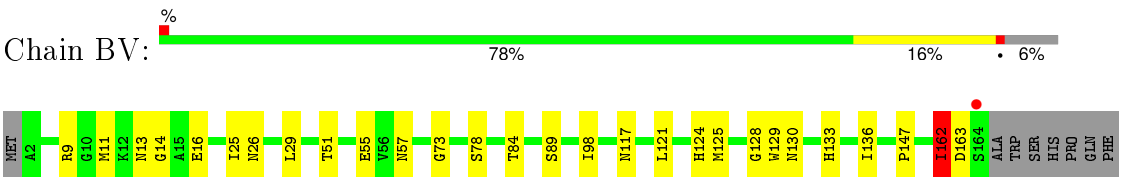
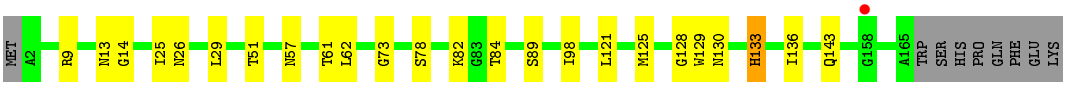


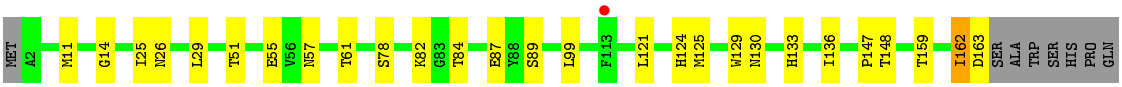
• Molecule 3: BPP

Chain BW:



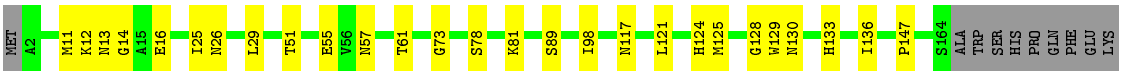
• Molecule 3: BPP

Chain BX:



• Molecule 3: BPP

Chain BY:



• Molecule 3: BPP

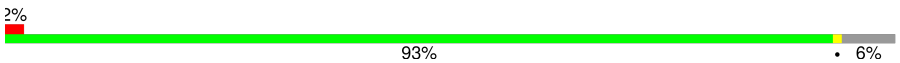
Chain BZ:

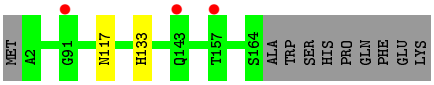
• Molecule 3: BPP

Chain Ba:

• Molecule 3: BPP

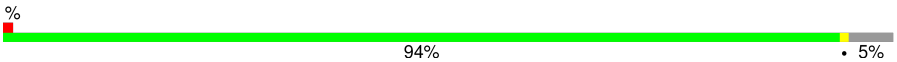
Chain Bb:

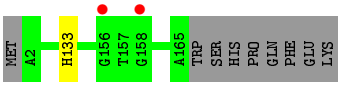




• Molecule 3: BPP

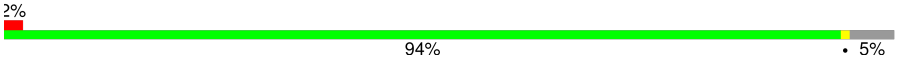
Chain Bc:

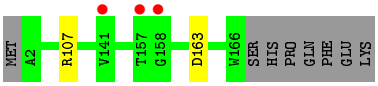




• Molecule 3: BPP

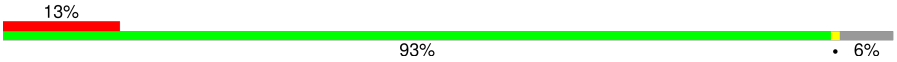
Chain Bd:

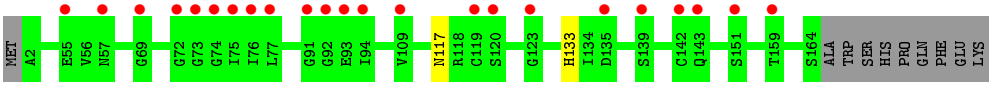




• Molecule 3: BPP

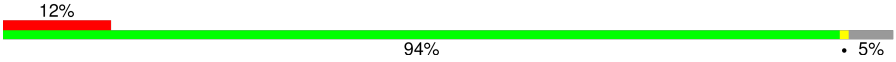
Chain Be:

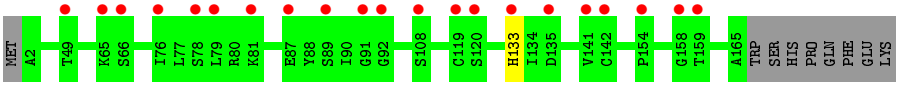




• Molecule 3: BPP

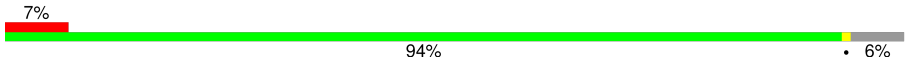
Chain Bf:

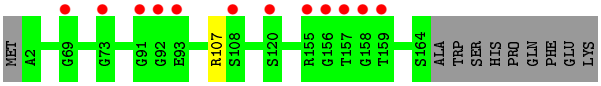




• Molecule 3: BPP

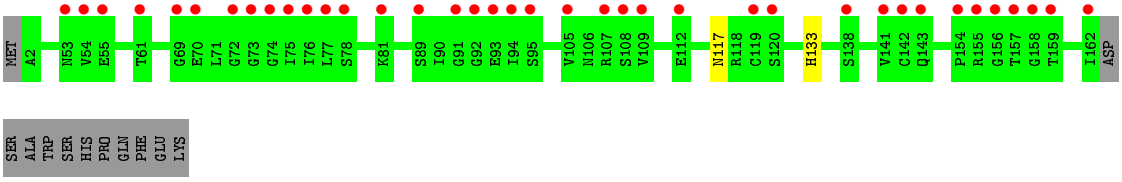
Chain Bg:





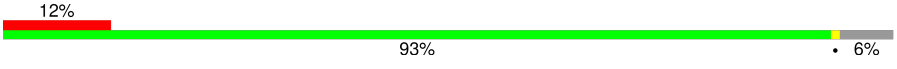
• Molecule 3: BPP

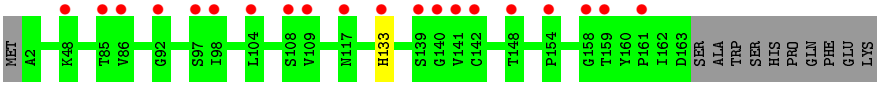
Chain Bh:



• Molecule 3: BPP

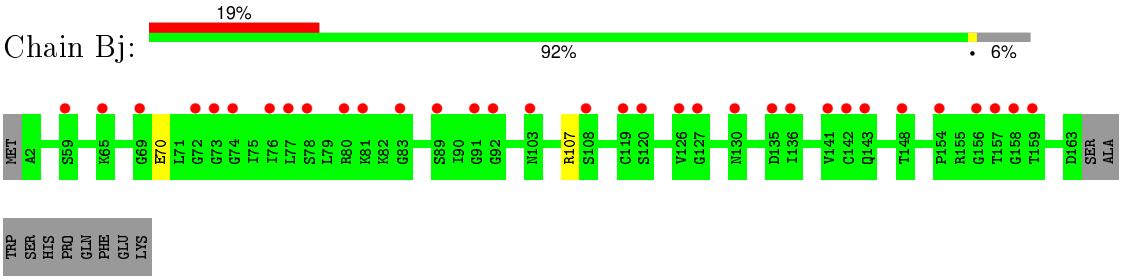
Chain Bi:





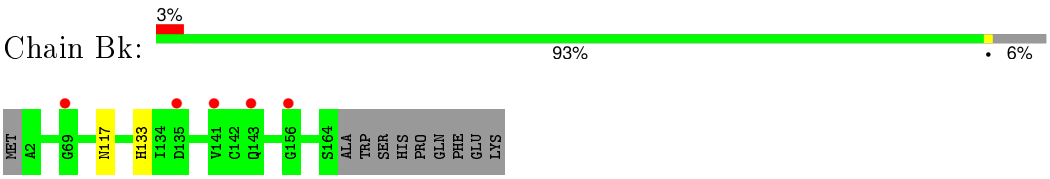
• Molecule 3: BPP

Chain Bj:



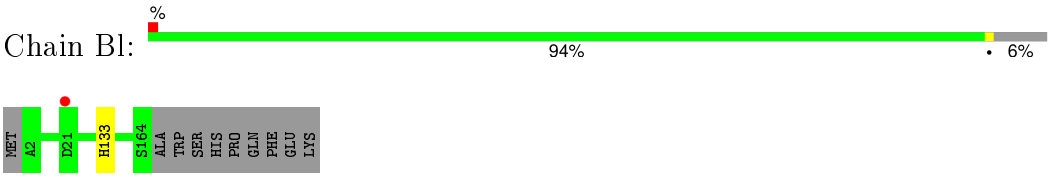
• Molecule 3: BPP

Chain Bk:



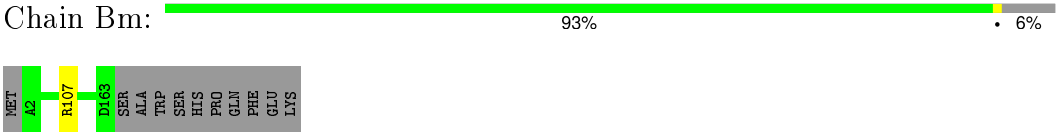
• Molecule 3: BPP

Chain Bl:



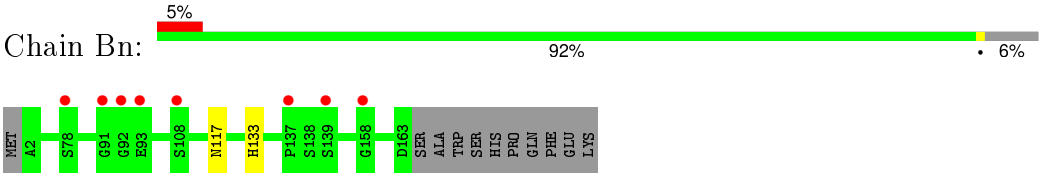
• Molecule 3: BPP

Chain Bm:



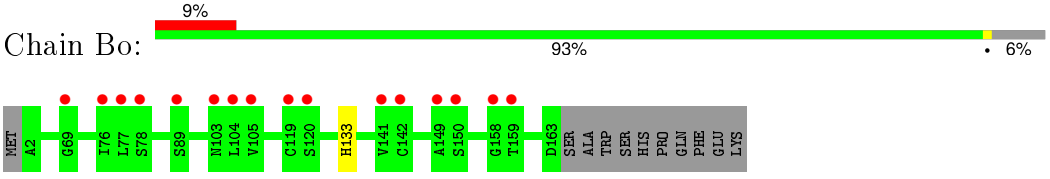
• Molecule 3: BPP

Chain Bn:



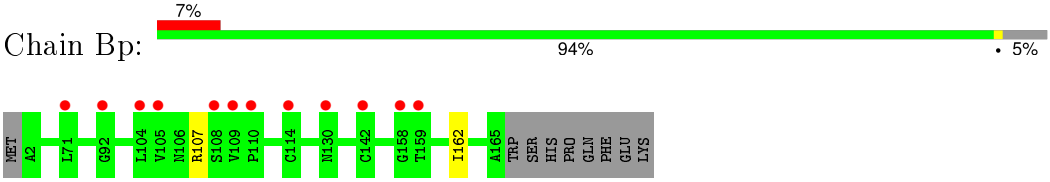
• Molecule 3: BPP

Chain Bo:



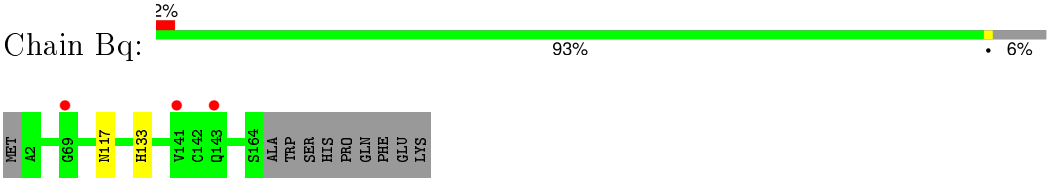
• Molecule 3: BPP

Chain Bp:



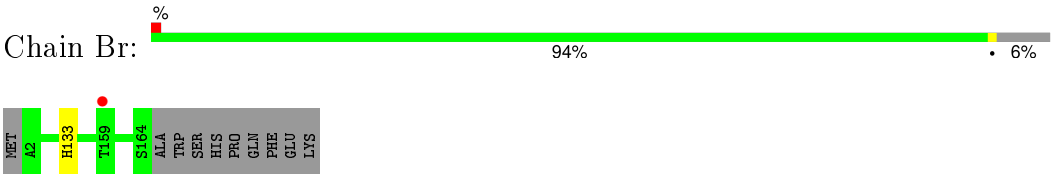
- Molecule 3: BPP

Chain Bq:



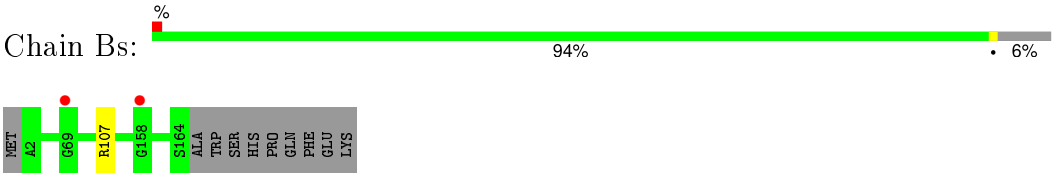
- Molecule 3: BPP

Chain Br:



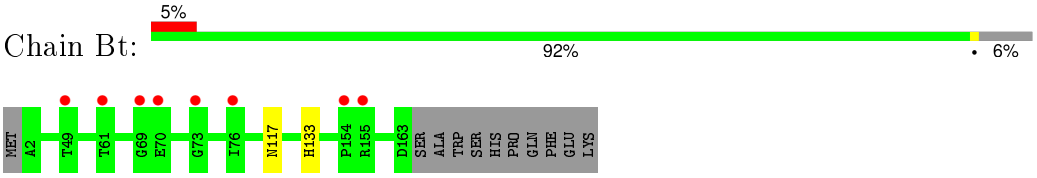
- Molecule 3: BPP

Chain Bs:



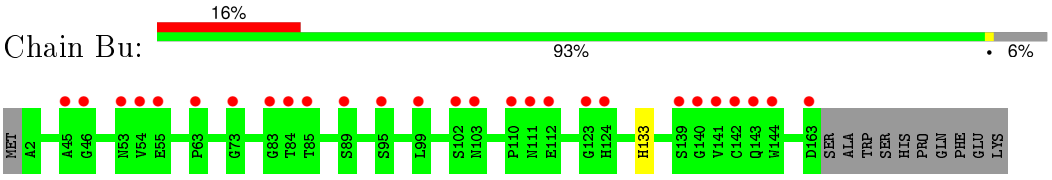
- Molecule 3: BPP

Chain Bt:



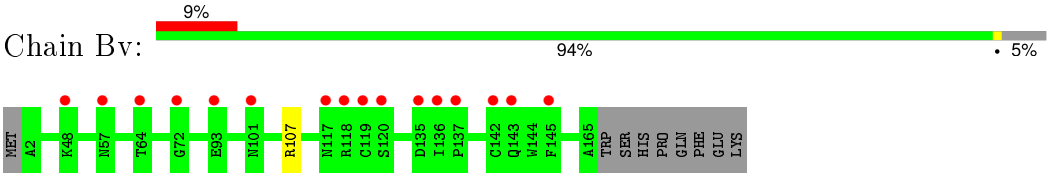
- Molecule 3: BPP

Chain Bu:



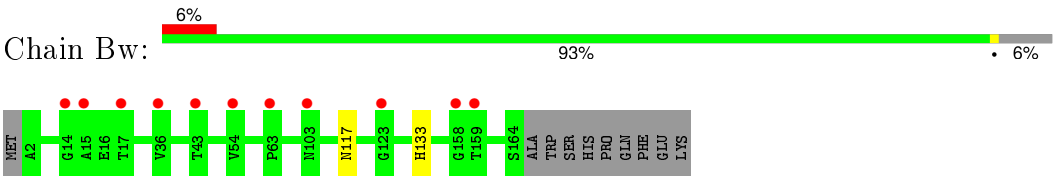
- Molecule 3: BPP

Chain Bv:



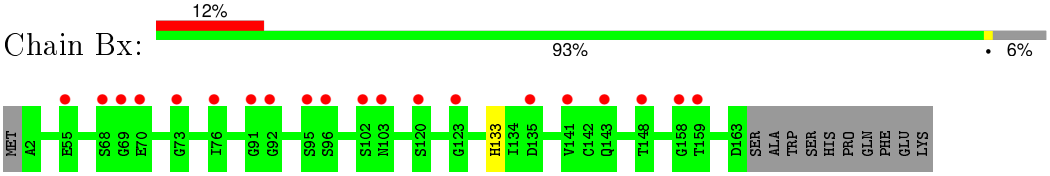
- Molecule 3: BPP

Chain Bw:



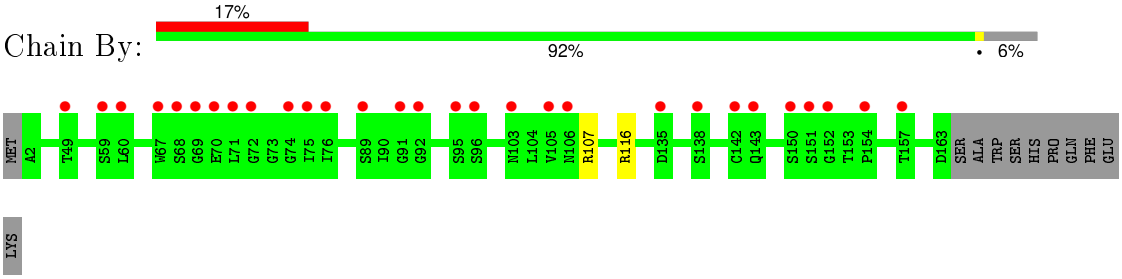
- Molecule 3: BPP

Chain Bx:



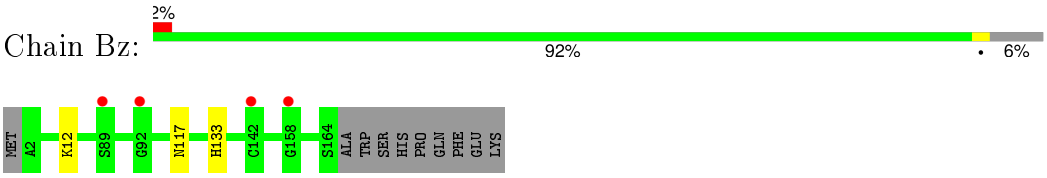
• Molecule 3: BPP

Chain By:



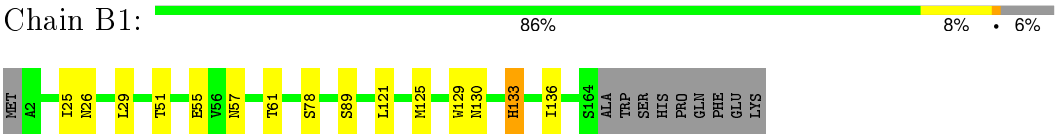
• Molecule 3: BPP

Chain Bz:



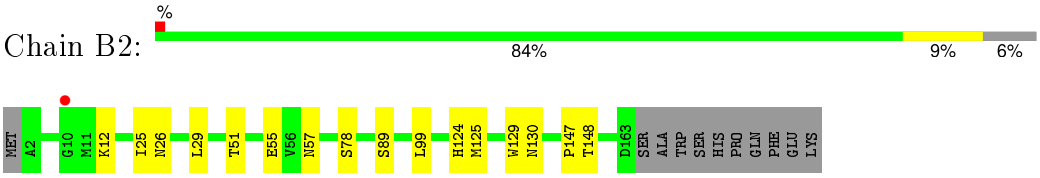
• Molecule 3: BPP

Chain B1:



• Molecule 3: BPP

Chain B2:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	163.53Å 287.36Å 323.14Å 90.00° 101.73° 90.00°	Depositor
Resolution (Å)	35.97 – 3.80 35.97 – 3.80	Depositor EDS
% Data completeness (in resolution range)	99.5 (35.97-3.80) 99.5 (35.97-3.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$< I/\sigma(I) >$ [1]	1.77 (at 3.76Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.237 , 0.264 0.252 , 0.259	Depositor DCC
R_{free} test set	1422 reflections (0.50%)	DCC
Wilson B-factor (Å^2)	123.5	Xtriage
Anisotropy	0.206	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.25 , 102.1	EDS
Estimated twinning fraction	0.022 for h,-k,-h-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 284701 reflections	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	118740	wwPDB-VP
Average B, all atoms (Å^2)	171.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.02% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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

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	AA	0.49	0/2444	0.74	3/3307 (0.1%)
1	AB	0.46	0/2398	0.69	1/3243 (0.0%)
1	AC	0.49	0/2444	0.72	1/3306 (0.0%)
1	AD	0.40	0/2448	0.63	1/3311 (0.0%)
1	AE	0.41	0/2390	0.60	0/3233
1	AF	0.41	0/2444	0.62	0/3307
1	AG	0.41	0/2441	0.61	2/3302 (0.1%)
1	AH	0.41	0/2396	0.59	0/3242
1	AI	0.42	0/2444	0.62	0/3307
1	AJ	0.41	0/2448	0.62	1/3311 (0.0%)
1	AK	0.42	0/2373	0.61	2/3214 (0.1%)
1	AL	0.45	0/2437	0.66	0/3298
1	AM	0.42	0/2444	0.62	1/3307 (0.0%)
1	AN	0.42	0/2381	0.62	1/3223 (0.0%)
1	AO	0.44	0/2448	0.65	0/3311
1	AP	0.41	0/2437	0.60	0/3298
1	AQ	0.40	0/2401	0.59	0/3250
1	AR	0.43	0/2445	0.65	1/3307 (0.0%)
2	AS	0.46	0/1972	0.65	0/2669
2	AT	0.46	0/1972	0.66	1/2670 (0.0%)
2	AU	0.46	0/1965	0.66	0/2661
2	AV	0.44	0/1938	0.64	0/2625
2	AW	0.43	0/1957	0.64	0/2649
2	AX	0.45	0/1952	0.64	0/2643
3	B1	0.32	0/1222	0.49	0/1655
3	B2	0.36	0/1216	0.50	0/1647
3	BA	0.40	0/1221	0.61	0/1655
3	BB	0.42	0/1216	0.63	0/1648
3	BC	0.42	0/1216	0.63	0/1648
3	BD	0.36	0/1221	0.50	0/1655
3	BE	0.34	0/1221	0.49	0/1655
3	BF	0.34	0/1216	0.49	0/1648
3	BG	0.36	0/1221	0.51	0/1655
3	BH	0.36	0/1227	0.50	0/1662

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
3	BI	0.34	0/1216	0.49	0/1648
3	BJ	0.36	0/1221	0.51	0/1655
3	BK	0.34	0/1216	0.48	0/1648
3	BL	0.36	0/1216	0.50	0/1648
3	BM	0.35	0/1216	0.50	0/1648
3	BN	0.36	0/1210	0.50	0/1640
3	BO	0.36	0/1210	0.53	1/1640 (0.1%)
3	BP	0.36	0/1216	0.49	0/1648
3	BQ	0.35	0/1216	0.48	0/1647
3	BR	0.35	0/1216	0.48	0/1648
3	BS	0.34	0/1216	0.48	0/1648
3	BT	0.35	0/1221	0.49	0/1655
3	BU	0.35	0/1221	0.48	0/1655
3	BV	0.38	0/1216	0.55	1/1648 (0.1%)
3	BW	0.36	0/1221	0.50	0/1655
3	BX	0.35	0/1210	0.58	2/1640 (0.1%)
3	BY	0.35	0/1216	0.49	0/1648
3	BZ	0.34	0/1216	0.49	0/1648
3	Ba	0.34	0/1216	0.49	0/1647
3	Bb	0.35	0/1216	0.48	0/1648
3	Bc	0.34	0/1220	0.48	0/1654
3	Bd	0.35	0/1231	0.50	0/1668
3	Be	0.35	0/1216	0.48	0/1648
3	Bf	0.35	0/1221	0.48	0/1655
3	Bg	0.34	0/1216	0.49	0/1648
3	Bh	0.35	0/1208	0.49	0/1636
3	Bi	0.34	0/1210	0.49	0/1640
3	Bj	0.35	0/1216	0.49	0/1647
3	Bk	0.34	0/1216	0.48	0/1648
3	Bl	0.34	0/1216	0.48	0/1648
3	Bm	0.36	0/1210	0.49	0/1640
3	Bn	0.35	0/1216	0.48	0/1647
3	Bo	0.34	0/1216	0.48	0/1647
3	Bp	0.35	0/1227	0.49	0/1662
3	Bq	0.35	0/1222	0.49	0/1655
3	Br	0.35	0/1216	0.50	0/1648
3	Bs	0.36	0/1216	0.50	0/1648
3	Bt	0.36	0/1210	0.49	0/1640
3	Bu	0.36	0/1216	0.49	0/1647
3	Bv	0.35	0/1221	0.49	0/1655
3	Bw	0.35	0/1216	0.48	0/1648
3	Bx	0.34	0/1216	0.48	0/1647
3	By	0.34	0/1216	0.48	0/1647

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
3	Bz	0.33	0/1222	0.49	0/1655
All	All	0.39	0/121148	0.57	19/164062 (0.0%)

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
3	BV	0	1

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	BX	163	ASP	N-CA-CB	-8.21	95.81	110.60
1	AR	179	ALA	CB-CA-C	7.90	121.95	110.10
3	BV	162	ILE	CB-CA-C	7.86	127.31	111.60
3	BX	162	ILE	CB-CA-C	7.70	126.99	111.60
1	AJ	83	ALA	CB-CA-C	7.48	121.31	110.10
1	AA	192	VAL	CB-CA-C	6.46	123.67	111.40
1	AG	192	VAL	CB-CA-C	6.20	123.17	111.40
1	AM	194	ALA	N-CA-C	6.19	127.70	111.00
3	BO	161	PRO	O-C-N	-6.14	112.88	122.70
1	AN	195	GLY	N-CA-C	6.04	128.20	113.10
2	AT	115	TYR	CB-CA-C	6.00	122.40	110.40
1	AA	268	ILE	CB-CA-C	5.70	123.00	111.60
1	AC	194	ALA	N-CA-C	5.59	126.11	111.00
1	AB	268	ILE	CB-CA-C	5.54	122.67	111.60
1	AK	268	ILE	CB-CA-C	5.33	122.27	111.60
1	AG	83	ALA	CB-CA-C	5.28	118.02	110.10
1	AK	195	GLY	N-CA-C	5.11	125.86	113.10
1	AD	162	GLU	CB-CG-CD	5.09	127.95	114.20
1	AA	179	ALA	CB-CA-C	5.01	117.61	110.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	BV	162	ILE	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	AA	2389	0	2333	57	0
1	AB	2345	0	2295	35	0
1	AC	2389	0	2340	46	0
1	AD	2393	0	2344	30	0
1	AE	2336	0	2292	26	0
1	AF	2389	0	2333	26	0
1	AG	2386	0	2338	31	0
1	AH	2343	0	2280	24	0
1	AI	2389	0	2333	34	0
1	AJ	2393	0	2344	29	0
1	AK	2320	0	2246	36	0
1	AL	2382	0	2330	38	0
1	AM	2389	0	2333	23	0
1	AN	2328	0	2253	28	0
1	AO	2393	0	2344	29	0
1	AP	2382	0	2327	31	0
1	AQ	2347	0	2281	20	0
1	AR	2390	0	2335	38	0
2	AS	1932	0	1882	30	0
2	AT	1931	0	1886	17	0
2	AU	1924	0	1879	19	0
2	AV	1899	0	1836	17	0
2	AW	1917	0	1865	31	0
2	AX	1913	0	1867	22	0
3	B1	1200	0	1182	14	0
3	B2	1194	0	1177	15	0
3	BA	1199	0	1176	36	0
3	BB	1194	0	1171	32	0
3	BC	1194	0	1171	37	0
3	BD	1199	0	1176	30	0
3	BE	1199	0	1176	25	0
3	BF	1194	0	1171	25	0
3	BG	1199	0	1176	29	0
3	BH	1205	0	1187	23	0
3	BI	1194	0	1171	31	0
3	BJ	1199	0	1176	28	0
3	BK	1194	0	1171	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	BL	1194	0	1171	20	0
3	BM	1194	0	1171	23	0
3	BN	1188	0	1166	22	0
3	BO	1188	0	1166	25	0
3	BP	1194	0	1171	35	0
3	BQ	1194	0	1177	22	0
3	BR	1194	0	1171	24	0
3	BS	1194	0	1171	28	0
3	BT	1199	0	1176	24	0
3	BU	1199	0	1176	26	0
3	BV	1194	0	1170	25	0
3	BW	1199	0	1176	22	0
3	BX	1188	0	1166	23	0
3	BY	1194	0	1171	24	0
3	BZ	1194	0	1171	29	0
3	Ba	1194	0	1177	0	0
3	Bb	1194	0	1171	0	0
3	Bc	1198	0	1173	0	0
3	Bd	1209	0	1186	0	0
3	Be	1194	0	1171	0	0
3	Bf	1199	0	1176	0	0
3	Bg	1194	0	1171	0	0
3	Bh	1186	0	1173	0	0
3	Bi	1188	0	1166	0	0
3	Bj	1194	0	1177	0	0
3	Bk	1194	0	1171	0	0
3	Bl	1194	0	1171	0	0
3	Bm	1188	0	1166	0	0
3	Bn	1194	0	1177	0	0
3	Bo	1194	0	1177	0	0
3	Bp	1205	0	1187	0	0
3	Bq	1200	0	1182	0	0
3	Br	1194	0	1171	0	0
3	Bs	1194	0	1171	0	0
3	Bt	1188	0	1166	0	0
3	Bu	1194	0	1177	0	0
3	Bv	1199	0	1176	0	0
3	Bw	1194	0	1171	0	0
3	Bx	1194	0	1177	0	0
3	By	1194	0	1177	0	0
3	Bz	1200	0	1182	0	0
All	All	118740	0	116287	1033	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 4.

All (1033) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:108:TRP:CZ2	1:AK:125:ILE:HD11	1.37	1.59
2:AW:127:VAL:HG23	2:AW:134:ILE:CD1	1.44	1.45
1:AI:108:TRP:CH2	1:AK:125:ILE:HD11	1.73	1.22
1:AI:108:TRP:CZ2	1:AK:125:ILE:CD1	2.29	1.15
2:AW:127:VAL:CG2	2:AW:134:ILE:CD1	2.27	1.11
3:BA:143:GLN:HE22	3:BG:95:SER:HB2	132.88	1.08
1:AO:21:LYS:HG3	1:AO:120:ILE:HG13	1.36	1.04
1:AR:21:LYS:HG2	1:AR:120:ILE:HD11	1.42	0.99
1:AI:108:TRP:HZ2	1:AK:125:ILE:CD1	1.71	0.98
2:AW:127:VAL:CG2	2:AW:134:ILE:HD11	1.92	0.95
2:AW:127:VAL:HG23	2:AW:134:ILE:HD11	0.95	0.95
2:AW:253:LEU:OXT	2:AX:96:LYS:HD2	1.66	0.95
1:AB:13:PRO:HA	1:AB:115:ARG:HE	1.29	0.95
1:AG:168:LEU:HD21	1:AH:168:LEU:HD11	1.49	0.94
1:AA:12:GLU:O	1:AA:115:ARG:HD3	1.71	0.91
1:AI:108:TRP:HZ2	1:AK:125:ILE:HD11	1.08	0.89
2:AV:253:LEU:OXT	2:AW:96:LYS:HD2	1.74	0.85
2:AS:253:LEU:OXT	2:AT:96:LYS:HD2	1.77	0.84
1:AR:179:ALA:O	1:AR:182:ILE:HG22	1.78	0.83
1:AP:177:LEU:HD11	1:AQ:181:VAL:HG11	1.59	0.83
2:AS:96:LYS:HD2	2:AX:253:LEU:OXT	1.79	0.83
2:AV:188:ARG:O	2:AV:226:PHE:HD2	1.62	0.82
1:AB:12:GLU:O	1:AB:115:ARG:HD3	1.80	0.82
1:AA:49:GLN:HE21	1:AA:50:PRO:HD2	1.44	0.82
2:AW:188:ARG:O	2:AW:226:PHE:HD2	1.63	0.81
1:AA:179:ALA:O	1:AA:182:ILE:HG22	1.81	0.80
1:AG:12:GLU:OE1	2:AS:150:LYS:HE2	1.81	0.80
1:AR:245:SER:HB2	1:AR:252:TYR:HB2	1.64	0.80
2:AU:188:ARG:O	2:AU:226:PHE:HD2	1.64	0.79
2:AT:188:ARG:O	2:AT:226:PHE:HD2	1.66	0.78
1:AA:165:ARG:HH22	1:AC:171:ILE:HG21	1.49	0.78
3:BA:143:GLN:NE2	3:BG:95:SER:HB2	132.21	0.77
2:AS:188:ARG:O	2:AS:226:PHE:HD2	1.68	0.77
1:AD:191:LYS:HD3	1:AE:193:PRO:O	1.83	0.76
2:AX:188:ARG:O	2:AX:226:PHE:HD2	1.67	0.76
1:AM:104:GLU:HB2	1:AM:109:ILE:HD11	1.66	0.75
1:AG:245:SER:HB3	1:AG:252:TYR:HB2	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:108:TRP:CH2	1:AK:125:ILE:CD1	2.62	0.75
1:AJ:12:GLU:OE1	2:AX:150:LYS:HE2	1.87	0.74
1:AA:13:PRO:HA	1:AA:115:ARG:HE	1.53	0.74
1:AJ:245:SER:HB3	1:AJ:252:TYR:HB2	1.67	0.74
1:AP:165:ARG:HH12	1:AR:171:ILE:HG22	1.50	0.74
3:BN:103:ASN:HD21	3:BN:141:VAL:HG12	1.52	0.73
3:BP:12:LYS:HG2	3:BP:13:ASN:ND2	2.04	0.73
1:AA:15:ASN:HD22	1:AA:15:ASN:H	1.35	0.72
1:AP:165:ARG:HH12	1:AR:171:ILE:CG2	2.02	0.72
3:BJ:138:SER:HB2	3:BU:107:ARG:NH2	2.05	0.71
1:AA:11:THR:HG21	1:AA:39:ASN:OD1	1.91	0.71
3:BP:13:ASN:HA	3:BR:9:ARG:HH21	1.55	0.71
3:BB:106:ASN:OD1	3:BF:138:SER:HB2	104.18	0.71
1:AJ:266:ILE:HD12	1:AJ:276:ILE:HD12	1.72	0.71
1:AO:245:SER:HB3	1:AO:252:TYR:HB2	1.73	0.71
1:AA:104:GLU:HB2	1:AA:109:ILE:HD11	1.72	0.70
1:AM:245:SER:HB3	1:AM:252:TYR:HB2	1.74	0.70
1:AD:245:SER:HB3	1:AD:252:TYR:HB2	1.73	0.70
1:AR:21:LYS:CG	1:AR:120:ILE:HD11	2.19	0.70
1:AI:245:SER:HB3	1:AI:252:TYR:HB2	1.71	0.70
3:BV:84:THR:HB	3:BV:163:ASP:OD1	1.91	0.70
1:AE:245:SER:HB3	1:AE:252:TYR:HB2	1.74	0.70
3:BP:12:LYS:HG2	3:BP:13:ASN:HD22	1.57	0.69
1:AN:167:ILE:HG12	1:AN:168:LEU:N	2.06	0.69
1:AH:245:SER:HB3	1:AH:252:TYR:HB2	1.74	0.69
3:BA:133:HIS:HD2	3:BB:124:HIS:ND1	1.90	0.69
2:AW:202:PHE:HB2	2:AW:210:PHE:HB2	1.75	0.69
3:BA:124:HIS:ND1	3:BC:133:HIS:HD2	1.91	0.69
1:AJ:177:LEU:HD11	1:AL:177:LEU:HD21	1.75	0.68
3:BA:76:ILE:HG12	3:BN:93:GLU:HG2	137.98	0.68
1:AL:85:ASP:HA	1:AL:88:LEU:HD12	1.75	0.68
2:AS:80:LEU:HB3	2:AS:134:ILE:HD11	1.75	0.68
1:AP:245:SER:HB2	1:AP:252:TYR:HB2	1.74	0.68
3:BB:133:HIS:HD2	3:BC:124:HIS:ND1	1.91	0.68
3:BZ:121:LEU:HD11	3:BZ:136:ILE:HD11	1.76	0.68
1:AI:15:ASN:ND2	2:AS:33:GLU:OE2	2.27	0.67
1:AN:245:SER:HB3	1:AN:252:TYR:HB2	1.76	0.67
3:BD:107:ARG:NH2	3:BD:138:SER:HB2	20.23	0.67
2:AW:127:VAL:CG2	2:AW:134:ILE:HD12	2.21	0.66
1:AO:93:ARG:HA	1:AO:120:ILE:HG22	1.77	0.66
1:AC:16:ASN:HB3	1:AC:118:HIS:HE1	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AS:80:LEU:O	2:AS:134:ILE:HG13	1.94	0.66
2:AW:253:LEU:OXT	2:AX:96:LYS:CD	2.41	0.66
1:AK:245:SER:HB3	1:AK:252:TYR:HB2	1.76	0.66
3:BW:121:LEU:HD11	3:BW:136:ILE:HD11	1.77	0.66
1:AM:12:GLU:OE1	2:AW:150:LYS:HE2	1.96	0.66
1:AL:245:SER:HB3	1:AL:252:TYR:HB2	1.77	0.65
3:BR:121:LEU:HD11	3:BR:136:ILE:HD11	3.01	0.65
1:AR:179:ALA:O	1:AR:182:ILE:CG2	2.44	0.65
1:AP:207:GLN:NE2	3:BP:13:ASN:OD1	2.29	0.65
3:BL:121:LEU:HD11	3:BL:136:ILE:HD11	3.00	0.65
1:AQ:245:SER:HB3	1:AQ:252:TYR:HB2	1.77	0.65
3:BT:121:LEU:HD11	3:BT:136:ILE:HD11	1.78	0.65
3:BN:121:LEU:HD11	3:BN:136:ILE:HD11	1.79	0.65
1:AD:167:ILE:HG12	1:AE:173:PRO:HG2	1.77	0.65
3:BU:121:LEU:HD11	3:BU:136:ILE:HD11	2.99	0.65
3:BE:121:LEU:HD11	3:BE:136:ILE:HD11	1.79	0.65
1:AA:192:VAL:O	1:AA:256:PRO:HG3	1.96	0.64
1:AM:15:ASN:H	1:AM:15:ASN:HD22	1.45	0.64
1:AP:15:ASN:H	1:AP:15:ASN:HD22	1.45	0.64
3:BH:121:LEU:HD11	3:BH:136:ILE:HD11	1.78	0.64
1:AB:245:SER:HB3	1:AB:252:TYR:HB2	1.79	0.64
1:AF:195:GLY:HA3	1:AF:257:LYS:HG2	1.80	0.64
1:AK:177:LEU:HD23	1:AL:177:LEU:HD22	1.80	0.64
3:BC:121:LEU:HD11	3:BC:136:ILE:HD11	3.17	0.64
1:AK:266:ILE:HD13	1:AK:276:ILE:HD12	1.80	0.64
3:BQ:121:LEU:HD11	3:BQ:136:ILE:HD11	1.80	0.64
1:AH:266:ILE:HD13	1:AH:276:ILE:HD12	1.79	0.64
2:AS:92:PHE:HZ	2:AS:134:ILE:CD1	2.10	0.63
3:BI:121:LEU:HD11	3:BI:136:ILE:HD11	3.02	0.63
3:BK:121:LEU:HD11	3:BK:136:ILE:HD11	1.80	0.63
1:AA:165:ARG:HH22	1:AC:171:ILE:CG2	2.11	0.63
3:BJ:95:SER:HB2	3:BP:143:GLN:HE22	122.63	0.63
3:BX:121:LEU:HD11	3:BX:136:ILE:HD11	2.97	0.63
3:B1:121:LEU:HD11	3:B1:136:ILE:HD11	1.79	0.63
1:AI:16:ASN:HB3	1:AI:118:HIS:HE1	1.62	0.63
3:BF:121:LEU:HD11	3:BF:136:ILE:HD11	2.99	0.63
3:BO:121:LEU:HD11	3:BO:136:ILE:HD11	3.01	0.63
1:AJ:15:ASN:HD22	1:AJ:15:ASN:H	1.44	0.63
1:AG:168:LEU:CD2	1:AH:168:LEU:HD11	2.26	0.62
1:AE:266:ILE:HD13	1:AE:276:ILE:HD12	1.80	0.62
1:AD:15:ASN:H	1:AD:15:ASN:HD22	1.45	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:191:LYS:HE3	1:AE:243:SER:OG	2.00	0.62
2:AS:92:PHE:HZ	2:AS:134:ILE:HD13	1.63	0.62
1:AD:179:ALA:O	1:AD:182:ILE:HG22	2.00	0.62
1:AH:6:ILE:HB	1:AH:17:ILE:HD11	1.80	0.62
1:AC:257:LYS:O	1:AC:260:THR:HG22	1.99	0.62
1:AA:267:LEU:HD23	1:AA:268:ILE:O	1.99	0.61
1:AL:16:ASN:HB3	1:AL:118:HIS:HE1	1.65	0.61
1:AQ:266:ILE:HD13	1:AQ:276:ILE:HD12	1.83	0.61
1:AN:266:ILE:HD13	1:AN:276:ILE:HD12	1.80	0.61
3:BA:25:ILE:HG23	3:BB:29:LEU:HD11	1.83	0.61
1:AG:15:ASN:H	1:AG:15:ASN:HD22	1.49	0.61
1:AR:21:LYS:HG2	1:AR:120:ILE:CD1	2.23	0.60
1:AP:171:ILE:HD11	1:AQ:177:LEU:HD11	1.82	0.60
3:BA:29:LEU:HD11	3:BC:25:ILE:HG23	1.84	0.60
1:AC:4:HIS:HB2	1:AC:32:ILE:HG22	1.83	0.60
3:BR:9:ARG:HH22	3:BS:13:ASN:HA	197.48	0.60
1:AR:101:ARG:NH1	1:AR:108:TRP:HE1	2.00	0.60
2:AT:202:PHE:HB2	2:AT:210:PHE:HB2	1.84	0.60
1:AG:188:VAL:HG21	1:AI:184:ILE:HD11	1.82	0.60
1:AK:125:ILE:HG23	1:AK:126:TYR:N	2.16	0.59
1:AD:191:LYS:NZ	1:AE:243:SER:HB2	2.16	0.59
1:AC:26:ASP:CB	1:AC:30:GLN:HE21	2.15	0.59
3:BV:9:ARG:HH22	3:BW:13:ASN:H	1.48	0.59
3:BJ:138:SER:HB2	3:BU:107:ARG:HH21	1.68	0.59
1:AK:177:LEU:CD2	1:AL:177:LEU:HD22	2.33	0.59
3:BN:125:MET:HB2	3:BN:130:ASN:HB2	1.97	0.59
3:BJ:118:ARG:HD2	3:BU:70:GLU:OE1	2.03	0.59
1:AC:24:HIS:CD2	1:AC:127:SER:HB3	2.37	0.59
3:BB:25:ILE:HG23	3:BC:29:LEU:HD11	1.85	0.59
1:AK:243:SER:HB3	1:AK:254:GLU:HB3	1.84	0.59
1:AB:266:ILE:HD13	1:AB:276:ILE:HD12	1.84	0.59
1:AG:206:TYR:HD1	3:BG:13:ASN:HD22	1.50	0.59
1:AP:219:ILE:HD13	3:BF:14:GLY:HA3	136.21	0.59
1:AB:192:VAL:O	1:AB:256:PRO:HG3	2.03	0.59
1:AC:245:SER:HB3	1:AC:252:TYR:HB2	1.85	0.58
1:AC:226:PHE:CZ	3:BB:18:ILE:HD11	2.38	0.58
1:AG:266:ILE:HD13	1:AG:276:ILE:HD12	1.84	0.58
1:AA:164:ASN:HD22	1:AB:168:LEU:HG	1.67	0.58
1:AF:15:ASN:ND2	2:AT:33:GLU:OE2	2.32	0.58
1:AG:164:ASN:HD22	1:AH:168:LEU:HD23	1.68	0.58
1:AK:177:LEU:HD23	1:AL:177:LEU:CD2	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:266:ILE:HD13	1:AM:276:ILE:HD12	1.85	0.58
2:AU:202:PHE:HB2	2:AU:210:PHE:HB2	1.85	0.58
1:AD:112:PHE:HA	1:AF:26:ASP:OD1	2.04	0.57
1:AH:243:SER:HB3	1:AH:254:GLU:HB3	1.85	0.57
3:BG:121:LEU:HD11	3:BG:136:ILE:HD11	1.87	0.57
2:AW:188:ARG:O	2:AW:226:PHE:CD2	2.53	0.57
1:AA:167:ILE:HG12	1:AB:173:PRO:HG2	1.86	0.57
1:AB:267:LEU:HD23	1:AB:268:ILE:O	2.05	0.57
1:AR:15:ASN:ND2	2:AV:33:GLU:OE2	2.36	0.57
3:BA:7:VAL:HG13	3:BA:11:MET:HE2	1.85	0.57
2:AV:202:PHE:HB2	2:AV:210:PHE:HB2	1.86	0.57
3:BY:121:LEU:HD11	3:BY:136:ILE:HD11	1.87	0.57
1:AN:36:ILE:HD11	1:AN:79:LEU:CD2	2.34	0.57
2:AS:96:LYS:CD	2:AX:253:LEU:OXT	2.52	0.57
1:AB:13:PRO:HA	1:AB:115:ARG:NE	2.11	0.57
3:BD:117:ASN:ND2	3:BD:165:ALA:HB3	9.31	0.56
2:AS:253:LEU:OXT	2:AT:96:LYS:CD	2.51	0.56
2:AU:253:LEU:OXT	2:AV:96:LYS:HD2	2.05	0.56
1:AQ:23:ARG:H	1:AQ:30:GLN:HE22	1.52	0.56
2:AU:216:ASN:O	2:AU:220:LEU:HB2	2.05	0.56
1:AP:195:GLY:HA3	1:AP:257:LYS:HE2	1.87	0.56
3:BA:125:MET:HB2	3:BA:130:ASN:HB2	2.46	0.56
3:BO:115:PRO:HB3	3:BO:162:ILE:HA	1.87	0.56
2:AV:253:LEU:OXT	2:AW:96:LYS:CD	2.52	0.56
1:AR:266:ILE:HD13	1:AR:276:ILE:HD12	1.88	0.56
1:AI:93:ARG:HA	1:AI:120:ILE:HG22	1.88	0.56
1:AL:93:ARG:HG2	1:AL:120:ILE:HD13	1.88	0.56
1:AQ:36:ILE:HD11	1:AQ:79:LEU:HD23	1.88	0.56
2:AV:188:ARG:O	2:AV:226:PHE:CD2	2.53	0.56
1:AK:184:ILE:HD11	1:AL:185:GLU:HG3	1.88	0.56
3:BP:121:LEU:HD11	3:BP:136:ILE:HD11	1.88	0.56
2:AS:202:PHE:HB2	2:AS:210:PHE:HB2	1.87	0.56
3:BX:84:THR:O	3:BX:162:ILE:HG22	2.06	0.56
1:AJ:102:LYS:HG2	1:AJ:109:ILE:HB	1.88	0.55
1:AA:257:LYS:O	1:AA:260:THR:HG22	2.06	0.55
1:AA:21:LYS:NZ	1:AR:15:ASN:HB2	2.21	0.55
1:AP:266:ILE:HD13	1:AP:276:ILE:HD12	1.86	0.55
1:AJ:299:ALA:O	1:AL:154:LYS:HE2	2.06	0.55
3:BC:64:THR:HA	3:BC:81:LYS:O	2.07	0.55
1:AA:38:GLU:OE1	1:AC:2:THR:HG22	2.06	0.55
2:AS:180:LEU:HB3	2:AS:191:SER:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:243:SER:HB3	1:AE:254:GLU:HB3	1.88	0.55
2:AU:253:LEU:OXT	2:AV:96:LYS:CE	2.55	0.55
1:AR:103:GLN:HE21	1:AR:106:GLY:H	1.55	0.55
1:AC:194:ALA:H	1:AC:256:PRO:HA	1.70	0.55
1:AF:266:ILE:HD13	1:AF:276:ILE:HD12	1.87	0.55
1:AG:12:GLU:OE1	2:AS:150:LYS:CE	2.55	0.55
1:AC:19:ILE:HD11	2:AU:113:LEU:HD12	1.89	0.55
3:BS:121:LEU:HD11	3:BS:136:ILE:HD11	1.89	0.55
1:AD:266:ILE:HD13	1:AD:276:ILE:HD12	1.87	0.55
2:AT:211:LEU:HD13	2:AT:220:LEU:HD21	1.89	0.55
1:AA:10:THR:HG21	1:AA:112:PHE:HE1	1.71	0.55
3:BG:13:ASN:HA	3:BI:9:ARG:NH2	2.22	0.55
3:BB:95:SER:HB2	3:BF:143:GLN:HE22	99.00	0.55
1:AC:10:THR:HG21	1:AC:112:PHE:HE1	1.71	0.55
1:AI:169:GLU:O	1:AI:176:VAL:HG22	2.07	0.55
3:BK:125:MET:HB2	3:BK:130:ASN:HB2	1.96	0.54
1:AD:299:ALA:O	1:AF:154:LYS:HE2	2.07	0.54
1:AL:147:ASN:HA	1:AL:150:ILE:HG22	1.89	0.54
1:AC:193:PRO:HB3	1:AC:254:GLU:O	2.07	0.54
3:BA:13:ASN:HA	3:BC:9:ARG:NH2	2.23	0.54
1:AB:23:ARG:HB2	1:AB:30:GLN:HE22	1.72	0.54
3:BV:125:MET:HB2	3:BV:130:ASN:HB2	1.88	0.54
3:BD:128:GLY:HA2	3:BF:147:PRO:HG3	1.90	0.54
3:BJ:121:LEU:HD11	3:BJ:136:ILE:HD11	1.89	0.54
1:AR:243:SER:HB3	1:AR:254:GLU:HB3	1.90	0.54
1:AO:15:ASN:ND2	2:AW:33:GLU:OE2	2.40	0.54
1:AB:179:ALA:O	1:AB:182:ILE:HG13	2.07	0.54
1:AA:110:GLU:HB2	1:AC:29:SER:HB3	1.89	0.54
3:BD:121:LEU:HD11	3:BD:136:ILE:HD11	1.90	0.54
3:BH:95:SER:HB2	3:BW:143:GLN:HE22	1.72	0.54
1:AI:261:LEU:HD11	1:AI:277:LYS:HB3	1.89	0.54
1:AD:191:LYS:HZ1	1:AE:243:SER:HB2	1.73	0.54
3:BY:125:MET:HB2	3:BY:130:ASN:HB2	1.90	0.54
1:AA:266:ILE:HD13	1:AA:276:ILE:HD12	1.89	0.54
3:BH:125:MET:HB2	3:BH:130:ASN:HB2	1.95	0.53
3:BX:125:MET:HB2	3:BX:130:ASN:HB2	1.90	0.53
1:AG:63:GLY:HA3	1:AG:90:PHE:HE2	1.74	0.53
3:BL:9:ARG:HH22	3:BM:13:ASN:HA	88.78	0.53
3:BB:125:MET:HB2	3:BB:130:ASN:HB2	2.46	0.53
3:BB:121:LEU:HD11	3:BB:136:ILE:HD11	2.26	0.53
1:AA:10:THR:OG1	1:AA:38:GLU:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:36:ILE:HD11	1:AN:79:LEU:HD23	1.89	0.53
3:BM:121:LEU:HD11	3:BM:136:ILE:HD11	1.90	0.53
3:BT:125:MET:HB2	3:BT:130:ASN:HB2	1.96	0.53
1:AI:266:ILE:HD13	1:AI:276:ILE:HD12	1.89	0.53
3:BE:13:ASN:HA	3:BG:9:ARG:HH21	96.79	0.53
2:AW:127:VAL:HG23	2:AW:134:ILE:HD13	1.72	0.53
3:BJ:125:MET:HB2	3:BJ:130:ASN:HB2	1.90	0.53
3:BM:125:MET:HB2	3:BM:130:ASN:HB2	1.91	0.53
3:BR:125:MET:HB2	3:BR:130:ASN:HB2	1.91	0.53
1:AC:266:ILE:HD13	1:AC:276:ILE:HD12	1.89	0.53
1:AL:266:ILE:HD13	1:AL:276:ILE:HD12	1.88	0.53
3:BQ:125:MET:HB2	3:BQ:130:ASN:HB2	1.96	0.53
1:AK:267:LEU:HD23	1:AK:268:ILE:O	2.08	0.53
3:BA:118:ARG:HD3	3:BA:135:ASP:OD2	2.09	0.53
1:AE:23:ARG:H	1:AE:30:GLN:HE22	1.57	0.53
2:AW:127:VAL:CG2	2:AW:134:ILE:HD13	2.34	0.53
3:BE:125:MET:HB2	3:BE:130:ASN:HB2	1.96	0.53
1:AL:16:ASN:HB3	1:AL:118:HIS:CE1	2.44	0.53
1:AC:219:ILE:HD13	1:AC:233:GLY:HA2	1.90	0.53
3:BA:133:HIS:CD2	3:BB:124:HIS:ND1	2.76	0.52
3:BD:125:MET:HB2	3:BD:130:ASN:HB2	1.90	0.52
3:BE:117:ASN:OD1	3:BE:164:SER:HB3	2.71	0.52
3:BE:163:ASP:O	3:BE:164:SER:HB2	4.28	0.52
3:BV:121:LEU:HD11	3:BV:136:ILE:HD11	1.92	0.52
3:BW:125:MET:HB2	3:BW:130:ASN:HB2	1.96	0.52
3:BC:7:VAL:HG13	3:BC:11:MET:CE	2.39	0.52
3:BL:125:MET:HB2	3:BL:130:ASN:HB2	1.90	0.52
1:AR:214:SER:HG	1:AR:259:TYR:HE1	1.56	0.52
1:AH:274:LEU:HD11	3:BP:8:TYR:CE2	222.88	0.52
1:AI:16:ASN:HB3	1:AI:118:HIS:CE1	2.44	0.52
1:AN:36:ILE:HD13	1:AN:100:PHE:CZ	2.44	0.52
3:BD:62:LEU:HD12	3:BD:82:LYS:HE2	5.62	0.52
3:BG:125:MET:HB2	3:BG:130:ASN:HB2	1.92	0.52
3:BP:125:MET:HB2	3:BP:130:ASN:HB2	1.90	0.52
1:AI:36:ILE:HG22	1:AI:43:LYS:HB3	1.92	0.52
1:AL:15:ASN:ND2	2:AX:33:GLU:OE2	2.39	0.52
1:AJ:219:ILE:HD13	3:BZ:14:GLY:HA3	1.91	0.52
2:AW:253:LEU:OXT	2:AX:96:LYS:CE	2.58	0.52
3:BS:125:MET:HB2	3:BS:130:ASN:HB2	1.91	0.52
1:AO:266:ILE:HD13	1:AO:276:ILE:HD12	1.91	0.52
3:BB:64:THR:HA	3:BB:81:LYS:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:54:LEU:HB3	1:AD:65:SER:HB3	1.92	0.52
1:AM:120:ILE:HD12	2:AX:17:PRO:HG3	1.92	0.52
1:AE:1:MET:HA	1:AE:28:ASN:HB3	1.92	0.52
3:BQ:43:THR:HG23	3:BS:49:THR:HB	167.92	0.52
1:AC:10:THR:HG21	1:AC:112:PHE:CE1	2.45	0.52
3:B2:125:MET:HB2	3:B2:130:ASN:HB2	1.90	0.52
1:AB:10:THR:HG21	1:AB:112:PHE:HE1	1.74	0.52
2:AW:173:PHE:HB2	2:AW:201:GLU:HB2	1.91	0.52
3:BF:125:MET:HB2	3:BF:130:ASN:HB2	1.91	0.52
1:AH:23:ARG:H	1:AH:30:GLN:HE22	1.56	0.52
3:BA:35:VAL:HG22	3:BA:37:HIS:CE1	2.44	0.52
1:AK:177:LEU:HD11	1:AL:178:LEU:HD23	1.92	0.51
2:AT:171:LEU:HD11	2:AT:229:ILE:HD11	1.92	0.51
1:AL:198:PHE:HB3	1:AL:253:VAL:HG23	1.92	0.51
3:BG:13:ASN:HA	3:BI:9:ARG:HH21	1.76	0.51
3:BA:7:VAL:HG13	3:BA:11:MET:CE	2.40	0.51
1:AH:91:VAL:HG11	1:AH:123:LYS:HG3	1.92	0.51
1:AP:181:VAL:HA	1:AP:184:ILE:HG22	1.92	0.51
1:AA:157:TRP:HZ3	1:AB:161:VAL:HG23	1.76	0.51
3:BD:13:ASN:HA	3:BF:9:ARG:NH2	2.25	0.51
1:AA:205:GLU:OE2	1:AA:248:ARG:HD3	2.10	0.51
1:AK:195:GLY:HA3	1:AK:257:LYS:HG2	1.92	0.51
3:BJ:25:ILE:HG23	3:BK:29:LEU:HD11	1.93	0.51
2:AX:24:MET:HE2	2:AX:107:ILE:HG12	1.93	0.51
3:BD:11:MET:HE3	3:BD:14:GLY:HA2	1.93	0.51
1:AN:23:ARG:HB2	1:AN:26:ASP:HB2	1.93	0.51
1:AR:86:ASN:O	1:AR:89:GLN:HG2	2.11	0.51
1:AR:93:ARG:HA	1:AR:120:ILE:HG22	1.92	0.51
1:AA:12:GLU:OE2	2:AU:150:LYS:HE2	2.11	0.51
1:AC:147:ASN:HA	1:AC:150:ILE:HG22	1.93	0.51
3:BD:78:SER:HB2	3:BD:89:SER:HB3	2.04	0.51
1:AH:177:LEU:HD11	1:AI:177:LEU:HD22	1.93	0.51
3:BZ:125:MET:HB2	3:BZ:130:ASN:HB2	1.93	0.51
1:AR:101:ARG:HH11	1:AR:108:TRP:HE1	1.57	0.50
1:AO:205:GLU:OE2	1:AO:248:ARG:HD3	2.11	0.50
3:BV:78:SER:HB2	3:BV:89:SER:HB3	2.04	0.50
3:BR:78:SER:HB2	3:BR:89:SER:HB3	1.93	0.50
1:AQ:163:ALA:HB3	1:AR:182:ILE:HD11	1.93	0.50
1:AL:205:GLU:OE2	1:AL:248:ARG:HD3	2.12	0.50
3:BW:62:LEU:HD12	3:BW:82:LYS:HE3	1.92	0.50
1:AA:245:SER:HB3	1:AA:252:TYR:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BP:13:ASN:HA	3:BR:9:ARG:NH2	2.24	0.50
3:BM:78:SER:HB2	3:BM:89:SER:HB3	2.05	0.50
1:AN:14:ASN:HB3	1:AN:17:ILE:HD12	1.92	0.50
1:AM:274:LEU:HD11	3:BI:8:TYR:CE2	165.34	0.50
1:AB:103:GLN:HG3	1:AB:108:TRP:CD2	2.46	0.50
1:AF:15:ASN:HB2	1:AG:21:LYS:NZ	2.26	0.50
3:BU:125:MET:HB2	3:BU:130:ASN:HB2	1.91	0.50
3:B2:78:SER:HB2	3:B2:89:SER:HB3	1.94	0.50
3:BX:78:SER:HB2	3:BX:89:SER:HB3	1.94	0.50
1:AK:164:ASN:ND2	1:AL:182:ILE:HD13	2.26	0.50
3:BI:125:MET:HB2	3:BI:130:ASN:HB2	1.92	0.50
1:AB:91:VAL:HG11	1:AB:123:LYS:HG3	1.93	0.50
3:BB:133:HIS:CD2	3:BC:124:HIS:ND1	2.76	0.50
1:AA:219:ILE:HD13	3:BC:14:GLY:HA3	48.48	0.50
1:AE:104:GLU:HB3	1:AE:109:ILE:HD12	1.93	0.50
3:BV:57:ASN:HB2	3:BW:51:THR:HA	1.92	0.50
1:AF:24:HIS:CG	1:AF:127:SER:HB3	2.47	0.50
3:BA:78:SER:HB2	3:BA:89:SER:HB3	2.50	0.50
3:BU:78:SER:HB2	3:BU:89:SER:HB3	1.94	0.50
1:AB:110:GLU:OE2	1:AB:113:SER:HB3	2.12	0.50
3:BN:103:ASN:HD21	3:BN:141:VAL:CG1	2.24	0.50
3:BG:25:ILE:HG23	3:BH:29:LEU:HD11	1.93	0.50
3:BM:29:LEU:HD11	3:BO:25:ILE:HG23	1.94	0.50
1:AA:146:PHE:CD2	1:AB:150:ILE:HD12	2.47	0.50
1:AN:141:GLU:HA	1:AN:144:ARG:HG2	1.94	0.50
1:AA:73:ASP:OD2	1:AA:76:ASN:HB2	2.11	0.50
1:AF:268:ILE:HB	1:AF:272:THR:HG23	1.94	0.50
1:AC:73:ASP:OD2	1:AC:76:ASN:HB2	2.12	0.50
2:AV:46:ARG:O	2:AW:96:LYS:NZ	2.44	0.49
1:AA:188:VAL:HA	1:AA:192:VAL:HG12	1.93	0.49
3:BB:7:VAL:HG13	3:BB:11:MET:HE2	1.94	0.49
3:BJ:78:SER:HB2	3:BJ:89:SER:HB3	2.05	0.49
1:AC:205:GLU:OE2	1:AC:248:ARG:HD3	2.11	0.49
1:AN:50:PRO:HG2	1:AN:69:VAL:HB	1.94	0.49
1:AO:112:PHE:HB3	1:AP:29:SER:HB3	1.93	0.49
1:AH:50:PRO:HG2	1:AH:69:VAL:HB	1.93	0.49
3:BG:78:SER:HB2	3:BG:89:SER:HB3	2.04	0.49
1:AO:167:ILE:HA	1:AO:171:ILE:HD12	1.94	0.49
1:AF:23:ARG:HG3	1:AF:24:HIS:N	2.27	0.49
1:AC:192:VAL:O	1:AC:256:PRO:HG3	2.11	0.49
3:BQ:25:ILE:HG23	3:BR:29:LEU:HD11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AV:171:LEU:HB2	2:AV:203:ASP:HB2	1.93	0.49
3:BP:118:ARG:HG2	3:BP:137:PRO:HA	1.95	0.49
2:AU:171:LEU:HB2	2:AU:203:ASP:HB2	1.92	0.49
2:AS:188:ARG:O	2:AS:226:PHE:CD2	2.58	0.49
3:BE:29:LEU:HD11	3:BG:25:ILE:HG23	82.74	0.49
3:BD:13:ASN:HA	3:BF:9:ARG:HH21	1.78	0.49
3:BC:118:ARG:HD3	3:BC:135:ASP:OD2	2.12	0.49
1:AG:102:LYS:HG2	1:AG:109:ILE:HB	1.93	0.49
1:AQ:50:PRO:HG2	1:AQ:69:VAL:HB	1.95	0.49
1:AA:202:HIS:HD2	1:AA:204:SER:H	1.57	0.49
1:AH:267:LEU:HD23	1:AH:268:ILE:O	2.13	0.49
1:AP:54:LEU:HB3	1:AP:65:SER:HB3	1.94	0.49
1:AQ:267:LEU:HD23	1:AQ:268:ILE:O	2.13	0.49
1:AL:58:GLU:HG3	1:AL:58:GLU:O	2.13	0.49
1:AF:104:GLU:HB2	1:AF:109:ILE:HD11	1.95	0.49
1:AA:12:GLU:O	1:AA:115:ARG:CD	2.55	0.49
3:BY:78:SER:HB2	3:BY:89:SER:HB3	2.05	0.49
1:AO:24:HIS:CG	1:AO:127:SER:HB3	2.47	0.49
1:AN:167:ILE:HD11	1:AO:178:LEU:CD1	2.42	0.49
1:AG:171:ILE:HD11	1:AH:177:LEU:HG	1.95	0.49
3:BR:11:MET:HE3	3:BR:14:GLY:HA2	2.05	0.49
1:AB:257:LYS:O	1:AB:260:THR:HG22	2.13	0.49
3:BW:57:ASN:HB2	3:BX:51:THR:HA	1.97	0.49
1:AP:56:ALA:HB2	1:AP:64:VAL:HG22	1.94	0.49
1:AC:169:GLU:HG3	1:AC:176:VAL:HG23	1.94	0.49
1:AC:202:HIS:HD2	1:AC:204:SER:H	1.60	0.49
1:AN:267:LEU:HD23	1:AN:268:ILE:O	2.12	0.49
2:AT:127:VAL:HG23	2:AT:134:ILE:CD1	2.43	0.49
1:AB:146:PHE:HD1	1:AC:150:ILE:HG13	1.77	0.49
1:AK:50:PRO:HG2	1:AK:69:VAL:HB	1.94	0.49
1:AF:169:GLU:O	1:AF:176:VAL:HG22	2.12	0.49
3:BL:57:ASN:HB2	3:BM:51:THR:HA	75.51	0.49
3:BA:124:HIS:ND1	3:BC:133:HIS:CD2	2.77	0.49
1:AJ:177:LEU:CD1	1:AL:177:LEU:HD11	2.43	0.49
1:AA:101:ARG:HD2	1:AA:108:TRP:CE2	2.48	0.49
3:BK:25:ILE:HG23	3:BL:29:LEU:HD11	1.99	0.49
1:AM:50:PRO:HB3	1:AM:100:PHE:CE2	2.48	0.49
3:BY:11:MET:HE3	3:BY:14:GLY:HA2	1.93	0.49
1:AC:19:ILE:HG12	1:AC:118:HIS:HB2	1.95	0.48
3:BS:29:LEU:HD11	3:BU:25:ILE:HG23	1.94	0.48
1:AJ:190:GLU:HG3	1:AJ:191:LYS:HD2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BG:11:MET:HE3	3:BG:14:GLY:HA2	1.95	0.48
2:AS:96:LYS:CE	2:AX:253:LEU:OXT	2.61	0.48
3:BQ:61:THR:HB	3:BR:55:GLU:HG3	2.03	0.48
2:AW:182:ALA:HB3	2:AW:189:LEU:HB3	1.94	0.48
1:AJ:11:THR:HB	2:AX:150:LYS:NZ	2.27	0.48
3:BN:128:GLY:HA2	3:BP:147:PRO:HG3	64.14	0.48
3:BT:29:LEU:HD11	3:BV:25:ILE:HG23	105.93	0.48
1:AK:125:ILE:HG23	1:AK:126:TYR:CD1	2.48	0.48
1:AK:168:LEU:HA	1:AK:173:PRO:HG3	1.96	0.48
1:AE:267:LEU:HD23	1:AE:268:ILE:O	2.14	0.48
3:BA:101:ASN:HA	3:BA:144:TRP:O	2.14	0.48
1:AD:181:VAL:HA	1:AD:184:ILE:HG22	1.95	0.48
1:AG:11:THR:HB	2:AS:150:LYS:HZ3	1.78	0.48
3:BH:29:LEU:HD11	3:BJ:25:ILE:HG23	78.23	0.48
3:BO:125:MET:HB2	3:BO:130:ASN:HB2	1.95	0.48
3:BA:51:THR:HA	3:BZ:57:ASN:HB2	168.55	0.48
3:BC:57:ASN:HB2	3:BD:51:THR:HA	74.35	0.48
3:BU:80:ARG:HH12	3:BU:82:LYS:HE3	1.78	0.48
3:BL:78:SER:HB2	3:BL:89:SER:HB3	1.94	0.48
3:BD:73:GLY:HA3	3:BD:98:ILE:HD11	1.95	0.48
1:AL:268:ILE:HB	1:AL:272:THR:HG23	1.96	0.48
3:BP:78:SER:HB2	3:BP:89:SER:HB3	2.04	0.48
3:BT:57:ASN:HB2	3:BU:51:THR:HA	1.94	0.48
1:AC:202:HIS:HB2	1:AC:286:MET:HE3	1.96	0.48
3:BH:57:ASN:HB2	3:BI:51:THR:HA	1.99	0.48
3:BE:11:MET:HE3	3:BE:14:GLY:HA2	2.02	0.48
1:AO:27:VAL:HG12	1:AO:28:ASN:HD22	1.78	0.48
3:BW:29:LEU:HD11	3:BY:25:ILE:HG23	181.21	0.48
3:BZ:29:LEU:HD11	3:B2:25:ILE:HG23	231.54	0.48
3:BF:78:SER:HB2	3:BF:89:SER:HB3	1.94	0.48
1:AM:146:PHE:HZ	1:AO:157:TRP:HB2	1.78	0.48
1:AE:50:PRO:HG2	1:AE:69:VAL:HB	1.94	0.48
1:AI:268:ILE:HB	1:AI:272:THR:HG23	1.96	0.48
3:BT:25:ILE:HG23	3:BU:29:LEU:HD11	2.00	0.48
3:BS:78:SER:HB2	3:BS:89:SER:HB3	2.05	0.48
1:AA:49:GLN:HE21	1:AA:50:PRO:CD	2.22	0.48
1:AJ:11:THR:HB	2:AX:150:LYS:HZ3	1.79	0.48
3:BZ:25:ILE:HG23	3:B1:29:LEU:HD11	233.96	0.48
1:AC:219:ILE:CD1	1:AC:233:GLY:HA2	2.44	0.48
3:BF:11:MET:HE3	3:BF:14:GLY:HA2	2.08	0.47
3:BA:35:VAL:HG22	3:BA:37:HIS:NE2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BS:57:ASN:HB2	3:BT:51:THR:HA	1.95	0.47
3:BR:57:ASN:HB2	3:BS:51:THR:HA	156.85	0.47
1:AI:181:VAL:HA	1:AI:184:ILE:HG22	1.95	0.47
3:BT:73:GLY:HA3	3:BT:98:ILE:HD11	2.06	0.47
3:BD:57:ASN:HB2	3:BE:51:THR:HA	1.96	0.47
1:AM:48:LEU:HG	1:AM:102:LYS:HB2	1.96	0.47
3:BB:145:PHE:O	3:BC:124:HIS:HE1	1.97	0.47
3:BG:57:ASN:HB2	3:BH:51:THR:HA	1.96	0.47
3:BE:57:ASN:HB2	3:BF:51:THR:HA	1.98	0.47
1:AG:50:PRO:HG2	1:AG:69:VAL:HB	1.94	0.47
1:AF:245:SER:OG	1:AF:252:TYR:HB2	2.15	0.47
3:BI:78:SER:HB2	3:BI:89:SER:HB3	1.96	0.47
1:AO:268:ILE:HB	1:AO:272:THR:HG23	1.95	0.47
1:AK:125:ILE:HG23	1:AK:126:TYR:H	1.79	0.47
3:BV:29:LEU:HD11	3:BX:25:ILE:HG23	1.97	0.47
3:BE:78:SER:HB2	3:BE:89:SER:HB3	1.97	0.47
3:BO:78:SER:HB2	3:BO:89:SER:HB3	1.95	0.47
3:BN:73:GLY:HA3	3:BN:98:ILE:HD11	2.06	0.47
3:BU:11:MET:HE3	3:BU:14:GLY:HA2	2.08	0.47
2:AU:182:ALA:HB3	2:AU:189:LEU:HB3	1.97	0.47
1:AE:164:ASN:OD1	1:AF:182:ILE:HD13	2.14	0.47
3:BH:73:GLY:HA3	3:BH:98:ILE:HD11	2.07	0.47
1:AB:13:PRO:CA	1:AB:115:ARG:HE	2.13	0.47
3:BB:29:LEU:HD11	3:BD:25:ILE:HG23	80.12	0.47
3:BC:125:MET:HB2	3:BC:130:ASN:HB2	2.46	0.47
3:BY:57:ASN:HB2	3:BZ:51:THR:HA	1.97	0.47
3:BQ:29:LEU:HD11	3:BS:25:ILE:HG23	178.51	0.47
3:BM:73:GLY:HA3	3:BM:98:ILE:HD11	1.96	0.47
2:AX:44:GLU:HB2	2:AX:75:THR:HG23	1.96	0.47
1:AI:205:GLU:OE2	1:AI:248:ARG:HD3	2.15	0.47
1:AO:14:ASN:HB3	1:AO:17:ILE:HG13	1.97	0.47
3:BB:118:ARG:HD3	3:BB:135:ASP:OD2	2.13	0.47
1:AR:268:ILE:HB	1:AR:272:THR:HG23	1.96	0.47
1:AA:11:THR:HB	2:AU:150:LYS:NZ	2.30	0.47
2:AS:253:LEU:OXT	2:AT:96:LYS:CE	2.63	0.47
2:AT:188:ARG:O	2:AT:226:PHE:CD2	2.57	0.47
3:BB:73:GLY:HA3	3:BB:98:ILE:HD11	2.16	0.47
3:BW:73:GLY:HA3	3:BW:98:ILE:HD11	2.05	0.47
1:AB:205:GLU:OE2	1:AB:248:ARG:HD3	2.14	0.47
3:BI:11:MET:HE3	3:BI:14:GLY:HA2	1.97	0.47
3:BS:61:THR:HB	3:BT:55:GLU:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BD:29:LEU:HD11	3:BF:25:ILE:HG23	1.97	0.47
1:AG:56:ALA:HB2	1:AG:64:VAL:HG22	1.96	0.47
3:BH:25:ILE:HG23	3:BI:29:LEU:HD11	1.96	0.47
3:BJ:11:MET:HE3	3:BJ:14:GLY:HA2	1.97	0.47
2:AS:182:ALA:HB3	2:AS:189:LEU:HB3	1.96	0.47
2:AT:84:ASP:OD2	2:AT:86:ARG:HG3	2.15	0.47
1:AM:102:LYS:HG2	1:AM:109:ILE:HD12	1.97	0.47
3:BY:25:ILE:HG23	3:BZ:29:LEU:HD11	1.97	0.47
1:AG:54:LEU:HB3	1:AG:65:SER:HB3	1.97	0.47
1:AJ:274:LEU:HD11	3:BZ:8:TYR:HE2	1.79	0.47
3:BB:5:LYS:HE3	3:BB:17:THR:HG23	1.97	0.47
1:AB:21:LYS:HG2	1:AB:120:ILE:CG2	2.45	0.47
1:AA:49:GLN:NE2	1:AA:50:PRO:HD2	2.21	0.47
1:AN:36:ILE:CD1	1:AN:100:PHE:HZ	2.28	0.47
1:AK:1:MET:HA	1:AK:28:ASN:HB3	1.97	0.47
3:B1:57:ASN:HB2	3:B2:51:THR:HA	1.97	0.47
3:BA:64:THR:HA	3:BA:81:LYS:O	2.15	0.47
3:BN:25:ILE:HG23	3:BO:29:LEU:HD11	2.00	0.47
3:BN:29:LEU:HD11	3:BP:25:ILE:HG23	78.66	0.46
3:BN:57:ASN:HB2	3:BO:51:THR:HA	1.97	0.46
1:AD:205:GLU:OE2	1:AD:248:ARG:HD3	2.15	0.46
3:BZ:73:GLY:HA3	3:BZ:98:ILE:HD11	2.07	0.46
1:AR:205:GLU:OE2	1:AR:248:ARG:HD3	2.15	0.46
3:BC:101:ASN:HA	3:BC:144:TRP:O	2.15	0.46
1:AM:134:ASN:HD22	1:AM:134:ASN:H	1.63	0.46
3:BQ:11:MET:HE3	3:BQ:14:GLY:HA2	2.03	0.46
1:AG:11:THR:HB	2:AS:150:LYS:NZ	2.30	0.46
3:BA:25:ILE:HG23	3:BY:29:LEU:HD11	175.92	0.46
1:AC:232:PHE:CZ	3:BC:18:ILE:HD11	2.50	0.46
2:AT:171:LEU:HB2	2:AT:203:ASP:HB2	1.97	0.46
3:BI:57:ASN:HB2	3:BJ:51:THR:HA	69.96	0.46
3:B1:125:MET:HB2	3:B1:130:ASN:HB2	1.96	0.46
1:AJ:146:PHE:HZ	1:AL:157:TRP:HB2	1.79	0.46
1:AM:205:GLU:OE2	1:AM:248:ARG:HD3	2.16	0.46
3:BP:64:THR:CG2	3:BP:80:ARG:HE	2.28	0.46
1:AL:102:LYS:HG2	1:AL:109:ILE:HD12	1.97	0.46
1:AG:165:ARG:HH22	1:AI:171:ILE:CG2	2.28	0.46
2:AX:182:ALA:HB3	2:AX:189:LEU:HB3	1.97	0.46
1:AP:22:LEU:HD11	1:AP:119:TYR:CD1	2.50	0.46
3:BP:73:GLY:HA3	3:BP:98:ILE:HD11	1.96	0.46
1:AD:165:ARG:HH22	1:AF:171:ILE:CG2	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B1:78:SER:HB2	3:B1:89:SER:HB3	1.98	0.46
3:BT:78:SER:HB2	3:BT:89:SER:HB3	1.98	0.46
1:AN:167:ILE:HG12	1:AN:168:LEU:H	1.80	0.46
3:BJ:29:LEU:HD11	3:BL:25:ILE:HG23	1.96	0.46
3:BC:7:VAL:HG13	3:BC:11:MET:HE1	1.98	0.46
3:BP:25:ILE:HG23	3:BQ:29:LEU:HD11	1.97	0.46
3:BO:57:ASN:HB2	3:BP:51:THR:HA	70.38	0.46
1:AC:268:ILE:HB	1:AC:272:THR:HG23	1.97	0.46
2:AT:182:ALA:HB3	2:AT:189:LEU:HB3	1.97	0.46
3:BK:57:ASN:HB2	3:BL:51:THR:HA	1.98	0.46
2:AS:188:ARG:NH1	2:AS:190:LYS:HE3	2.30	0.46
3:BK:29:LEU:HD11	3:BM:25:ILE:HG23	83.82	0.46
1:AB:146:PHE:O	1:AB:150:ILE:HG12	2.14	0.46
3:BK:73:GLY:HA3	3:BK:98:ILE:HD11	2.07	0.46
3:BP:57:ASN:HB2	3:BQ:51:THR:HA	1.96	0.46
3:BN:78:SER:HB2	3:BN:89:SER:HB3	1.97	0.46
1:AQ:205:GLU:OE2	1:AQ:248:ARG:HD3	2.16	0.46
3:BG:29:LEU:HD11	3:BI:25:ILE:HG23	1.98	0.46
3:BA:51:THR:HA	3:BC:57:ASN:HB2	1.98	0.46
3:BV:73:GLY:HA3	3:BV:98:ILE:HD11	1.97	0.46
3:BG:73:GLY:HA3	3:BG:98:ILE:HD11	1.98	0.46
1:AF:205:GLU:OE2	1:AF:248:ARG:HD3	2.15	0.46
1:AB:73:ASP:OD2	1:AB:76:ASN:HB2	2.15	0.46
3:BH:11:MET:HE3	3:BH:14:GLY:HA2	2.01	0.46
1:AA:15:ASN:ND2	1:AA:15:ASN:H	2.08	0.46
3:BC:25:ILE:HG23	3:BD:29:LEU:HD11	77.19	0.46
3:BB:7:VAL:HG13	3:BB:11:MET:CE	2.45	0.46
1:AA:101:ARG:HD3	1:AA:111:GLN:NE2	2.31	0.46
3:BY:73:GLY:HA3	3:BY:98:ILE:HD11	1.97	0.46
1:AG:146:PHE:HZ	1:AI:157:TRP:HB2	1.81	0.46
2:AS:188:ARG:HH12	2:AS:190:LYS:HE3	1.80	0.46
3:BM:57:ASN:HB2	3:BN:51:THR:HA	1.97	0.46
1:AG:192:VAL:O	1:AG:256:PRO:HG3	2.16	0.46
2:AX:188:ARG:O	2:AX:226:PHE:CD2	2.58	0.46
3:BM:26:ASN:HA	3:BM:29:LEU:HD12	1.97	0.46
1:AA:48:LEU:HD23	1:AA:102:LYS:HB2	1.97	0.46
3:BW:25:ILE:HG23	3:BX:29:LEU:HD11	1.98	0.46
3:BF:26:ASN:HA	3:BF:29:LEU:HD12	1.98	0.46
2:AU:188:ARG:O	2:AU:226:PHE:CD2	2.55	0.46
1:AC:16:ASN:HB3	1:AC:118:HIS:CE1	2.45	0.46
1:AB:276:ILE:HG12	1:AB:281:VAL:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:205:GLU:OE2	1:AG:248:ARG:HD3	2.16	0.46
3:BY:61:THR:HB	3:BZ:55:GLU:HG3	1.98	0.46
1:AN:179:ALA:O	1:AN:182:ILE:HG13	2.16	0.46
3:BB:57:ASN:HB2	3:BC:51:THR:HA	2.01	0.46
3:BQ:73:GLY:HA3	3:BQ:98:ILE:HD11	2.09	0.46
1:AC:16:ASN:HB2	2:AU:30:TRP:HZ2	1.82	0.45
3:BD:26:ASN:HA	3:BD:29:LEU:HD12	2.00	0.45
3:BJ:57:ASN:HB2	3:BK:51:THR:HA	1.96	0.45
3:BN:51:THR:HA	3:BP:57:ASN:HB2	57.95	0.45
1:AM:185:GLU:HB3	1:AO:184:ILE:HD11	1.98	0.45
2:AV:45:GLY:O	2:AV:72:ARG:HD2	2.16	0.45
1:AD:15:ASN:H	1:AD:15:ASN:ND2	2.13	0.45
3:BZ:11:MET:HE3	3:BZ:14:GLY:HA2	2.05	0.45
1:AB:165:ARG:NH2	1:AB:170:SER:OG	2.49	0.45
1:AJ:56:ALA:HB2	1:AJ:64:VAL:HG22	1.98	0.45
1:AR:168:LEU:HD12	1:AR:179:ALA:HB2	1.99	0.45
1:AP:177:LEU:CD1	1:AQ:181:VAL:HG11	2.39	0.45
2:AU:253:LEU:OXT	2:AV:96:LYS:HE3	2.16	0.45
3:BV:130:ASN:HA	3:BW:129:TRP:HB3	1.98	0.45
3:BU:130:ASN:HA	3:BV:129:TRP:HB3	81.07	0.45
3:BE:130:ASN:HA	3:BF:129:TRP:HB3	1.98	0.45
3:BW:130:ASN:HA	3:BX:129:TRP:HB3	1.99	0.45
3:BL:130:ASN:HA	3:BM:129:TRP:HB3	65.42	0.45
1:AB:10:THR:HG21	1:AB:112:PHE:CE1	2.50	0.45
3:BV:25:ILE:HG23	3:BW:29:LEU:HD11	1.98	0.45
1:AJ:274:LEU:HD11	3:BZ:8:TYR:CE2	2.52	0.45
3:BO:26:ASN:HA	3:BO:29:LEU:HD12	1.98	0.45
1:AL:169:GLU:O	1:AL:176:VAL:HG22	2.16	0.45
1:AD:103:GLN:HG2	1:AD:108:TRP:HD1	1.81	0.45
2:AW:171:LEU:HD11	2:AW:229:ILE:HD11	1.98	0.45
3:BD:25:ILE:HG23	3:BE:29:LEU:HD11	1.97	0.45
3:BP:26:ASN:HA	3:BP:29:LEU:HD12	2.00	0.45
3:BS:26:ASN:HA	3:BS:29:LEU:HD12	2.01	0.45
1:AO:15:ASN:HB2	1:AP:21:LYS:NZ	2.32	0.45
1:AH:36:ILE:HG13	1:AH:100:PHE:HZ	1.81	0.45
1:AF:225:GLY:HA3	3:BE:10:GLY:HA2	1.99	0.45
3:BH:78:SER:HB2	3:BH:89:SER:HB3	1.97	0.45
1:AG:164:ASN:ND2	1:AH:168:LEU:HD23	2.30	0.45
3:BC:130:ASN:HA	3:BD:129:TRP:HB3	62.59	0.45
3:BF:57:ASN:HB2	3:BG:51:THR:HA	74.18	0.45
3:BL:26:ASN:HA	3:BL:29:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BS:25:ILE:HG23	3:BT:29:LEU:HD11	1.98	0.45
1:AM:219:ILE:HD13	3:BI:14:GLY:HA3	179.77	0.45
3:BI:26:ASN:HA	3:BI:29:LEU:HD12	1.98	0.45
3:BE:73:GLY:HA3	3:BE:98:ILE:HD11	2.05	0.45
1:AM:194:ALA:H	1:AM:256:PRO:HA	1.82	0.45
3:B1:130:ASN:HA	3:B2:129:TRP:HB3	1.98	0.45
1:AQ:195:GLY:HA3	1:AQ:257:LYS:HG3	1.98	0.45
1:AA:1:MET:HB2	1:AA:29:SER:O	2.16	0.45
3:BJ:95:SER:HB2	3:BP:143:GLN:NE2	122.58	0.45
3:BU:25:ILE:HG23	3:BV:29:LEU:HD11	101.17	0.45
1:AA:112:PHE:HA	1:AC:26:ASP:OD2	2.17	0.45
1:AF:23:ARG:HB3	1:AF:26:ASP:OD2	2.16	0.45
3:BQ:130:ASN:HA	3:BR:129:TRP:HB3	1.99	0.45
3:BU:26:ASN:HA	3:BU:29:LEU:HD12	1.98	0.45
3:BE:25:ILE:HG23	3:BF:29:LEU:HD11	1.99	0.45
2:AW:171:LEU:HB2	2:AW:203:ASP:HB2	1.97	0.45
3:BV:11:MET:HE3	3:BV:14:GLY:HA2	1.99	0.45
3:BZ:78:SER:HB2	3:BZ:89:SER:HB3	1.99	0.45
1:AO:22:LEU:HD22	1:AO:30:GLN:HB3	1.99	0.45
3:BB:61:THR:HB	3:BC:55:GLU:HG3	2.71	0.45
1:AJ:168:LEU:O	1:AJ:171:ILE:HG22	2.16	0.45
2:AS:92:PHE:CZ	2:AS:134:ILE:CD1	2.96	0.45
3:BP:29:LEU:HD11	3:BR:25:ILE:HG23	1.99	0.45
3:BB:26:ASN:HA	3:BB:29:LEU:HD12	2.73	0.45
3:BG:26:ASN:HA	3:BG:29:LEU:HD12	2.00	0.45
3:BT:130:ASN:HA	3:BU:129:TRP:HB3	1.98	0.45
3:BZ:130:ASN:HA	3:B1:129:TRP:HB3	210.04	0.45
3:BG:51:THR:HA	3:BI:57:ASN:HB2	1.99	0.45
3:BX:57:ASN:HB2	3:BY:51:THR:HA	154.46	0.45
1:AO:16:ASN:HB3	1:AO:118:HIS:HE1	1.81	0.45
1:AR:166:GLU:O	1:AR:170:SER:HB2	2.17	0.45
1:AN:205:GLU:OE2	1:AN:248:ARG:HD3	2.17	0.45
1:AJ:12:GLU:OE1	2:AX:150:LYS:CE	2.61	0.45
3:BJ:26:ASN:HA	3:BJ:29:LEU:HD12	1.99	0.45
3:BY:130:ASN:HA	3:BZ:129:TRP:HB3	1.99	0.45
3:BH:130:ASN:HA	3:BI:129:TRP:HB3	1.99	0.45
3:BF:130:ASN:HA	3:BG:129:TRP:HB3	56.64	0.45
1:AO:16:ASN:HB3	1:AO:118:HIS:CE1	2.52	0.45
3:BZ:61:THR:HB	3:B1:55:GLU:HG3	228.82	0.45
1:AM:56:ALA:HB2	1:AM:64:VAL:HB	1.98	0.45
1:AA:10:THR:HG21	1:AA:112:PHE:CE1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BX:26:ASN:HA	3:BX:29:LEU:HD12	1.99	0.44
1:AI:26:ASP:CG	1:AI:30:GLN:HE21	2.21	0.44
1:AI:164:ASN:HA	1:AI:167:ILE:HD12	1.99	0.44
1:AK:36:ILE:HG13	1:AK:100:PHE:HZ	1.83	0.44
3:BG:61:THR:HB	3:BH:55:GLU:HG3	2.00	0.44
1:AB:207:GLN:NE2	3:BC:13:ASN:OD1	50.91	0.44
3:B1:25:ILE:HG23	3:B2:29:LEU:HD11	1.99	0.44
1:AP:149:TYR:CE1	1:AQ:154:LYS:HG2	2.52	0.44
3:BA:13:ASN:HA	3:BC:9:ARG:HH22	1.81	0.44
3:BD:130:ASN:HA	3:BE:129:TRP:HB3	1.99	0.44
3:BB:11:MET:HE3	3:BB:14:GLY:HA2	2.38	0.44
1:AK:205:GLU:OE2	1:AK:248:ARG:HD3	2.18	0.44
1:AA:95:GLU:HG3	1:AA:118:HIS:NE2	2.32	0.44
1:AM:11:THR:HB	2:AW:150:LYS:NZ	2.32	0.44
3:BC:26:ASN:HA	3:BC:29:LEU:HD12	2.76	0.44
3:BB:130:ASN:HA	3:BC:129:TRP:HB3	2.42	0.44
1:AL:15:ASN:HB2	1:AM:21:LYS:NZ	2.33	0.44
1:AD:146:PHE:O	1:AD:150:ILE:HG12	2.17	0.44
1:AQ:10:THR:HG22	1:AQ:114:THR:HA	1.99	0.44
1:AD:192:VAL:O	1:AD:256:PRO:HG3	2.18	0.44
1:AR:165:ARG:O	1:AR:169:GLU:HG2	2.18	0.44
3:BM:15:ALA:HB1	3:BO:7:VAL:HG12	1.99	0.44
1:AP:168:LEU:HB3	1:AR:172:ASP:OD1	2.18	0.44
1:AE:10:THR:HG22	1:AE:114:THR:HA	1.99	0.44
3:BA:26:ASN:HA	3:BA:29:LEU:HD12	2.74	0.44
1:AL:102:LYS:HB2	1:AL:102:LYS:HE2	1.84	0.44
1:AM:128:GLN:HB3	1:AN:126:TYR:CZ	2.53	0.44
1:AC:44:ASN:ND2	1:AC:46:GLU:OE2	2.50	0.44
3:BK:61:THR:HB	3:BL:55:GLU:HG3	2.02	0.44
1:AL:24:HIS:CG	1:AL:127:SER:HB3	2.53	0.44
3:BE:26:ASN:HA	3:BE:29:LEU:HD12	2.00	0.44
3:BX:25:ILE:HG23	3:BY:29:LEU:HD11	174.86	0.44
3:BM:130:ASN:HA	3:BN:129:TRP:HB3	2.00	0.44
3:BR:26:ASN:HA	3:BR:29:LEU:HD12	2.00	0.44
3:BH:9:ARG:HH22	3:BI:13:ASN:HA	3.27	0.44
1:AN:239:ASN:HD22	1:AO:244:LEU:HB2	1.82	0.44
3:BK:78:SER:HB2	3:BK:89:SER:HB3	1.98	0.44
3:BC:136:ILE:HG13	3:BC:142:CYS:SG	2.58	0.44
3:BF:25:ILE:HG23	3:BG:29:LEU:HD11	78.99	0.44
3:BK:26:ASN:HA	3:BK:29:LEU:HD12	2.00	0.44
3:BZ:57:ASN:HB2	3:B1:51:THR:HA	225.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:21:LYS:HG2	1:AB:120:ILE:HG23	2.00	0.44
3:BQ:78:SER:HB2	3:BQ:89:SER:HB3	1.99	0.44
3:BB:101:ASN:HA	3:BB:144:TRP:O	2.17	0.44
1:AH:10:THR:HG22	1:AH:114:THR:HA	1.99	0.44
3:BN:130:ASN:HA	3:BO:129:TRP:HB3	1.99	0.44
3:BG:130:ASN:HA	3:BH:129:TRP:HB3	1.99	0.44
3:BP:130:ASN:HA	3:BQ:129:TRP:HB3	2.00	0.44
3:BU:57:ASN:HB2	3:BV:51:THR:HA	90.47	0.44
3:B2:26:ASN:HA	3:B2:29:LEU:HD12	1.99	0.44
1:AG:31:ALA:HA	1:AG:82:VAL:HA	2.00	0.44
3:BQ:57:ASN:HB2	3:BR:51:THR:HA	1.99	0.44
1:AJ:213:THR:HG21	3:BZ:12:LYS:HE3	2.00	0.44
1:AD:50:PRO:HG2	1:AD:69:VAL:HB	1.99	0.44
3:BI:25:ILE:HG23	3:BJ:29:LEU:HD11	75.35	0.44
3:BV:26:ASN:HA	3:BV:29:LEU:HD12	2.01	0.44
3:BC:8:TYR:O	3:BC:11:MET:HB3	2.18	0.44
3:BM:129:TRP:HB3	3:BO:130:ASN:HA	2.00	0.44
1:AC:62:GLN:HG2	1:AE:125:ILE:HG22	2.00	0.44
1:AC:108:TRP:CH2	1:AE:125:ILE:HD11	2.53	0.44
3:BW:61:THR:HB	3:BX:55:GLU:HG3	2.05	0.44
2:AS:24:MET:HE2	2:AS:107:ILE:HG12	2.00	0.44
3:BS:73:GLY:HA3	3:BS:98:ILE:HD11	2.00	0.44
1:AH:239:ASN:HD22	1:AI:244:LEU:HB2	1.82	0.44
1:AG:274:LEU:HD11	3:BT:8:TYR:HE2	1.83	0.44
3:BD:61:THR:HB	3:BE:55:GLU:HG3	2.00	0.44
3:BT:26:ASN:HA	3:BT:29:LEU:HD12	2.00	0.44
3:BP:51:THR:HA	3:BR:57:ASN:HB2	2.00	0.44
1:AJ:22:LEU:HD22	1:AJ:30:GLN:HB3	1.99	0.44
1:AA:192:VAL:C	1:AA:256:PRO:HG3	2.38	0.43
3:BL:25:ILE:HG23	3:BM:29:LEU:HD11	80.47	0.43
3:BY:26:ASN:HA	3:BY:29:LEU:HD12	2.00	0.43
1:AP:171:ILE:HG12	1:AQ:177:LEU:CD1	2.48	0.43
3:BK:130:ASN:HA	3:BL:129:TRP:HB3	1.99	0.43
3:BI:130:ASN:HA	3:BJ:129:TRP:HB3	56.04	0.43
1:AJ:136:TRP:HB2	1:AL:142:LEU:HD11	1.99	0.43
3:BV:128:GLY:HA2	3:BX:147:PRO:HG3	2.00	0.43
3:BT:115:PRO:HA	3:BT:162:ILE:HG13	2.25	0.43
1:AA:44:ASN:ND2	1:AA:46:GLU:OE2	2.50	0.43
1:AK:184:ILE:HD11	1:AL:185:GLU:CG	2.48	0.43
3:BS:130:ASN:HA	3:BT:129:TRP:HB3	2.01	0.43
3:BX:130:ASN:HA	3:BY:129:TRP:HB3	143.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BD:13:ASN:HB3	3:BD:16:GLU:HB2	1.99	0.43
3:B2:99:LEU:HA	3:B2:148:THR:HG23	2.00	0.43
1:AH:205:GLU:OE2	1:AH:248:ARG:HD3	2.18	0.43
3:BA:147:PRO:HG3	3:BY:128:GLY:HA2	139.16	0.43
3:BT:51:THR:HA	3:BV:57:ASN:HB2	93.19	0.43
2:AX:171:LEU:HB2	2:AX:203:ASP:HB2	2.00	0.43
1:AK:239:ASN:HD22	1:AL:244:LEU:HB2	1.84	0.43
3:BP:61:THR:HB	3:BQ:55:GLU:HG3	2.01	0.43
1:AE:205:GLU:OE2	1:AE:248:ARG:HD3	2.18	0.43
3:BJ:130:ASN:HA	3:BK:129:TRP:HB3	2.00	0.43
3:BM:13:ASN:HB3	3:BM:16:GLU:HB2	2.00	0.43
1:AA:157:TRP:CZ3	1:AB:161:VAL:HG23	2.53	0.43
3:BS:11:MET:HE3	3:BS:14:GLY:HA2	1.99	0.43
1:AK:23:ARG:H	1:AK:30:GLN:HE22	1.66	0.43
1:AB:12:GLU:O	1:AB:115:ARG:CD	2.59	0.43
1:AN:36:ILE:HD11	1:AN:79:LEU:HD21	2.01	0.43
3:BR:130:ASN:HA	3:BS:129:TRP:HB3	134.23	0.43
3:BZ:26:ASN:HA	3:BZ:29:LEU:HD12	2.00	0.43
1:AM:237:ILE:HG21	3:BI:12:LYS:HE3	168.62	0.43
2:AV:50:SER:HB3	2:AW:123:THR:HG22	2.00	0.43
1:AO:132:ASP:HB3	1:AO:137:TRP:CD1	2.53	0.43
1:AR:192:VAL:O	1:AR:256:PRO:HG3	2.19	0.43
1:AE:195:GLY:HA3	1:AE:257:LYS:HB3	2.00	0.43
2:AW:135:ILE:O	2:AW:135:ILE:HG23	2.17	0.43
1:AQ:125:ILE:C	1:AQ:125:ILE:HD13	2.39	0.43
1:AB:13:PRO:HB3	1:AB:115:ARG:HH21	1.84	0.43
3:BO:130:ASN:HA	3:BP:129:TRP:HB3	50.85	0.43
1:AK:36:ILE:HD12	1:AK:114:THR:HG21	2.00	0.43
1:AB:242:VAL:HG12	1:AB:255:MET:HG2	1.99	0.43
1:AP:205:GLU:OE2	1:AP:248:ARG:HD3	2.19	0.43
3:BL:11:MET:HE3	3:BL:14:GLY:HA2	2.03	0.43
3:BV:13:ASN:HB3	3:BV:16:GLU:HB2	4.67	0.43
3:BJ:61:THR:HB	3:BK:55:GLU:HG3	2.01	0.43
1:AA:93:ARG:HB2	2:AV:15:ASN:HD22	1.84	0.43
1:AO:54:LEU:HB3	1:AO:65:SER:HB3	2.00	0.43
1:AP:192:VAL:O	1:AP:256:PRO:HG3	2.18	0.43
3:BV:129:TRP:HB3	3:BX:130:ASN:HA	2.00	0.43
1:AI:194:ALA:H	1:AI:256:PRO:HA	1.84	0.43
1:AC:223:THR:HG23	1:AC:279:THR:CG2	2.48	0.43
2:AS:105:VAL:HA	2:AS:106:PRO:HD3	1.90	0.43
1:AA:146:PHE:HZ	1:AC:157:TRP:HB2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BM:61:THR:HB	3:BN:55:GLU:HG3	2.00	0.43
1:AI:54:LEU:HB3	1:AI:65:SER:HB3	2.01	0.43
1:AJ:54:LEU:HB3	1:AJ:65:SER:HB2	2.01	0.43
1:AD:177:LEU:CD2	1:AE:181:VAL:HG21	2.48	0.43
2:AT:121:PHE:HA	2:AT:140:VAL:HG12	2.00	0.43
1:AF:54:LEU:HB3	1:AF:65:SER:HB3	2.01	0.43
3:BT:61:THR:HB	3:BU:55:GLU:HG3	2.02	0.43
1:AD:134:ASN:N	1:AD:134:ASN:HD22	2.16	0.43
1:AK:10:THR:HG22	1:AK:114:THR:HA	2.00	0.43
3:BW:78:SER:HB2	3:BW:89:SER:HB3	2.00	0.43
1:AJ:165:ARG:HH12	1:AL:171:ILE:CG2	2.32	0.43
1:AN:54:LEU:HD21	1:AN:87:ALA:HA	2.00	0.43
3:BC:78:SER:HB2	3:BC:89:SER:HB3	2.50	0.43
1:AJ:177:LEU:HD11	1:AL:177:LEU:HD11	2.01	0.43
3:BH:26:ASN:HA	3:BH:29:LEU:HD12	2.01	0.43
3:BE:61:THR:HB	3:BF:55:GLU:HG3	2.02	0.43
3:BC:112:GLU:O	3:BC:162:ILE:HD11	2.19	0.43
1:AC:19:ILE:HD11	2:AU:113:LEU:CD1	2.48	0.42
1:AA:21:LYS:O	1:AR:115:ARG:NH2	2.52	0.42
3:BZ:129:TRP:HB3	3:B2:130:ASN:HA	206.86	0.42
1:AC:202:HIS:CB	1:AC:286:MET:HE3	2.49	0.42
3:BW:26:ASN:HA	3:BW:29:LEU:HD12	2.01	0.42
3:BN:61:THR:HB	3:BO:55:GLU:HG3	2.04	0.42
1:AP:48:LEU:HD21	1:AP:110:GLU:HG3	2.01	0.42
2:AW:35:ILE:HD13	2:AW:95:LEU:HG	2.01	0.42
1:AI:112:PHE:HB3	1:AJ:29:SER:HB2	2.00	0.42
3:BA:99:LEU:HA	3:BA:148:THR:HG23	2.61	0.42
1:AA:268:ILE:HG22	1:AA:270:ASP:OD1	2.19	0.42
3:BJ:51:THR:HA	3:BL:57:ASN:HB2	2.00	0.42
3:BN:26:ASN:HA	3:BN:29:LEU:HD12	5.42	0.42
3:BQ:26:ASN:HA	3:BQ:29:LEU:HD12	2.01	0.42
3:BN:51:THR:HG22	3:BP:57:ASN:HD22	55.27	0.42
2:AX:127:VAL:HG23	2:AX:134:ILE:CD1	2.50	0.42
3:BI:118:ARG:HD2	3:BQ:70:GLU:CD	133.41	0.42
1:AA:134:ASN:H	1:AA:134:ASN:HD22	1.68	0.42
1:AA:21:LYS:HZ2	1:AR:15:ASN:HB2	1.84	0.42
1:AQ:37:VAL:HG13	1:AQ:40:GLY:H	1.84	0.42
3:BA:112:GLU:O	3:BA:162:ILE:HD11	2.19	0.42
1:AH:207:GLN:NE2	3:BT:13:ASN:OD1	2.53	0.42
1:AL:186:LYS:O	1:AL:190:GLU:HG2	2.19	0.42
3:BJ:73:GLY:HA3	3:BJ:98:ILE:HD11	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:191:LYS:HE2	1:AQ:254:GLU:OE1	2.19	0.42
1:AJ:15:ASN:ND2	1:AJ:15:ASN:H	2.15	0.42
3:BB:129:TRP:HB3	3:BD:130:ASN:HA	65.78	0.42
1:AG:274:LEU:HD11	3:BT:8:TYR:CE2	2.54	0.42
1:AR:23:ARG:HB3	1:AR:26:ASP:OD2	2.19	0.42
3:BJ:13:ASN:HB3	3:BJ:16:GLU:HB2	2.01	0.42
1:AI:225:GLY:HA3	3:BH:10:GLY:HA2	2.01	0.42
1:AG:22:LEU:HD22	1:AG:30:GLN:HB3	2.02	0.42
1:AC:26:ASP:HB2	1:AC:30:GLN:HE21	1.84	0.42
1:AE:36:ILE:HD12	1:AE:114:THR:HG21	2.02	0.42
1:AP:299:ALA:O	1:AR:154:LYS:HE2	2.19	0.42
2:AS:35:ILE:HD13	2:AS:95:LEU:HG	2.02	0.42
3:BK:11:MET:HE3	3:BK:14:GLY:HA2	2.05	0.42
3:BR:7:VAL:HB	3:BS:19:ASN:HB2	181.11	0.42
1:AF:168:LEU:HD21	1:AF:179:ALA:HB2	2.01	0.42
3:BO:87:GLU:HG2	3:BO:159:THR:HG22	2.09	0.42
1:AR:147:ASN:O	1:AR:150:ILE:HG22	2.19	0.42
2:AW:78:TYR:CZ	2:AW:136:SER:HB3	2.54	0.42
3:BW:128:GLY:HA2	3:BY:147:PRO:HG3	154.41	0.42
1:AD:157:TRP:HZ3	1:AE:161:VAL:HG13	1.84	0.42
3:BJ:128:GLY:HA2	3:BL:147:PRO:HG3	2.01	0.42
3:BC:11:MET:HE3	3:BC:14:GLY:HA2	2.18	0.42
3:BD:51:THR:HA	3:BF:57:ASN:HB2	2.01	0.42
1:AO:128:GLN:HA	1:AO:129:PRO:HD3	1.88	0.42
3:BC:61:THR:HB	3:BD:55:GLU:HG3	64.79	0.42
3:BM:13:ASN:HA	3:BO:9:ARG:NH2	2.35	0.42
3:BT:51:THR:HG22	3:BV:57:ASN:HD22	90.77	0.42
1:AA:202:HIS:HB3	1:AA:286:MET:HE1	2.01	0.42
3:BK:9:ARG:HH22	3:BL:13:ASN:HA	3.43	0.42
1:AI:101:ARG:HB3	1:AI:111:GLN:HG3	2.00	0.42
1:AJ:205:GLU:OE2	1:AJ:248:ARG:HD3	2.20	0.42
1:AP:146:PHE:HZ	1:AR:157:TRP:HB2	1.85	0.42
2:AT:192:SER:HB3	2:AT:222:LEU:HD13	2.01	0.42
2:AT:47:GLU:H	2:AT:47:GLU:HG2	1.04	0.42
1:AK:125:ILE:CG2	1:AK:126:TYR:N	2.82	0.42
3:BH:129:TRP:HB3	3:BJ:130:ASN:HA	59.84	0.42
3:BG:129:TRP:HB3	3:BI:130:ASN:HA	2.02	0.42
3:BC:101:ASN:OD1	3:BE:95:SER:HB2	45.43	0.42
1:AD:146:PHE:HZ	1:AF:157:TRP:HB2	1.84	0.42
1:AK:23:ARG:HB2	1:AK:26:ASP:HB2	2.02	0.42
3:BM:99:LEU:HA	3:BM:148:THR:HG23	2.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BW:133:HIS:HD2	3:BX:124:HIS:ND1	2.18	0.42
1:AR:16:ASN:HB2	2:AV:30:TRP:HZ2	1.84	0.42
2:AW:47:GLU:HG2	2:AW:47:GLU:H	1.00	0.42
1:AE:23:ARG:HB2	1:AE:26:ASP:HB2	2.02	0.42
1:AA:204:SER:HB2	1:AA:289:ALA:HB2	2.01	0.42
1:AO:24:HIS:HB3	1:AO:124:SER:HB3	2.01	0.42
3:B1:133:HIS:HB3	3:B2:124:HIS:HB3	2.02	0.42
1:AE:239:ASN:HD22	1:AF:244:LEU:HB2	1.85	0.42
2:AW:177:THR:HG22	2:AW:178:GLU:H	1.85	0.42
1:AH:158:GLU:HA	1:AH:161:VAL:HG12	2.02	0.42
1:AL:202:HIS:CE1	1:AL:251:VAL:HG23	2.55	0.42
1:AJ:171:ILE:HG12	1:AK:177:LEU:HD22	2.01	0.41
1:AA:21:LYS:HZ3	1:AR:15:ASN:HB2	1.85	0.41
3:BT:129:TRP:HB3	3:BV:130:ASN:HA	85.33	0.41
1:AN:23:ARG:H	1:AN:30:GLN:HE22	1.68	0.41
3:BU:80:ARG:NH1	3:BU:82:LYS:HE3	2.34	0.41
3:BP:51:THR:HG22	3:BR:57:ASN:HD22	1.85	0.41
1:AA:24:HIS:CD2	1:AA:126:TYR:O	2.73	0.41
3:BF:99:LEU:HA	3:BF:148:THR:HG23	2.03	0.41
2:AU:44:GLU:HB2	2:AU:75:THR:HG23	2.02	0.41
1:AO:168:LEU:HD21	1:AO:178:LEU:HD23	2.02	0.41
3:BJ:129:TRP:HB3	3:BL:130:ASN:HA	2.01	0.41
1:AN:54:LEU:HD13	1:AN:65:SER:HB3	2.01	0.41
3:BZ:128:GLY:HA2	3:B2:147:PRO:HG3	209.66	0.41
3:BA:55:GLU:HG3	3:BZ:61:THR:HB	151.58	0.41
1:AL:24:HIS:CD2	1:AL:127:SER:HB3	2.55	0.41
3:BE:9:ARG:HH22	3:BF:13:ASN:HA	3.37	0.41
1:AC:148:LYS:HA	1:AC:151:GLU:HG2	2.02	0.41
1:AP:10:THR:HG22	1:AP:114:THR:HA	2.02	0.41
3:BT:128:GLY:HA2	3:BV:147:PRO:HG3	87.03	0.41
1:AN:162:GLU:O	1:AN:166:GLU:HB2	2.20	0.41
3:BX:99:LEU:HA	3:BX:148:THR:HG23	2.02	0.41
1:AP:171:ILE:CD1	1:AQ:177:LEU:HD11	2.48	0.41
3:BC:7:VAL:HG13	3:BC:11:MET:HE2	2.02	0.41
1:AC:108:TRP:CH2	1:AE:125:ILE:CD1	3.03	0.41
1:AL:190:GLU:HG3	1:AL:191:LYS:HD2	2.02	0.41
1:AO:61:GLY:H	1:AO:64:VAL:HG22	1.85	0.41
3:BB:112:GLU:O	3:BB:162:ILE:HD11	2.20	0.41
2:AS:44:GLU:HB2	2:AS:75:THR:HG23	2.02	0.41
1:AR:36:ILE:HD12	1:AR:114:THR:HG21	2.01	0.41
3:BR:133:HIS:HB3	3:BS:124:HIS:HB3	144.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BD:129:TRP:HB3	3:BF:130:ASN:HA	2.01	0.41
1:AK:257:LYS:O	1:AK:260:THR:HG22	2.21	0.41
3:BA:129:TRP:HB3	3:BZ:130:ASN:HA	129.33	0.41
3:BS:51:THR:HA	3:BU:57:ASN:HB2	2.03	0.41
3:BQ:70:GLU:OE1	3:BQ:74:GLY:HA2	2.20	0.41
3:BR:133:HIS:HD2	3:BS:124:HIS:ND1	144.24	0.41
2:AX:105:VAL:HA	2:AX:106:PRO:HD3	1.90	0.41
2:AU:35:ILE:HD13	2:AU:95:LEU:HG	2.01	0.41
3:BO:61:THR:HB	3:BP:55:GLU:HG3	57.25	0.41
1:AO:169:GLU:O	1:AO:176:VAL:HG22	2.20	0.41
3:BI:133:HIS:HB3	3:BJ:124:HIS:HB3	56.94	0.41
1:AD:219:ILE:HD13	3:BW:14:GLY:HA3	2.01	0.41
3:BA:124:HIS:HB3	3:BZ:133:HIS:HB3	130.98	0.41
3:BO:25:ILE:HG23	3:BP:29:LEU:HD11	75.08	0.41
2:AU:253:LEU:OXT	2:AV:96:LYS:CD	2.67	0.41
3:BW:51:THR:HA	3:BY:57:ASN:HB2	160.21	0.41
1:AR:16:ASN:HB3	1:AR:118:HIS:HE1	1.85	0.41
3:BX:61:THR:HB	3:BY:55:GLU:HG3	151.14	0.41
1:AA:2:THR:HG21	1:AR:10:THR:HB	2.02	0.41
2:AS:108:ILE:HG12	2:AS:116:THR:HG23	2.02	0.41
1:AN:6:ILE:HD11	1:AN:18:GLY:H	1.86	0.41
3:BQ:87:GLU:HG2	3:BQ:159:THR:HG22	2.02	0.41
1:AG:248:ARG:HG3	3:BI:9:ARG:HB3	2.03	0.41
3:BB:51:THR:HA	3:BD:57:ASN:HB2	63.43	0.41
1:AF:62:GLN:HB2	1:AH:122:GLU:HB2	2.03	0.41
2:AU:192:SER:HB3	2:AU:222:LEU:HD13	2.03	0.41
1:AP:134:ASN:HD22	1:AP:134:ASN:C	2.23	0.41
3:BD:51:THR:HG22	3:BF:57:ASN:HD22	1.85	0.41
3:BA:57:ASN:HB2	3:BY:51:THR:HA	147.09	0.41
1:AD:22:LEU:HD22	1:AD:30:GLN:HB3	2.03	0.41
3:BQ:133:HIS:HB3	3:BR:124:HIS:HB3	2.03	0.41
2:AU:47:GLU:H	2:AU:47:GLU:HG2	1.16	0.41
1:AH:165:ARG:NH2	1:AH:170:SER:OG	2.53	0.41
2:AW:210:PHE:CE1	2:AW:215:VAL:HG22	2.56	0.41
3:B1:26:ASN:HA	3:B1:29:LEU:HD12	2.01	0.41
1:AC:232:PHE:O	3:BC:9:ARG:HA	2.21	0.41
3:BK:129:TRP:HB3	3:BM:130:ASN:HA	69.47	0.41
1:AO:165:ARG:O	1:AO:169:GLU:HB3	2.20	0.41
3:BW:84:THR:OG1	3:BX:82:LYS:NZ	2.54	0.41
1:AP:84:SER:H	1:AP:87:ALA:HB3	1.86	0.41
3:BH:61:THR:HB	3:BI:55:GLU:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BV:124:HIS:ND1	3:BX:133:HIS:HD2	2.19	0.41
1:AR:31:ALA:HB2	1:AR:82:VAL:HG22	2.03	0.41
3:BS:99:LEU:HA	3:BS:148:THR:HG23	2.06	0.41
1:AN:91:VAL:HG11	1:AN:123:LYS:HB2	2.03	0.41
3:BY:13:ASN:HB3	3:BY:16:GLU:HB2	4.70	0.41
3:BG:128:GLY:HA2	3:BI:147:PRO:HG3	2.02	0.41
3:BA:124:HIS:ND1	3:BZ:133:HIS:HD2	126.83	0.41
1:AI:16:ASN:HB2	2:AS:30:TRP:HZ2	1.86	0.41
3:BA:118:ARG:HH21	3:BG:70:GLU:CD	138.86	0.41
3:BA:57:ASN:HD22	3:BY:51:THR:HG22	146.57	0.41
3:BH:51:THR:HA	3:BJ:57:ASN:HB2	60.70	0.41
3:BO:7:VAL:HB	3:BP:19:ASN:HB2	80.41	0.41
1:AK:22:LEU:HB3	1:AK:30:GLN:OE1	2.21	0.41
2:AX:43:VAL:HG22	2:AX:76:ILE:HG23	2.03	0.41
3:BP:128:GLY:HA2	3:BR:147:PRO:HG3	2.02	0.41
3:BE:128:GLY:HA2	3:BG:147:PRO:HG3	67.79	0.41
1:AD:151:GLU:HG3	1:AD:152:ASP:N	2.34	0.41
1:AI:49:GLN:NE2	1:AI:68:SER:OG	2.54	0.41
1:AA:6:ILE:HD12	1:AA:8:LEU:HD21	2.01	0.41
3:BO:133:HIS:HD2	3:BP:124:HIS:ND1	52.28	0.41
1:AQ:147:ASN:HA	1:AQ:150:ILE:HG12	2.03	0.41
1:AD:56:ALA:HB2	1:AD:64:VAL:HG13	2.02	0.41
1:AJ:167:ILE:H	1:AJ:167:ILE:HG13	1.63	0.41
3:BH:128:GLY:HA2	3:BJ:147:PRO:HG3	65.52	0.41
3:BR:25:ILE:HG23	3:BS:29:LEU:HD11	170.16	0.40
3:BW:129:TRP:HB3	3:BY:130:ASN:HA	151.53	0.40
3:BS:129:TRP:HB3	3:BU:130:ASN:HA	2.02	0.40
3:BM:16:GLU:OE2	3:BO:9:ARG:NH1	2.55	0.40
3:BZ:51:THR:HG22	3:B2:57:ASN:HD22	212.15	0.40
1:AA:101:ARG:HH11	1:AA:108:TRP:HE1	1.69	0.40
3:BS:51:THR:HG22	3:BU:57:ASN:HD22	1.86	0.40
1:AD:151:GLU:CG	1:AD:152:ASP:N	2.84	0.40
1:AF:16:ASN:HB3	1:AF:118:HIS:HE1	1.86	0.40
2:AX:202:PHE:HB2	2:AX:210:PHE:HB2	2.02	0.40
3:BB:128:GLY:HA2	3:BD:147:PRO:HG3	72.08	0.40
1:AG:219:ILE:HG22	3:BU:15:ALA:HB2	2.02	0.40
1:AB:149:TYR:CZ	1:AC:154:LYS:HG2	2.56	0.40
3:BH:133:HIS:HD2	3:BI:124:HIS:ND1	2.19	0.40
1:AE:37:VAL:HG13	1:AE:40:GLY:H	1.86	0.40
3:BP:11:MET:HE3	3:BP:14:GLY:HA2	2.02	0.40
3:BK:133:HIS:HD2	3:BL:124:HIS:ND1	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BA:29:LEU:HD11	3:BZ:25:ILE:HG23	173.08	0.40
1:AF:24:HIS:CD2	1:AF:127:SER:HB3	2.56	0.40
1:AD:299:ALA:O	1:AF:154:LYS:CE	2.68	0.40
3:BQ:129:TRP:HB3	3:BS:130:ASN:HA	145.10	0.40
1:AM:274:LEU:HD11	3:BI:8:TYR:HE2	165.31	0.40
3:BZ:51:THR:HA	3:B2:57:ASN:HB2	212.45	0.40
1:AP:7:THR:HG23	1:AP:35:GLN:HB3	2.02	0.40
3:BL:99:LEU:HA	3:BL:148:THR:HG23	2.03	0.40
1:AL:225:GLY:HA3	3:BK:10:GLY:HA2	2.03	0.40
1:AB:46:GLU:OE1	1:AB:75:LYS:HG2	2.21	0.40
3:BM:128:GLY:HA2	3:BO:147:PRO:HG3	2.03	0.40
1:AN:7:THR:HG23	1:AN:35:GLN:HB3	2.03	0.40
3:BX:11:MET:HE3	3:BX:14:GLY:HA2	2.06	0.40
3:BS:128:GLY:HA2	3:BU:147:PRO:HG3	2.03	0.40
3:BR:99:LEU:HA	3:BR:148:THR:HG23	2.04	0.40
3:BB:78:SER:HB2	3:BB:89:SER:HB3	2.50	0.40
1:AM:167:ILE:HG13	1:AM:167:ILE:H	1.72	0.40
3:BQ:128:GLY:HA2	3:BS:147:PRO:HG3	153.39	0.40
3:BT:133:HIS:HB3	3:BU:124:HIS:HB3	2.03	0.40
3:BN:129:TRP:HB3	3:BP:130:ASN:HA	57.10	0.40
1:AG:102:LYS:HE2	1:AG:110:GLU:HG2	2.03	0.40
1:AO:16:ASN:HB2	2:AW:30:TRP:HZ2	1.86	0.40
1:AK:36:ILE:HD11	1:AK:79:LEU:HD21	2.04	0.40
3:BX:133:HIS:HD2	3:BY:124:HIS:ND1	154.56	0.40
3:BT:133:HIS:HD2	3:BU:124:HIS:ND1	2.20	0.40
3:B1:61:THR:HB	3:B2:55:GLU:HG3	2.03	0.40
2:AS:152:GLN:NE2	2:AS:160:GLU:OE1	2.55	0.40
2:AV:35:ILE:HD13	2:AV:95:LEU:HG	2.03	0.40
1:AI:61:GLY:H	1:AI:64:VAL:HG22	1.87	0.40
1:AL:261:LEU:HD21	1:AL:275:VAL:HG12	2.04	0.40
1:AC:48:LEU:HD23	1:AC:102:LYS:HB2	2.03	0.40
2:AT:43:VAL:HG13	2:AT:76:ILE:HG22	2.03	0.40
3:BB:8:TYR:O	3:BB:11:MET:HB3	2.22	0.40
3:BA:57:ASN:HB2	3:BB:51:THR:HA	2.03	0.40
3:B1:133:HIS:HD2	3:B2:124:HIS:ND1	2.19	0.40
3:BH:133:HIS:HB3	3:BI:124:HIS:HB3	2.04	0.40
3:BU:61:THR:HB	3:BV:55:GLU:HG3	86.83	0.40
3:BG:55:GLU:HG3	3:BI:61:THR:HB	2.04	0.40
3:BN:133:HIS:HD2	3:BO:124:HIS:ND1	2.20	0.40
3:BE:133:HIS:HD2	3:BF:124:HIS:ND1	2.19	0.40
3:BX:87:GLU:HG2	3:BX:159:THR:HG22	2.11	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BI:99:LEU:HA	3:BI:148:THR:HG23	2.04	0.40
3:BC:133:HIS:HD2	3:BD:124:HIS:ND1	60.62	0.40
3:BE:129:TRP:HB3	3:BG:130:ASN:HA	61.95	0.40
3:BE:51:THR:HA	3:BG:57:ASN:HB2	63.47	0.40
1:AN:207:GLN:NE2	3:BI:13:ASN:OD1	177.30	0.40
1:AH:248:ARG:HG3	3:BS:9:ARG:HB3	2.04	0.40
1:AN:123:LYS:HD3	1:AN:125:ILE:HD11	2.04	0.40
3:BN:133:HIS:HB3	3:BO:124:HIS:HB3	2.03	0.40
1:AF:101:ARG:HB3	1:AF:111:GLN:HG3	2.03	0.40
3:BK:128:GLY:HA2	3:BM:147:PRO:HG3	74.86	0.40
1:AI:128:GLN:HA	1:AI:129:PRO:HD3	2.01	0.40
3:BO:99:LEU:HA	3:BO:148:THR:HG23	2.03	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	AA	297/299 (99%)	284 (96%)	11 (4%)	2 (1%)	26 72
1	AB	290/299 (97%)	273 (94%)	17 (6%)	0	100 100
1	AC	297/299 (99%)	274 (92%)	23 (8%)	0	100 100
1	AD	297/299 (99%)	276 (93%)	19 (6%)	2 (1%)	26 72
1	AE	287/299 (96%)	268 (93%)	19 (7%)	0	100 100
1	AF	297/299 (99%)	277 (93%)	19 (6%)	1 (0%)	46 83
1	AG	297/299 (99%)	278 (94%)	14 (5%)	5 (2%)	11 56
1	AH	290/299 (97%)	271 (93%)	18 (6%)	1 (0%)	46 83
1	AI	297/299 (99%)	275 (93%)	20 (7%)	2 (1%)	26 72
1	AJ	297/299 (99%)	275 (93%)	20 (7%)	2 (1%)	26 72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AK	289/299 (97%)	270 (93%)	19 (7%)	0	100	100
1	AL	296/299 (99%)	276 (93%)	19 (6%)	1 (0%)	46	83
1	AM	297/299 (99%)	276 (93%)	19 (6%)	2 (1%)	26	72
1	AN	290/299 (97%)	270 (93%)	20 (7%)	0	100	100
1	AO	297/299 (99%)	276 (93%)	20 (7%)	1 (0%)	46	83
1	AP	297/299 (99%)	281 (95%)	13 (4%)	3 (1%)	19	66
1	AQ	291/299 (97%)	269 (92%)	21 (7%)	1 (0%)	46	83
1	AR	297/299 (99%)	277 (93%)	17 (6%)	3 (1%)	19	66
2	AS	240/253 (95%)	215 (90%)	24 (10%)	1 (0%)	39	80
2	AT	240/253 (95%)	218 (91%)	22 (9%)	0	100	100
2	AU	240/253 (95%)	215 (90%)	25 (10%)	0	100	100
2	AV	239/253 (94%)	217 (91%)	22 (9%)	0	100	100
2	AW	239/253 (94%)	217 (91%)	22 (9%)	0	100	100
2	AX	239/253 (94%)	217 (91%)	22 (9%)	0	100	100
3	B1	161/173 (93%)	157 (98%)	4 (2%)	0	100	100
3	B2	160/173 (92%)	154 (96%)	6 (4%)	0	100	100
3	BA	162/173 (94%)	159 (98%)	3 (2%)	0	100	100
3	BB	161/173 (93%)	158 (98%)	3 (2%)	0	100	100
3	BC	161/173 (93%)	158 (98%)	3 (2%)	0	100	100
3	BD	162/173 (94%)	154 (95%)	8 (5%)	0	100	100
3	BE	162/173 (94%)	157 (97%)	5 (3%)	0	100	100
3	BF	161/173 (93%)	155 (96%)	6 (4%)	0	100	100
3	BG	162/173 (94%)	155 (96%)	7 (4%)	0	100	100
3	BH	162/173 (94%)	157 (97%)	5 (3%)	0	100	100
3	BI	161/173 (93%)	154 (96%)	7 (4%)	0	100	100
3	BJ	162/173 (94%)	156 (96%)	6 (4%)	0	100	100
3	BK	161/173 (93%)	157 (98%)	4 (2%)	0	100	100
3	BL	161/173 (93%)	154 (96%)	7 (4%)	0	100	100
3	BM	161/173 (93%)	155 (96%)	6 (4%)	0	100	100
3	BN	160/173 (92%)	156 (98%)	4 (2%)	0	100	100
3	BO	160/173 (92%)	153 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	BP	161/173 (93%)	154 (96%)	7 (4%)	0	100	100
3	BQ	160/173 (92%)	156 (98%)	4 (2%)	0	100	100
3	BR	161/173 (93%)	154 (96%)	7 (4%)	0	100	100
3	BS	161/173 (93%)	156 (97%)	5 (3%)	0	100	100
3	BT	162/173 (94%)	157 (97%)	5 (3%)	0	100	100
3	BU	162/173 (94%)	154 (95%)	8 (5%)	0	100	100
3	BV	161/173 (93%)	155 (96%)	6 (4%)	0	100	100
3	BW	162/173 (94%)	157 (97%)	5 (3%)	0	100	100
3	BX	160/173 (92%)	153 (96%)	7 (4%)	0	100	100
3	BY	161/173 (93%)	155 (96%)	6 (4%)	0	100	100
3	BZ	161/173 (93%)	157 (98%)	4 (2%)	0	100	100
3	Ba	160/173 (92%)	151 (94%)	9 (6%)	0	100	100
3	Bb	161/173 (93%)	155 (96%)	6 (4%)	0	100	100
3	Bc	162/173 (94%)	158 (98%)	4 (2%)	0	100	100
3	Bd	163/173 (94%)	155 (95%)	8 (5%)	0	100	100
3	Be	161/173 (93%)	155 (96%)	6 (4%)	0	100	100
3	Bf	162/173 (94%)	157 (97%)	5 (3%)	0	100	100
3	Bg	161/173 (93%)	154 (96%)	7 (4%)	0	100	100
3	Bh	159/173 (92%)	154 (97%)	5 (3%)	0	100	100
3	Bi	160/173 (92%)	156 (98%)	4 (2%)	0	100	100
3	Bj	160/173 (92%)	155 (97%)	5 (3%)	0	100	100
3	Bk	161/173 (93%)	155 (96%)	6 (4%)	0	100	100
3	Bl	161/173 (93%)	157 (98%)	4 (2%)	0	100	100
3	Bm	160/173 (92%)	154 (96%)	6 (4%)	0	100	100
3	Bn	160/173 (92%)	154 (96%)	6 (4%)	0	100	100
3	Bo	160/173 (92%)	156 (98%)	4 (2%)	0	100	100
3	Bp	162/173 (94%)	154 (95%)	8 (5%)	0	100	100
3	Bq	161/173 (93%)	155 (96%)	6 (4%)	0	100	100
3	Br	161/173 (93%)	157 (98%)	4 (2%)	0	100	100
3	Bs	161/173 (93%)	154 (96%)	7 (4%)	0	100	100
3	Bt	160/173 (92%)	154 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Bu	160/173 (92%)	156 (98%)	4 (2%)	0	100	100
3	Bv	162/173 (94%)	154 (95%)	8 (5%)	0	100	100
3	Bw	161/173 (93%)	155 (96%)	6 (4%)	0	100	100
3	Bx	160/173 (92%)	156 (98%)	4 (2%)	0	100	100
3	By	160/173 (92%)	153 (96%)	7 (4%)	0	100	100
3	Bz	161/173 (93%)	155 (96%)	6 (4%)	0	100	100
All	All	15429/16242 (95%)	14631 (95%)	771 (5%)	27 (0%)	52	86

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AF	269	ASP
1	AA	175	GLY
1	AM	175	GLY
1	AD	27	VAL
1	AG	27	VAL
1	AG	175	GLY
1	AJ	27	VAL
1	AJ	175	GLY
1	AP	27	VAL
1	AP	175	GLY
1	AA	27	VAL
1	AG	193	PRO
1	AL	28	ASN
1	AM	27	VAL
1	AD	175	GLY
1	AI	269	ASP
1	AP	106	GLY
1	AR	269	ASP
1	AQ	63	GLY
1	AR	105	GLY
1	AR	171	ILE
1	AH	193	PRO
1	AG	105	GLY
1	AO	235	GLY
1	AG	106	GLY
2	AS	197	GLY
1	AI	235	GLY

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	AA	260/261 (100%)	245 (94%)	15 (6%)	25 66
1	AB	255/261 (98%)	244 (96%)	11 (4%)	35 74
1	AC	260/261 (100%)	247 (95%)	13 (5%)	30 70
1	AD	261/261 (100%)	247 (95%)	14 (5%)	27 68
1	AE	256/261 (98%)	250 (98%)	6 (2%)	58 84
1	AF	260/261 (100%)	251 (96%)	9 (4%)	43 78
1	AG	259/261 (99%)	249 (96%)	10 (4%)	39 75
1	AH	254/261 (97%)	242 (95%)	12 (5%)	32 72
1	AI	260/261 (100%)	245 (94%)	15 (6%)	25 66
1	AJ	261/261 (100%)	247 (95%)	14 (5%)	27 68
1	AK	250/261 (96%)	239 (96%)	11 (4%)	35 73
1	AL	259/261 (99%)	246 (95%)	13 (5%)	30 70
1	AM	260/261 (100%)	249 (96%)	11 (4%)	36 74
1	AN	250/261 (96%)	238 (95%)	12 (5%)	31 71
1	AO	261/261 (100%)	250 (96%)	11 (4%)	36 74
1	AP	258/261 (99%)	242 (94%)	16 (6%)	23 64
1	AQ	254/261 (97%)	244 (96%)	10 (4%)	39 75
1	AR	260/261 (100%)	253 (97%)	7 (3%)	52 82
2	AS	212/229 (93%)	205 (97%)	7 (3%)	45 79
2	AT	212/229 (93%)	200 (94%)	12 (6%)	25 67
2	AU	209/229 (91%)	202 (97%)	7 (3%)	45 79
2	AV	204/229 (89%)	196 (96%)	8 (4%)	39 75
2	AW	209/229 (91%)	203 (97%)	6 (3%)	50 81
2	AX	209/229 (91%)	197 (94%)	12 (6%)	25 67
3	B1	133/142 (94%)	132 (99%)	1 (1%)	86 94
3	B2	132/142 (93%)	131 (99%)	1 (1%)	86 94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	BA	132/142 (93%)	127 (96%)	5 (4%)	40 76
3	BB	132/142 (93%)	126 (96%)	6 (4%)	34 73
3	BC	132/142 (93%)	124 (94%)	8 (6%)	23 65
3	BD	132/142 (93%)	129 (98%)	3 (2%)	58 84
3	BE	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	BF	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	BG	132/142 (93%)	129 (98%)	3 (2%)	58 84
3	BH	133/142 (94%)	131 (98%)	2 (2%)	72 90
3	BI	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	BJ	132/142 (93%)	130 (98%)	2 (2%)	72 90
3	BK	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	BL	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	BM	132/142 (93%)	130 (98%)	2 (2%)	72 90
3	BN	131/142 (92%)	128 (98%)	3 (2%)	58 84
3	BO	131/142 (92%)	129 (98%)	2 (2%)	72 90
3	BP	132/142 (93%)	130 (98%)	2 (2%)	72 90
3	BQ	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	BR	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	BS	132/142 (93%)	130 (98%)	2 (2%)	72 90
3	BT	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	BU	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	BV	132/142 (93%)	129 (98%)	3 (2%)	58 84
3	BW	132/142 (93%)	130 (98%)	2 (2%)	72 90
3	BX	131/142 (92%)	131 (100%)	0	100 100
3	BY	132/142 (93%)	128 (97%)	4 (3%)	48 80
3	BZ	132/142 (93%)	130 (98%)	2 (2%)	72 90
3	Ba	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	Bb	132/142 (93%)	130 (98%)	2 (2%)	72 90
3	Bc	131/142 (92%)	130 (99%)	1 (1%)	86 94
3	Bd	132/142 (93%)	130 (98%)	2 (2%)	72 90
3	Be	132/142 (93%)	130 (98%)	2 (2%)	72 90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	Bf	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	Bg	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	Bh	131/142 (92%)	129 (98%)	2 (2%)	72 90
3	Bi	131/142 (92%)	130 (99%)	1 (1%)	86 94
3	Bj	132/142 (93%)	130 (98%)	2 (2%)	72 90
3	Bk	132/142 (93%)	130 (98%)	2 (2%)	72 90
3	Bl	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	Bm	131/142 (92%)	130 (99%)	1 (1%)	86 94
3	Bn	132/142 (93%)	130 (98%)	2 (2%)	72 90
3	Bo	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	Bp	133/142 (94%)	131 (98%)	2 (2%)	72 90
3	Bq	133/142 (94%)	131 (98%)	2 (2%)	72 90
3	Br	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	Bs	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	Bt	131/142 (92%)	129 (98%)	2 (2%)	72 90
3	Bu	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	Bv	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	Bw	132/142 (93%)	130 (98%)	2 (2%)	72 90
3	Bx	132/142 (93%)	131 (99%)	1 (1%)	86 94
3	By	132/142 (93%)	130 (98%)	2 (2%)	72 90
3	Bz	133/142 (94%)	130 (98%)	3 (2%)	58 84
All	All	13018/13740 (95%)	12654 (97%)	364 (3%)	51 81

All (364) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AA	15	ASN
1	AA	49	GLN
1	AA	62	GLN
1	AA	64	VAL
1	AA	101	ARG
1	AA	134	ASN
1	AA	139	PHE
1	AA	140	LYS
1	AA	171	ILE

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Mol	Chain	Res	Type
1	AA	186	LYS
1	AA	224	ASP
1	AA	248	ARG
1	AA	250	LYS
1	AA	267	LEU
1	AA	272	THR
1	AB	37	VAL
1	AB	75	LYS
1	AB	85	ASP
1	AB	125	ILE
1	AB	132	ASP
1	AB	151	GLU
1	AB	219	ILE
1	AB	224	ASP
1	AB	248	ARG
1	AB	267	LEU
1	AB	298	VAL
1	AC	2	THR
1	AC	27	VAL
1	AC	62	GLN
1	AC	107	ARG
1	AC	116	THR
1	AC	159	GLN
1	AC	168	LEU
1	AC	178	LEU
1	AC	186	LYS
1	AC	189	ASN
1	AC	224	ASP
1	AC	248	ARG
1	AC	267	LEU
1	AD	15	ASN
1	AD	62	GLN
1	AD	75	LYS
1	AD	116	THR
1	AD	132	ASP
1	AD	134	ASN
1	AD	140	LYS
1	AD	144	ARG
1	AD	147	ASN
1	AD	167	ILE
1	AD	178	LEU
1	AD	191	LYS

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Mol	Chain	Res	Type
1	AD	224	ASP
1	AD	248	ARG
1	AE	85	ASP
1	AE	125	ILE
1	AE	189	ASN
1	AE	219	ILE
1	AE	224	ASP
1	AE	248	ARG
1	AF	2	THR
1	AF	6	ILE
1	AF	91	VAL
1	AF	158	GLU
1	AF	168	LEU
1	AF	216	LYS
1	AF	224	ASP
1	AF	248	ARG
1	AF	267	LEU
1	AG	15	ASN
1	AG	28	ASN
1	AG	49	GLN
1	AG	62	GLN
1	AG	102	LYS
1	AG	103	GLN
1	AG	134	ASN
1	AG	155	LYS
1	AG	224	ASP
1	AG	248	ARG
1	AH	85	ASP
1	AH	89	GLN
1	AH	125	ILE
1	AH	132	ASP
1	AH	155	LYS
1	AH	165	ARG
1	AH	168	LEU
1	AH	169	GLU
1	AH	219	ILE
1	AH	224	ASP
1	AH	248	ARG
1	AH	257	LYS
1	AI	2	THR
1	AI	12	GLU
1	AI	27	VAL

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Mol	Chain	Res	Type
1	AI	62	GLN
1	AI	75	LYS
1	AI	108	TRP
1	AI	159	GLN
1	AI	168	LEU
1	AI	177	LEU
1	AI	178	LEU
1	AI	184	ILE
1	AI	189	ASN
1	AI	224	ASP
1	AI	248	ARG
1	AI	267	LEU
1	AJ	15	ASN
1	AJ	28	ASN
1	AJ	62	GLN
1	AJ	88	LEU
1	AJ	102	LYS
1	AJ	116	THR
1	AJ	132	ASP
1	AJ	134	ASN
1	AJ	139	PHE
1	AJ	140	LYS
1	AJ	148	LYS
1	AJ	154	LYS
1	AJ	224	ASP
1	AJ	248	ARG
1	AK	85	ASP
1	AK	89	GLN
1	AK	132	ASP
1	AK	154	LYS
1	AK	155	LYS
1	AK	165	ARG
1	AK	177	LEU
1	AK	219	ILE
1	AK	224	ASP
1	AK	248	ARG
1	AK	298	VAL
1	AL	2	THR
1	AL	22	LEU
1	AL	58	GLU
1	AL	62	GLN
1	AL	85	ASP

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Mol	Chain	Res	Type
1	AL	108	TRP
1	AL	165	ARG
1	AL	182	ILE
1	AL	185	GLU
1	AL	248	ARG
1	AL	253	VAL
1	AL	261	LEU
1	AL	267	LEU
1	AM	15	ASN
1	AM	27	VAL
1	AM	55	MET
1	AM	62	GLN
1	AM	88	LEU
1	AM	116	THR
1	AM	132	ASP
1	AM	134	ASN
1	AM	139	PHE
1	AM	224	ASP
1	AM	248	ARG
1	AN	43	LYS
1	AN	85	ASP
1	AN	89	GLN
1	AN	132	ASP
1	AN	167	ILE
1	AN	168	LEU
1	AN	177	LEU
1	AN	178	LEU
1	AN	184	ILE
1	AN	219	ILE
1	AN	224	ASP
1	AN	248	ARG
1	AO	23	ARG
1	AO	27	VAL
1	AO	62	GLN
1	AO	116	THR
1	AO	159	GLN
1	AO	165	ARG
1	AO	170	SER
1	AO	219	ILE
1	AO	224	ASP
1	AO	248	ARG
1	AO	267	LEU

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Mol	Chain	Res	Type
1	AP	15	ASN
1	AP	22	LEU
1	AP	57	GLN
1	AP	62	GLN
1	AP	102	LYS
1	AP	116	THR
1	AP	132	ASP
1	AP	134	ASN
1	AP	139	PHE
1	AP	148	LYS
1	AP	181	VAL
1	AP	191	LYS
1	AP	192	VAL
1	AP	209	GLU
1	AP	224	ASP
1	AP	248	ARG
1	AQ	125	ILE
1	AQ	132	ASP
1	AQ	155	LYS
1	AQ	165	ARG
1	AQ	178	LEU
1	AQ	219	ILE
1	AQ	224	ASP
1	AQ	248	ARG
1	AQ	277	LYS
1	AQ	298	VAL
1	AR	2	THR
1	AR	62	GLN
1	AR	115	ARG
1	AR	116	THR
1	AR	150	ILE
1	AR	224	ASP
1	AR	248	ARG
2	AS	47	GLU
2	AS	95	LEU
2	AS	177	THR
2	AS	200	LEU
2	AS	221	ASP
2	AS	232	THR
2	AS	243	GLU
2	AT	47	GLU
2	AT	76	ILE

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Mol	Chain	Res	Type
2	AT	86	ARG
2	AT	95	LEU
2	AT	134	ILE
2	AT	135	ILE
2	AT	177	THR
2	AT	200	LEU
2	AT	221	ASP
2	AT	232	THR
2	AT	244	LEU
2	AT	246	ILE
2	AU	47	GLU
2	AU	76	ILE
2	AU	95	LEU
2	AU	177	THR
2	AU	200	LEU
2	AU	220	LEU
2	AU	232	THR
2	AV	47	GLU
2	AV	58	MET
2	AV	95	LEU
2	AV	135	ILE
2	AV	177	THR
2	AV	198	ASP
2	AV	200	LEU
2	AV	232	THR
2	AW	47	GLU
2	AW	86	ARG
2	AW	95	LEU
2	AW	177	THR
2	AW	200	LEU
2	AW	232	THR
2	AX	46	ARG
2	AX	47	GLU
2	AX	79	LYS
2	AX	88	LEU
2	AX	95	LEU
2	AX	134	ILE
2	AX	135	ILE
2	AX	177	THR
2	AX	200	LEU
2	AX	221	ASP
2	AX	232	THR

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Mol	Chain	Res	Type
2	AX	244	LEU
3	BA	35	VAL
3	BA	70	GLU
3	BA	97	SER
3	BA	107	ARG
3	BA	117	ASN
3	BB	35	VAL
3	BB	70	GLU
3	BB	97	SER
3	BB	107	ARG
3	BB	117	ASN
3	BB	162	ILE
3	BC	12	LYS
3	BC	35	VAL
3	BC	70	GLU
3	BC	97	SER
3	BC	107	ARG
3	BC	117	ASN
3	BC	162	ILE
3	BC	163	ASP
3	BD	117	ASN
3	BD	118	ARG
3	BD	133	HIS
3	BE	133	HIS
3	BF	107	ARG
3	BG	5	LYS
3	BG	117	ASN
3	BG	133	HIS
3	BH	12	LYS
3	BH	133	HIS
3	BI	107	ARG
3	BJ	117	ASN
3	BJ	133	HIS
3	BK	133	HIS
3	BL	107	ARG
3	BM	117	ASN
3	BM	133	HIS
3	BN	103	ASN
3	BN	133	HIS
3	BN	141	VAL
3	BO	5	LYS
3	BO	107	ARG

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Mol	Chain	Res	Type
3	BP	117	ASN
3	BP	133	HIS
3	BQ	133	HIS
3	BR	107	ARG
3	BS	117	ASN
3	BS	133	HIS
3	BT	133	HIS
3	BU	107	ARG
3	BV	117	ASN
3	BV	133	HIS
3	BV	162	ILE
3	BW	9	ARG
3	BW	133	HIS
3	BY	12	LYS
3	BY	81	LYS
3	BY	117	ASN
3	BY	133	HIS
3	BZ	107	ARG
3	BZ	133	HIS
3	Ba	107	ARG
3	Bb	117	ASN
3	Bb	133	HIS
3	Bc	133	HIS
3	Bd	107	ARG
3	Bd	163	ASP
3	Be	117	ASN
3	Be	133	HIS
3	Bf	133	HIS
3	Bg	107	ARG
3	Bh	117	ASN
3	Bh	133	HIS
3	Bi	133	HIS
3	Bj	70	GLU
3	Bj	107	ARG
3	Bk	117	ASN
3	Bk	133	HIS
3	Bl	133	HIS
3	Bm	107	ARG
3	Bn	117	ASN
3	Bn	133	HIS
3	Bo	133	HIS
3	Bp	107	ARG

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Mol	Chain	Res	Type
3	Bp	162	ILE
3	Bq	117	ASN
3	Bq	133	HIS
3	Br	133	HIS
3	Bs	107	ARG
3	Bt	117	ASN
3	Bt	133	HIS
3	Bu	133	HIS
3	Bv	107	ARG
3	Bw	117	ASN
3	Bw	133	HIS
3	Bx	133	HIS
3	By	107	ARG
3	By	116	ARG
3	Bz	12	LYS
3	Bz	117	ASN
3	Bz	133	HIS
3	B1	133	HIS
3	B2	12	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (243) such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	15	ASN
1	AA	44	ASN
1	AA	49	GLN
1	AA	62	GLN
1	AA	89	GLN
1	AA	134	ASN
1	AA	164	ASN
1	AA	202	HIS
1	AA	280	GLN
1	AB	30	GLN
1	AC	24	HIS
1	AC	30	GLN
1	AC	44	ASN
1	AC	111	GLN
1	AC	159	GLN
1	AC	189	ASN
1	AC	202	HIS
1	AD	15	ASN
1	AD	134	ASN

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Mol	Chain	Res	Type
1	AE	239	ASN
1	AF	111	GLN
1	AG	15	ASN
1	AG	62	GLN
1	AG	164	ASN
1	AH	103	GLN
1	AH	164	ASN
1	AH	239	ASN
1	AI	24	HIS
1	AI	30	GLN
1	AI	49	GLN
1	AI	62	GLN
1	AI	89	GLN
1	AI	111	GLN
1	AJ	15	ASN
1	AJ	62	GLN
1	AK	147	ASN
1	AK	164	ASN
1	AK	239	ASN
1	AL	24	HIS
1	AL	118	HIS
1	AL	202	HIS
1	AM	15	ASN
1	AM	62	GLN
1	AM	89	GLN
1	AM	111	GLN
1	AM	134	ASN
1	AN	147	ASN
1	AN	239	ASN
1	AO	24	HIS
1	AO	28	ASN
1	AO	49	GLN
1	AO	62	GLN
1	AO	89	GLN
1	AO	111	GLN
1	AO	147	ASN
1	AP	15	ASN
1	AP	62	GLN
1	AQ	30	GLN
1	AQ	239	ASN
1	AR	24	HIS
1	AR	62	GLN

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Mol	Chain	Res	Type
1	AR	111	GLN
2	AS	59	GLN
2	AS	66	ASN
2	AS	102	GLN
2	AS	205	GLN
2	AT	59	GLN
2	AT	66	ASN
2	AT	102	GLN
2	AT	205	GLN
2	AU	15	ASN
2	AU	59	GLN
2	AU	66	ASN
2	AU	89	GLN
2	AU	102	GLN
2	AU	217	ASN
2	AV	15	ASN
2	AV	66	ASN
2	AV	102	GLN
2	AW	102	GLN
2	AW	217	ASN
2	AX	15	ASN
2	AX	59	GLN
2	AX	102	GLN
3	BA	133	HIS
3	BA	143	GLN
3	BB	133	HIS
3	BC	133	HIS
3	BD	19	ASN
3	BD	26	ASN
3	BD	133	HIS
3	BE	19	ASN
3	BE	133	HIS
3	BF	19	ASN
3	BF	57	ASN
3	BF	103	ASN
3	BF	133	HIS
3	BG	19	ASN
3	BG	26	ASN
3	BG	133	HIS
3	BH	19	ASN
3	BH	133	HIS
3	BI	19	ASN

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Mol	Chain	Res	Type
3	BI	57	ASN
3	BI	103	ASN
3	BI	133	HIS
3	BJ	19	ASN
3	BJ	26	ASN
3	BJ	133	HIS
3	BK	19	ASN
3	BK	133	HIS
3	BL	19	ASN
3	BL	57	ASN
3	BL	103	ASN
3	BL	133	HIS
3	BM	19	ASN
3	BM	26	ASN
3	BM	133	HIS
3	BN	19	ASN
3	BN	103	ASN
3	BN	133	HIS
3	BO	19	ASN
3	BO	57	ASN
3	BO	133	HIS
3	BP	19	ASN
3	BP	133	HIS
3	BP	143	GLN
3	BQ	19	ASN
3	BQ	133	HIS
3	BR	19	ASN
3	BR	57	ASN
3	BR	103	ASN
3	BR	133	HIS
3	BS	19	ASN
3	BS	26	ASN
3	BS	133	HIS
3	BT	19	ASN
3	BT	133	HIS
3	BU	19	ASN
3	BU	57	ASN
3	BU	103	ASN
3	BU	133	HIS
3	BV	19	ASN
3	BV	26	ASN
3	BV	133	HIS

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Mol	Chain	Res	Type
3	BW	19	ASN
3	BW	133	HIS
3	BW	143	GLN
3	BX	19	ASN
3	BX	57	ASN
3	BX	103	ASN
3	BX	133	HIS
3	BY	19	ASN
3	BY	133	HIS
3	BZ	19	ASN
3	BZ	133	HIS
3	Ba	19	ASN
3	Ba	57	ASN
3	Ba	103	ASN
3	Ba	133	HIS
3	Bb	19	ASN
3	Bb	133	HIS
3	Bc	19	ASN
3	Bc	133	HIS
3	Bd	19	ASN
3	Bd	57	ASN
3	Bd	103	ASN
3	Bd	133	HIS
3	Be	19	ASN
3	Be	26	ASN
3	Be	133	HIS
3	Bf	19	ASN
3	Bf	133	HIS
3	Bf	143	GLN
3	Bg	19	ASN
3	Bg	57	ASN
3	Bg	103	ASN
3	Bg	133	HIS
3	Bh	19	ASN
3	Bh	26	ASN
3	Bh	133	HIS
3	Bi	19	ASN
3	Bi	133	HIS
3	Bj	19	ASN
3	Bj	57	ASN
3	Bj	103	ASN
3	Bj	133	HIS

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Mol	Chain	Res	Type
3	Bk	19	ASN
3	Bk	26	ASN
3	Bk	133	HIS
3	Bl	19	ASN
3	Bl	133	HIS
3	Bm	19	ASN
3	Bm	57	ASN
3	Bm	103	ASN
3	Bm	133	HIS
3	Bn	19	ASN
3	Bn	26	ASN
3	Bn	133	HIS
3	Bo	19	ASN
3	Bo	133	HIS
3	Bp	19	ASN
3	Bp	57	ASN
3	Bp	103	ASN
3	Bp	133	HIS
3	Bq	19	ASN
3	Bq	26	ASN
3	Bq	133	HIS
3	Br	19	ASN
3	Br	133	HIS
3	Bs	13	ASN
3	Bs	19	ASN
3	Bs	57	ASN
3	Bs	103	ASN
3	Bs	133	HIS
3	Bt	19	ASN
3	Bt	133	HIS
3	Bu	19	ASN
3	Bu	133	HIS
3	Bv	13	ASN
3	Bv	19	ASN
3	Bv	57	ASN
3	Bv	103	ASN
3	Bv	133	HIS
3	Bw	19	ASN
3	Bw	26	ASN
3	Bw	133	HIS
3	Bx	19	ASN
3	Bx	133	HIS

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Mol	Chain	Res	Type
3	By	13	ASN
3	By	19	ASN
3	By	57	ASN
3	By	103	ASN
3	By	133	HIS
3	Bz	19	ASN
3	Bz	26	ASN
3	Bz	133	HIS
3	B1	19	ASN
3	B1	133	HIS
3	B2	19	ASN
3	B2	57	ASN
3	B2	103	ASN
3	B2	133	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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, 95^{th} 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	AA	299/299 (100%)	-0.36	1 (0%) 94 89	84, 119, 162, 188	0
1	AB	294/299 (98%)	-0.10	9 (3%) 52 36	94, 149, 206, 237	0
1	AC	299/299 (100%)	-0.29	0 100 100	95, 124, 160, 180	0
1	AD	299/299 (100%)	-0.36	0 100 100	86, 128, 175, 206	0
1	AE	291/299 (97%)	-0.07	6 (2%) 67 51	89, 159, 213, 249	0
1	AF	299/299 (100%)	-0.28	2 (0%) 89 80	90, 132, 167, 183	0
1	AG	299/299 (100%)	-0.35	2 (0%) 89 80	95, 133, 180, 203	0
1	AH	294/299 (98%)	-0.11	6 (2%) 68 53	103, 176, 237, 261	0
1	AI	299/299 (100%)	-0.30	0 100 100	94, 135, 163, 180	0
1	AJ	299/299 (100%)	-0.38	0 100 100	88, 121, 160, 183	0
1	AK	293/299 (97%)	-0.13	8 (2%) 58 42	94, 140, 229, 255	0
1	AL	298/299 (99%)	-0.33	2 (0%) 89 80	92, 122, 157, 172	0
1	AM	299/299 (100%)	-0.28	2 (0%) 89 80	85, 124, 188, 230	0
1	AN	294/299 (98%)	0.04	11 (3%) 45 30	92, 156, 235, 269	0
1	AO	299/299 (100%)	-0.30	1 (0%) 94 89	91, 129, 164, 182	0
1	AP	299/299 (100%)	-0.36	0 100 100	92, 129, 171, 193	0
1	AQ	295/299 (98%)	-0.17	1 (0%) 94 89	111, 172, 217, 240	0
1	AR	299/299 (100%)	-0.18	2 (0%) 89 80	95, 138, 197, 218	0
2	AS	242/253 (95%)	-0.40	1 (0%) 93 87	84, 124, 195, 234	0
2	AT	242/253 (95%)	-0.37	2 (0%) 87 77	88, 122, 191, 233	0
2	AU	242/253 (95%)	-0.41	1 (0%) 93 87	83, 121, 188, 235	0
2	AV	241/253 (95%)	-0.40	0 100 100	82, 125, 205, 257	0
2	AW	241/253 (95%)	-0.32	0 100 100	83, 125, 200, 246	0
2	AX	241/253 (95%)	-0.40	1 (0%) 93 87	86, 119, 192, 232	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
3	B1	163/173 (94%)	-0.17	0 100 100	134, 174, 213, 233	0
3	B2	162/173 (93%)	-0.27	1 (0%) 90 82	106, 137, 159, 179	0
3	BA	164/173 (94%)	0.26	9 (5%) 29 19	103, 260, 278, 283	0
3	BB	163/173 (94%)	0.45	17 (10%) 8 6	112, 254, 272, 279	0
3	BC	163/173 (94%)	0.43	19 (11%) 6 5	113, 261, 278, 280	0
3	BD	164/173 (94%)	-0.25	2 (1%) 81 67	112, 160, 181, 206	0
3	BE	164/173 (94%)	-0.27	0 100 100	112, 157, 189, 219	0
3	BF	163/173 (94%)	-0.10	5 (3%) 52 36	118, 183, 239, 258	0
3	BG	164/173 (94%)	-0.19	5 (3%) 54 37	97, 159, 203, 216	0
3	BH	164/173 (94%)	-0.11	3 (1%) 71 56	102, 148, 177, 214	0
3	BI	163/173 (94%)	-0.07	5 (3%) 52 36	99, 177, 221, 229	0
3	BJ	164/173 (94%)	-0.03	2 (1%) 81 67	106, 179, 218, 232	0
3	BK	163/173 (94%)	-0.11	3 (1%) 71 56	107, 171, 210, 235	0
3	BL	163/173 (94%)	-0.06	4 (2%) 61 44	116, 190, 228, 239	0
3	BM	163/173 (94%)	1.10	35 (21%) 1 1	133, 280, 292, 295	0
3	BN	162/173 (93%)	0.88	34 (20%) 1 1	149, 265, 278, 282	0
3	BO	162/173 (93%)	1.15	35 (21%) 1 1	147, 276, 292, 295	0
3	BP	163/173 (94%)	0.84	29 (17%) 2 2	162, 274, 286, 288	0
3	BQ	162/173 (93%)	0.93	27 (16%) 2 2	176, 241, 272, 278	0
3	BR	163/173 (94%)	0.91	31 (19%) 2 1	179, 271, 290, 294	0
3	BS	163/173 (94%)	-0.00	2 (1%) 81 67	163, 198, 224, 233	0
3	BT	164/173 (94%)	-0.03	2 (1%) 81 67	149, 196, 218, 227	0
3	BU	164/173 (94%)	0.15	8 (4%) 33 22	148, 204, 241, 256	0
3	BV	163/173 (94%)	-0.36	1 (0%) 90 82	125, 150, 191, 214	0
3	BW	164/173 (94%)	-0.24	1 (0%) 90 82	121, 146, 163, 187	0
3	BX	162/173 (93%)	-0.25	1 (0%) 90 82	118, 143, 179, 200	0
3	BY	163/173 (94%)	-0.25	0 100 100	127, 154, 182, 202	0
3	BZ	163/173 (94%)	-0.23	1 (0%) 90 82	116, 151, 180, 209	0
3	Ba	162/173 (93%)	-0.24	0 100 100	124, 148, 179, 196	0
3	Bb	163/173 (94%)	-0.10	3 (1%) 71 56	144, 200, 239, 255	0
3	Bc	164/173 (94%)	-0.20	2 (1%) 81 67	119, 196, 228, 240	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
3	Bd	165/173 (95%)	-0.03	3 (1%) 71 56	120, 187, 209, 215	0
3	Be	163/173 (94%)	0.57	23 (14%) 4 3	128, 282, 288, 291	0
3	Bf	164/173 (94%)	0.55	21 (12%) 5 4	107, 277, 289, 291	0
3	Bg	163/173 (94%)	0.38	12 (7%) 17 11	109, 273, 286, 288	0
3	Bh	161/173 (93%)	1.11	38 (23%) 1 1	194, 259, 275, 278	0
3	Bi	162/173 (93%)	0.61	20 (12%) 5 5	164, 256, 274, 276	0
3	Bj	162/173 (93%)	1.03	33 (20%) 1 1	181, 259, 276, 278	0
3	Bk	163/173 (94%)	0.04	5 (3%) 52 36	160, 187, 214, 231	0
3	Bl	163/173 (94%)	-0.09	1 (0%) 90 82	161, 184, 203, 232	0
3	Bm	162/173 (93%)	-0.07	0 100 100	156, 181, 202, 213	0
3	Bn	162/173 (93%)	0.28	8 (4%) 33 22	146, 208, 256, 274	0
3	Bo	162/173 (93%)	0.32	16 (9%) 9 6	142, 203, 230, 238	0
3	Bp	164/173 (94%)	0.31	12 (7%) 18 11	133, 210, 240, 252	0
3	Bq	163/173 (94%)	-0.02	3 (1%) 71 56	108, 192, 220, 232	0
3	Br	163/173 (94%)	-0.07	1 (0%) 90 82	100, 172, 207, 237	0
3	Bs	163/173 (94%)	-0.08	2 (1%) 81 67	99, 168, 208, 227	0
3	Bt	162/173 (93%)	0.41	8 (4%) 33 22	146, 213, 232, 257	0
3	Bu	162/173 (93%)	0.63	27 (16%) 2 2	138, 239, 271, 275	0
3	Bv	164/173 (94%)	0.61	16 (9%) 10 6	128, 225, 251, 257	0
3	Bw	163/173 (94%)	0.53	11 (6%) 21 12	182, 216, 245, 253	0
3	Bx	162/173 (93%)	0.59	20 (12%) 5 5	203, 239, 274, 280	0
3	By	162/173 (93%)	0.81	29 (17%) 2 2	195, 252, 267, 272	0
3	Bz	163/173 (94%)	-0.12	4 (2%) 61 44	130, 170, 232, 238	0
All	All	15597/16242 (96%)	0.01	658 (4%) 40 26	82, 163, 274, 295	0

All (658) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	BQ	135	ASP	13.7
3	BO	91	GLY	13.5
3	BR	69	GLY	12.6
3	BO	92	GLY	11.4
3	BQ	120	SER	9.8
3	BM	91	GLY	8.9

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Mol	Chain	Res	Type	RSRZ
3	Bh	76	ILE	8.6
3	BO	78	SER	8.5
3	BB	73	GLY	8.3
3	Bh	92	GLY	8.3
3	Bh	91	GLY	7.8
3	BN	108	SER	7.8
3	BM	133	HIS	7.7
3	Bt	69	GLY	7.4
3	Bg	69	GLY	7.4
3	Bj	91	GLY	7.4
3	BO	135	ASP	7.3
3	BO	76	ILE	7.3
3	BO	89	SER	7.2
3	BR	70	GLU	7.1
3	Bj	69	GLY	7.1
3	Bf	89	SER	7.0
3	Bj	120	SER	7.0
3	BQ	145	PHE	7.0
3	BQ	119	CYS	7.0
3	Bj	74	GLY	6.5
3	Bg	158	GLY	6.4
3	BM	158	GLY	6.3
3	Bg	157	THR	6.3
3	BM	131	ALA	6.2
3	BN	109	VAL	6.1
3	Bv	135	ASP	6.0
3	BN	159	THR	6.0
3	Bv	118	ARG	5.9
3	BU	92	GLY	5.9
3	BR	76	ILE	5.8
3	BP	83	GLY	5.8
3	Bf	159	THR	5.8
3	BP	158	GLY	5.7
1	AE	34	ALA	5.7
3	BO	139	SER	5.7
3	By	92	GLY	5.7
3	Bh	74	GLY	5.6
3	Bj	119	CYS	5.5
3	BC	133	HIS	5.5
3	BR	159	THR	5.4
3	BU	91	GLY	5.4
3	Bp	108	SER	5.4

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Mol	Chain	Res	Type	RSRZ
3	BM	120	SER	5.4
3	BB	74	GLY	5.3
3	Bf	78	SER	5.3
3	Be	73	GLY	5.3
3	BA	91	GLY	5.3
3	BM	76	ILE	5.2
3	Bi	159	THR	5.2
2	AT	12	HIS	5.2
3	BR	155	ARG	5.2
3	Bj	73	GLY	5.2
3	Bv	57	ASN	5.2
3	BQ	133	HIS	5.2
3	Bx	158	GLY	5.1
3	BO	120	SER	5.1
3	BO	145	PHE	5.1
3	Bh	120	SER	5.1
3	BM	154	PRO	5.1
3	BR	154	PRO	5.1
3	Be	142	CYS	5.0
3	BC	132	PHE	5.0
3	By	69	GLY	5.0
1	AE	56	ALA	5.0
3	BB	69	GLY	5.0
3	Be	74	GLY	5.0
3	Bj	157	THR	4.9
3	BO	142	CYS	4.9
3	Bh	156	GLY	4.9
3	BN	69	GLY	4.8
3	Bg	92	GLY	4.8
3	Be	69	GLY	4.8
3	Bf	120	SER	4.8
3	BO	141	VAL	4.7
3	By	91	GLY	4.7
3	Be	76	ILE	4.7
3	Bx	141	VAL	4.7
3	Bh	159	THR	4.7
3	Bv	119	CYS	4.7
3	BN	140	GLY	4.7
3	BU	156	GLY	4.6
3	By	143	GLN	4.6
1	AF	16	ASN	4.6
3	Bw	15	ALA	4.6

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Mol	Chain	Res	Type	RSRZ
3	BQ	118	ARG	4.6
3	Be	92	GLY	4.6
3	BO	154	PRO	4.6
3	Bg	120	SER	4.6
3	BP	159	THR	4.6
3	BM	89	SER	4.5
3	BP	143	GLN	4.5
3	Bt	70	GLU	4.5
3	Bi	158	GLY	4.5
3	BM	112	GLU	4.5
3	BO	74	GLY	4.5
3	Bh	73	GLY	4.5
3	BP	139	SER	4.4
3	BM	103	ASN	4.4
3	BR	75	ILE	4.4
3	Bu	143	GLN	4.4
3	BP	135	ASP	4.4
3	BA	142	CYS	4.3
3	BR	123	GLY	4.3
3	Bg	73	GLY	4.3
3	BP	141	VAL	4.3
3	BP	142	CYS	4.3
3	Bt	76	ILE	4.3
3	Bt	154	PRO	4.2
3	Bc	158	GLY	4.2
3	BR	157	THR	4.2
3	BQ	143	GLN	4.2
3	Bn	92	GLY	4.2
3	BM	90	ILE	4.2
3	BP	84	THR	4.2
3	Be	109	VAL	4.2
3	BM	101	ASN	4.1
3	Be	135	ASP	4.1
3	BH	156	GLY	4.1
3	BM	159	THR	4.1
3	Bn	91	GLY	4.1
1	AN	49	GLN	4.1
3	Bh	75	ILE	4.1
3	Bj	135	ASP	4.1
3	BO	108	SER	4.1
3	BT	120	SER	4.0
3	BC	123	GLY	4.0

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Mol	Chain	Res	Type	RSRZ
3	BN	133	HIS	4.0
3	BR	117	ASN	4.0
3	Bi	104	LEU	4.0
3	BM	132	PHE	4.0
3	BN	55	GLU	4.0
3	Bp	92	GLY	4.0
3	Bj	142	CYS	4.0
3	Bi	117	ASN	3.9
3	Bi	141	VAL	3.9
3	BB	142	CYS	3.9
3	BN	110	PRO	3.9
3	BO	133	HIS	3.9
3	BA	92	GLY	3.9
3	Bf	108	SER	3.9
3	Bf	76	ILE	3.9
3	Bx	76	ILE	3.8
3	Bv	143	GLN	3.8
1	AN	106	GLY	3.8
3	BB	75	ILE	3.8
3	Bh	108	SER	3.8
3	Bu	163	ASP	3.8
3	Bh	93	GLU	3.8
3	Bx	103	ASN	3.8
3	BN	92	GLY	3.8
3	BA	148	THR	3.8
3	Bh	77	LEU	3.8
3	Bi	161	PRO	3.8
3	Bp	105	VAL	3.8
3	Bh	72	GLY	3.8
3	Bu	103	ASN	3.8
3	BN	44	ILE	3.8
3	Bj	81	LYS	3.8
3	BR	142	CYS	3.8
3	Bx	70	GLU	3.8
3	BQ	136	ILE	3.8
3	By	76	ILE	3.7
3	BH	158	GLY	3.7
3	Be	72	GLY	3.7
3	Bx	55	GLU	3.7
3	Bg	93	GLU	3.7
3	BN	154	PRO	3.7
3	BB	91	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
3	Bf	91	GLY	3.7
3	Bi	108	SER	3.6
3	BR	141	VAL	3.6
3	Bf	65	LYS	3.6
1	AQ	269	ASP	3.6
3	Bn	93	GLU	3.6
1	AH	261	LEU	3.6
1	AK	105	GLY	3.6
3	BM	156	GLY	3.6
3	Bv	101	ASN	3.6
3	BI	158	GLY	3.6
3	Bt	155	ARG	3.6
3	BO	137	PRO	3.6
3	BC	97	SER	3.6
3	Bj	92	GLY	3.6
3	BU	113	PHE	3.6
3	BG	120	SER	3.6
3	Bp	109	VAL	3.6
3	BN	158	GLY	3.6
3	BQ	96	SER	3.6
3	Bj	77	LEU	3.6
3	BR	108	SER	3.5
3	BP	56	VAL	3.5
3	Bj	141	VAL	3.5
3	BN	74	GLY	3.5
3	Bz	158	GLY	3.5
3	Bf	142	CYS	3.5
3	BR	156	GLY	3.5
3	BN	85	THR	3.5
3	BR	118	ARG	3.5
3	Bf	141	VAL	3.5
3	BP	82	LYS	3.5
1	AH	105	GLY	3.5
3	BP	157	THR	3.4
3	BR	74	GLY	3.4
3	Bx	69	GLY	3.4
3	By	70	GLU	3.4
3	BR	103	ASN	3.4
3	Bh	142	CYS	3.4
3	Bv	137	PRO	3.4
3	BP	55	GLU	3.4
3	BN	84	THR	3.4

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Mol	Chain	Res	Type	RSRZ
3	Bi	140	GLY	3.4
3	BB	72	GLY	3.4
3	BU	158	GLY	3.4
3	Bi	142	CYS	3.4
3	BB	94	ILE	3.4
1	AL	15	ASN	3.4
3	Bv	64	THR	3.3
3	By	72	GLY	3.3
3	BR	72	GLY	3.3
3	BN	73	GLY	3.3
1	AG	269	ASP	3.3
3	Bs	158	GLY	3.3
3	Bx	95	SER	3.3
3	Bx	159	THR	3.3
3	BM	123	GLY	3.3
3	By	71	LEU	3.3
3	BQ	63	PRO	3.3
3	BN	149	ALA	3.3
1	AN	105	GLY	3.3
3	Bf	79	LEU	3.3
3	BM	111	ASN	3.3
3	BC	73	GLY	3.2
3	Bh	157	THR	3.2
3	BF	69	GLY	3.2
3	BB	76	ILE	3.2
3	Be	91	GLY	3.2
3	Bq	69	GLY	3.2
3	BO	105	VAL	3.2
3	BP	10	GLY	3.2
3	BU	157	THR	3.2
3	Bj	78	SER	3.2
3	Bo	150	SER	3.2
3	BR	143	GLN	3.2
3	Bf	158	GLY	3.2
3	BP	85	THR	3.2
3	Bh	78	SER	3.2
3	Bi	98	ILE	3.2
3	Bu	83	GLY	3.2
3	Bj	127	GLY	3.2
3	Bo	69	GLY	3.2
3	Bw	54	VAL	3.2
3	Bf	66	SER	3.2

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Mol	Chain	Res	Type	RSRZ
3	BA	135	ASP	3.2
3	Bh	138	SER	3.2
3	Bo	89	SER	3.2
3	Bu	46	GLY	3.1
3	Bv	120	SER	3.1
3	Bu	102	SER	3.1
3	BO	119	CYS	3.1
3	Bu	45	ALA	3.1
3	Bw	158	GLY	3.1
3	BG	158	GLY	3.1
3	Bg	156	GLY	3.1
3	BO	136	ILE	3.1
3	Bo	141	VAL	3.1
3	BM	77	LEU	3.1
3	BR	158	GLY	3.1
3	Bg	159	THR	3.1
3	Bo	142	CYS	3.1
3	Bp	142	CYS	3.1
3	Bx	123	GLY	3.1
3	Bk	156	GLY	3.1
3	By	68	SER	3.0
1	AB	34	ALA	3.0
3	BH	157	THR	3.0
1	AH	269	ASP	3.0
3	BA	137	PRO	3.0
3	Be	75	ILE	3.0
3	Bv	48	LYS	3.0
3	Bf	49	THR	3.0
1	AE	261	LEU	3.0
3	BQ	97	SER	3.0
3	By	135	ASP	3.0
1	AK	106	GLY	3.0
1	AN	100	PHE	3.0
3	Bh	112	GLU	3.0
3	BQ	95	SER	3.0
3	By	67	TRP	3.0
3	Bu	142	CYS	3.0
3	Bv	136	ILE	3.0
3	BP	102	SER	3.0
3	Bo	149	ALA	3.0
3	Bp	104	LEU	3.0
3	BO	144	TRP	3.0

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Mol	Chain	Res	Type	RSRZ
1	AN	98	PHE	3.0
3	Bo	105	VAL	3.0
3	Be	143	GLN	3.0
3	Bj	148	THR	3.0
3	BR	73	GLY	2.9
3	Bi	133	HIS	2.9
3	Bi	148	THR	2.9
3	Bw	63	PRO	2.9
3	Bb	143	GLN	2.9
3	BQ	142	CYS	2.9
3	By	142	CYS	2.9
3	BU	155	ARG	2.9
3	Bv	145	PHE	2.9
1	AH	30	GLN	2.9
3	Bt	61	THR	2.9
3	Bu	123	GLY	2.9
1	AN	108	TRP	2.9
3	BC	162	ILE	2.9
3	BF	76	ILE	2.9
3	Bu	54	VAL	2.9
3	BB	92	GLY	2.9
3	BM	66	SER	2.9
3	Bp	159	THR	2.9
3	BC	108	SER	2.9
3	Bj	159	THR	2.9
3	BK	158	GLY	2.9
3	BO	103	ASN	2.9
3	BO	143	GLN	2.9
3	Bo	159	THR	2.8
3	BM	155	ARG	2.8
3	BP	140	GLY	2.8
3	BP	155	ARG	2.8
3	Bh	141	VAL	2.8
3	BO	107	ARG	2.8
3	Bj	59	SER	2.8
3	Bn	78	SER	2.8
3	BI	76	ILE	2.8
3	BQ	81	LYS	2.8
3	Bu	53	ASN	2.8
3	BJ	120	SER	2.8
3	Be	93	GLU	2.8
3	BM	143	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
3	Bj	136	ILE	2.8
3	Be	55	GLU	2.8
3	BQ	108	SER	2.8
3	Bo	76	ILE	2.8
3	By	75	ILE	2.8
3	BM	157	THR	2.8
3	BP	103	ASN	2.8
3	Bn	137	PRO	2.8
3	BR	67	TRP	2.8
1	AN	103	GLN	2.8
3	By	60	LEU	2.8
3	BM	113	PHE	2.8
3	Bh	105	VAL	2.8
3	Bj	156	GLY	2.8
2	AX	13	TYR	2.8
3	BB	77	LEU	2.7
3	Bw	36	VAL	2.7
3	By	154	PRO	2.7
3	BM	102	SER	2.7
1	AB	36	ILE	2.7
3	BN	68	SER	2.7
3	BN	78	SER	2.7
3	Bu	55	GLU	2.7
3	Bo	77	LEU	2.7
3	BB	143	GLN	2.7
3	Bd	157	THR	2.7
3	BB	89	SER	2.7
1	AK	43	LYS	2.7
3	BL	143	GLN	2.7
3	BM	110	PRO	2.7
3	BO	159	THR	2.7
3	Bx	73	GLY	2.7
1	AE	79	LEU	2.7
3	Bb	91	GLY	2.7
3	Bh	89	SER	2.7
3	Bx	102	SER	2.7
3	Bn	139	SER	2.7
3	Bq	143	GLN	2.7
3	Bx	92	GLY	2.7
3	Bh	55	GLU	2.6
3	BR	71	LEU	2.6
3	BQ	73	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
3	By	152	GLY	2.6
3	BC	119	CYS	2.6
3	BN	54	VAL	2.6
1	AN	1	MET	2.6
3	Bf	87	GLU	2.6
3	Bu	89	SER	2.6
3	By	151	SER	2.6
3	BP	51	THR	2.6
3	Be	159	THR	2.6
3	Bh	158	GLY	2.6
3	BI	69	GLY	2.6
3	BM	65	LYS	2.6
3	BC	141	VAL	2.6
3	BQ	157	THR	2.6
3	Bu	95	SER	2.6
3	BC	95	SER	2.6
3	BN	120	SER	2.6
3	Bf	92	GLY	2.6
3	Bh	95	SER	2.6
3	Be	123	GLY	2.6
3	BQ	86	VAL	2.6
3	Bj	154	PRO	2.6
3	Bv	93	GLU	2.6
3	BN	156	GLY	2.6
3	BQ	101	ASN	2.6
3	Be	119	CYS	2.6
3	Bv	142	CYS	2.6
3	By	59	SER	2.6
3	Bf	154	PRO	2.6
3	BM	141	VAL	2.6
3	By	95	SER	2.6
1	AA	269	ASP	2.6
3	BC	92	GLY	2.6
3	Bk	141	VAL	2.5
1	AB	43	LYS	2.5
3	Bk	69	GLY	2.5
3	BG	159	THR	2.5
3	Bw	159	THR	2.5
3	BM	150	SER	2.5
3	BN	113	PHE	2.5
1	AN	99	SER	2.5
3	BC	54	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
3	Bh	143	GLN	2.5
3	Bu	139	SER	2.5
3	BR	119	CYS	2.5
3	BO	106	ASN	2.5
3	Bo	119	CYS	2.5
3	BC	109	VAL	2.5
3	Be	77	LEU	2.5
3	BP	81	LYS	2.5
3	Bt	49	THR	2.5
3	BC	75	ILE	2.5
3	Bj	126	VAL	2.5
3	Bp	158	GLY	2.5
1	AR	269	ASP	2.5
3	Bi	48	LYS	2.5
3	Bn	108	SER	2.5
3	BP	72	GLY	2.5
3	Bh	155	ARG	2.5
1	AB	269	ASP	2.5
3	Bj	65	LYS	2.5
3	BN	105	VAL	2.5
3	Be	139	SER	2.5
3	BO	77	LEU	2.5
3	BZ	158	GLY	2.5
3	By	150	SER	2.5
3	Bu	141	VAL	2.5
3	Bx	135	ASP	2.5
3	BM	50	PHE	2.5
1	AM	299	ALA	2.5
1	AR	299	ALA	2.5
3	Bh	119	CYS	2.4
3	BS	154	PRO	2.4
3	By	89	SER	2.4
3	BR	135	ASP	2.4
3	Bj	108	SER	2.4
3	By	103	ASN	2.4
3	Br	159	THR	2.4
3	Bl	21	ASP	2.4
3	Bs	69	GLY	2.4
3	BM	121	LEU	2.4
3	Bh	154	PRO	2.4
3	Bf	133	HIS	2.4
3	BO	93	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
3	Bu	110	PRO	2.4
3	Bv	117	ASN	2.4
3	Bi	109	VAL	2.4
3	BM	130	ASN	2.4
3	Bx	68	SER	2.4
3	BP	99	LEU	2.4
3	Bx	96	SER	2.4
3	Bw	17	THR	2.4
3	BO	87	GLU	2.4
3	Bg	108	SER	2.4
3	Bx	120	SER	2.4
3	BC	69	GLY	2.4
3	BC	76	ILE	2.4
3	BR	164	SER	2.4
3	Be	57	ASN	2.4
3	Bh	61	THR	2.4
3	BD	158	GLY	2.4
3	BU	89	SER	2.4
3	Bo	158	GLY	2.4
3	Bh	53	ASN	2.4
3	Bh	70	GLU	2.4
3	BR	109	VAL	2.4
1	AB	18	GLY	2.4
3	Bf	135	ASP	2.4
3	BP	154	PRO	2.3
3	Bn	158	GLY	2.3
1	AB	4	HIS	2.3
3	BO	104	LEU	2.3
3	Bz	142	CYS	2.3
1	AN	104	GLU	2.3
3	BP	126	VAL	2.3
3	BC	144	TRP	2.3
3	By	96	SER	2.3
1	AH	106	GLY	2.3
3	BL	69	GLY	2.3
3	Bj	72	GLY	2.3
3	BP	98	ILE	2.3
3	Bu	111	ASN	2.3
3	BN	142	CYS	2.3
3	Be	151	SER	2.3
3	Bi	139	SER	2.3
3	BX	113	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
3	BG	157	THR	2.3
3	Bo	104	LEU	2.3
3	Bu	85	THR	2.3
3	By	157	THR	2.3
3	Bg	91	GLY	2.3
3	BD	157	THR	2.3
3	BM	140	GLY	2.3
3	Bi	85	THR	2.3
3	Bk	135	ASP	2.3
3	BQ	134	ILE	2.3
3	Bu	84	THR	2.3
3	BN	112	GLU	2.3
3	BR	161	PRO	2.3
3	BN	72	GLY	2.3
1	AM	269	ASP	2.3
3	Bu	144	TRP	2.3
1	AL	16	ASN	2.3
3	Be	120	SER	2.3
3	Bw	14	GLY	2.3
3	Bp	114	CYS	2.3
3	BA	118	ARG	2.3
3	BA	66	SER	2.2
3	Bj	83	GLY	2.2
3	Bu	140	GLY	2.2
3	Bi	97	SER	2.2
3	Bk	143	GLN	2.2
1	AG	243	SER	2.2
3	BK	157	THR	2.2
3	BO	140	GLY	2.2
3	BA	143	GLN	2.2
3	BO	69	GLY	2.2
3	Bf	81	LYS	2.2
3	BN	79	LEU	2.2
3	BN	95	SER	2.2
3	BW	158	GLY	2.2
3	By	74	GLY	2.2
3	B2	10	GLY	2.2
1	AN	50	PRO	2.2
3	Bh	69	GLY	2.2
3	Bh	107	ARG	2.2
3	BM	99	LEU	2.2
3	BB	155	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
3	Bi	86	VAL	2.2
3	Bj	130	ASN	2.2
3	BC	157	THR	2.2
3	BN	161	PRO	2.2
1	AK	269	ASP	2.2
3	BP	29	LEU	2.2
3	BP	64	THR	2.2
3	Bx	148	THR	2.2
3	BN	141	VAL	2.2
1	AB	8	LEU	2.2
3	BT	165	ALA	2.2
3	Bb	157	THR	2.2
3	BQ	144	TRP	2.2
3	Bh	54	VAL	2.2
3	Bh	162	ILE	2.2
3	Bo	103	ASN	2.2
1	AE	32	ILE	2.2
3	Be	94	ILE	2.2
3	Bh	94	ILE	2.2
3	BF	157	THR	2.2
3	BN	43	THR	2.2
3	BG	156	GLY	2.2
3	BI	144	TRP	2.2
1	AK	50	PRO	2.2
3	BI	157	THR	2.1
1	AK	34	ALA	2.1
3	BB	141	VAL	2.1
3	BF	92	GLY	2.1
3	Bg	155	ARG	2.1
3	Bj	76	ILE	2.1
3	Bx	143	GLN	2.1
3	Bj	103	ASN	2.1
3	Bq	141	VAL	2.1
3	Bj	143	GLN	2.1
3	Bo	120	SER	2.1
3	BQ	50	PHE	2.1
3	Bp	110	PRO	2.1
3	BO	138	SER	2.1
3	BQ	78	SER	2.1
3	Bt	73	GLY	2.1
3	By	105	VAL	2.1
3	By	49	THR	2.1

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Mol	Chain	Res	Type	RSRZ
2	AU	12	HIS	2.1
3	Bw	123	GLY	2.1
3	BR	2	ALA	2.1
1	AB	35	GLN	2.1
3	BM	95	SER	2.1
3	BV	164	SER	2.1
3	Bd	158	GLY	2.1
3	Bu	124	HIS	2.1
3	Bx	91	GLY	2.1
3	BN	63	PRO	2.1
3	BQ	107	ARG	2.1
3	Bh	109	VAL	2.1
3	BF	158	GLY	2.1
3	BB	95	SER	2.1
3	BB	133	HIS	2.1
3	BL	135	ASP	2.1
3	BJ	165	ALA	2.1
3	BP	104	LEU	2.1
3	BN	87	GLU	2.1
3	Bz	89	SER	2.1
3	BQ	146	GLY	2.1
1	AB	1	MET	2.1
3	Bw	43	THR	2.1
1	AF	15	ASN	2.1
3	Bu	112	GLU	2.1
3	By	106	ASN	2.1
3	BO	158	GLY	2.1
3	Bv	72	GLY	2.1
3	BL	119	CYS	2.1
3	BR	136	ILE	2.1
3	Bd	141	VAL	2.1
3	BM	109	VAL	2.1
3	BR	132	PHE	2.1
1	AE	36	ILE	2.0
3	BC	72	GLY	2.0
3	BK	156	GLY	2.0
3	Bf	119	CYS	2.0
3	Bu	99	LEU	2.0
3	Bp	130	ASN	2.0
3	BO	156	GLY	2.0
3	Bu	73	GLY	2.0
3	Bj	89	SER	2.0

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Mol	Chain	Res	Type	RSRZ
3	Bu	63	PRO	2.0
1	AO	269	ASP	2.0
3	BQ	112	GLU	2.0
3	Bw	103	ASN	2.0
1	AK	36	ILE	2.0
2	AT	13	TYR	2.0
3	Bh	81	LYS	2.0
3	By	138	SER	2.0
3	BS	153	THR	2.0
1	AH	47	GLY	2.0
3	Bc	156	GLY	2.0
3	Bj	158	GLY	2.0
3	BQ	155	ARG	2.0
3	Bj	80	ARG	2.0
3	Bp	71	LEU	2.0
3	BO	90	ILE	2.0
3	Bi	92	GLY	2.0
3	Bi	154	PRO	2.0
2	AS	13	TYR	2.0
3	Bo	78	SER	2.0
3	Bz	92	GLY	2.0
1	AK	8	LEU	2.0

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.