Full wwPDB EM Validation Report ⓘ

Nov 28, 2022 – 11:15 AM EST

PDB ID	:	7SPB
EMDB ID	:	EMD-24769
Title	:	Models for C13 reconstruction of Outer Membrane Core Complex (OMCC) of Type IV Secretion System (T4SS) encoded by F-plasmid (pED208).
Authors	:	Liu, X.; Khara, P.; Baker, M.L.; Christie, P.J.; Hu, B.
Deposited on	:	2021-11-02
Resolution	:	3.31 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

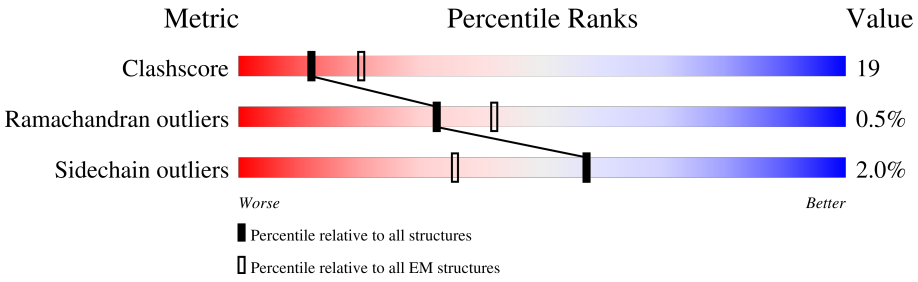
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.31 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)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A1	204	18% 9% 73%
1	A10	204	19% 8% 73%
1	A11	204	17% 10% 73%
1	A12	204	19% 8% 73%
1	A13	204	18% 9% 73%
1	A2	204	19% 8% 73%
1	A3	204	19% 8% 73%
1	A4	204	19% 8% 73%

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Mol	Chain	Length	Quality of chain
1	A5	204	19% 8% 73%
1	A6	204	19% 8% 73%
1	A7	204	19% 8% 73%
1	A8	204	19% 8% 73%
1	A9	204	18% 9% 73%
1	B1	204	25% 7% 68%
1	B10	204	24% 8% 68%
1	B11	204	24% 8% 68%
1	B12	204	24% 8% 68%
1	B13	204	25% 7% 68%
1	B2	204	24% 8% 68%
1	B3	204	24% 8% 68%
1	B4	204	24% 8% 68%
1	B5	204	24% 8% 68%
1	B6	204	24% 8% 68%
1	B7	204	24% 8% 68%
1	B8	204	25% 7% 68%
1	B9	204	24% 8% 68%
2	C1	246	68% 20% 12%
2	C10	246	68% 20% 12%
2	C11	246	68% 20% 12%
2	C12	246	67% 20% 12%
2	C13	246	67% 21% 12%
2	C2	246	66% 22% 12%
2	C3	246	68% 20% 12%

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Mol	Chain	Length	Quality of chain
2	C4	246	68% 20% 12%
2	C5	246	67% 21% 12%
2	C6	246	68% 20% 12%
2	C7	246	68% 20% 12%
2	C8	246	67% 20% 12%
2	C9	246	68% 20% 12%
2	D1	246	10% 66% 22% 12%
2	D10	246	10% 65% 23% 12%
2	D11	246	10% 65% 23% 12%
2	D12	246	11% 65% 23% 12%
2	D13	246	11% 65% 23% 12%
2	D2	246	10% 66% 22% 12%
2	D3	246	9% 65% 22% 12%
2	D4	246	9% 65% 22% 12%
2	D5	246	11% 65% 23% 12%
2	D6	246	9% 65% 23% 12%
2	D7	246	9% 64% 24% 12%
2	D8	246	10% 65% 23% 12%
2	D9	246	10% 65% 23% 12%
3	E1	453	98%
3	E10	453	98%
3	E11	453	98%
3	E12	453	98%
3	E13	453	98%
3	E2	453	98%

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Mol	Chain	Length	Quality of chain
3	E3	453	98%
3	E4	453	98%
3	E5	453	98%
3	E6	453	98%
3	E7	453	98%
3	E8	453	98%
3	E9	453	98%
3	F1	453	98%
3	F10	453	98%
3	F11	453	98%
3	F12	453	98%
3	F13	453	98%
3	F2	453	98%
3	F3	453	98%
3	F4	453	98%
3	F5	453	98%
3	F6	453	98%
3	F7	453	98%
3	F8	453	98%
3	F9	453	98%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 57408 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 TraV.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	55	Total	C	N	O	S	0	0
			436	275	83	77	1		
1	A2	55	Total	C	N	O	S	0	0
			436	275	83	77	1		
1	A3	55	Total	C	N	O	S	0	0
			436	275	83	77	1		
1	A4	55	Total	C	N	O	S	0	0
			436	275	83	77	1		
1	A5	55	Total	C	N	O	S	0	0
			436	275	83	77	1		
1	A6	55	Total	C	N	O	S	0	0
			436	275	83	77	1		
1	A7	55	Total	C	N	O	S	0	0
			436	275	83	77	1		
1	A8	55	Total	C	N	O	S	0	0
			436	275	83	77	1		
1	A9	55	Total	C	N	O	S	0	0
			436	275	83	77	1		
1	A10	55	Total	C	N	O	S	0	0
			436	275	83	77	1		
1	A11	55	Total	C	N	O	S	0	0
			436	275	83	77	1		
1	A12	55	Total	C	N	O	S	0	0
			436	275	83	77	1		
1	A13	55	Total	C	N	O	S	0	0
			436	275	83	77	1		
1	B1	65	Total	C	N	O	S	0	0
			498	314	92	91	1		
1	B2	65	Total	C	N	O	S	0	0
			498	314	92	91	1		
1	B3	65	Total	C	N	O	S	0	0
			498	314	92	91	1		
1	B4	65	Total	C	N	O	S	0	0
			498	314	92	91	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	B5	65	Total	C	N	O	S	0	0
			498	314	92	91	1		
1	B6	65	Total	C	N	O	S	0	0
			498	314	92	91	1		
1	B7	65	Total	C	N	O	S	0	0
			498	314	92	91	1		
1	B8	65	Total	C	N	O	S	0	0
			498	314	92	91	1		
1	B9	65	Total	C	N	O	S	0	0
			498	314	92	91	1		
1	B10	65	Total	C	N	O	S	0	0
			498	314	92	91	1		
1	B11	65	Total	C	N	O	S	0	0
			498	314	92	91	1		
1	B12	65	Total	C	N	O	S	0	0
			498	314	92	91	1		
1	B13	65	Total	C	N	O	S	0	0
			498	314	92	91	1		

- Molecule 2 is a protein called TraK.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C1	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	C2	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	C3	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	C4	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	C5	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	C6	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	C7	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	C8	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	C9	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	C10	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	C11	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	C12	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	C13	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	D1	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	D2	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	D3	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	D4	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	D5	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	D6	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	D7	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	D8	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	D9	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	D10	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	D11	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	D12	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		
2	D13	217	Total	C	N	O	S	0	0
			1654	1041	299	308	6		

- Molecule 3 is a protein called TraB.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E1	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	E2	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	E3	11	Total	C	N	O	S	0	0
			87	52	15	18	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	E4	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	E5	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	E6	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	E7	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	E8	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	E9	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	E10	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	E11	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	E12	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	E13	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	F1	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	F2	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	F3	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	F4	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	F5	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	F6	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	F7	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	F8	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	F9	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	F10	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	F11	11	Total	C	N	O	S	0	0
			87	52	15	18	2		

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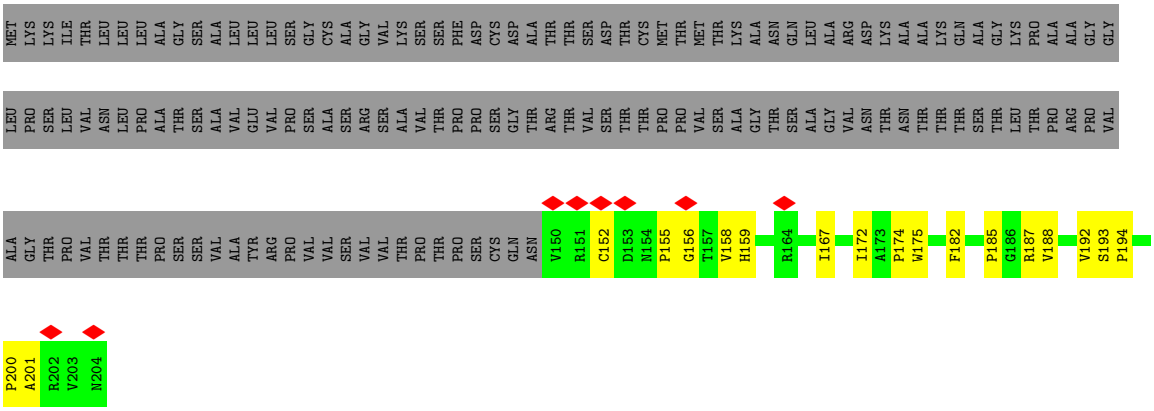
Mol	Chain	Residues	Atoms					AltConf	Trace
3	F12	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	F13	11	Total	C	N	O	S	0	0
			87	52	15	18	2		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

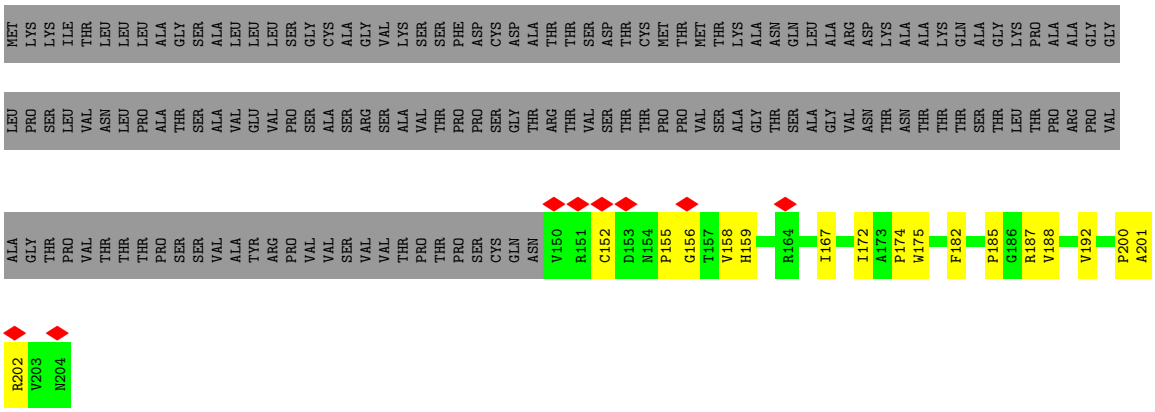
• Molecule 1: TraV

Chain A1:



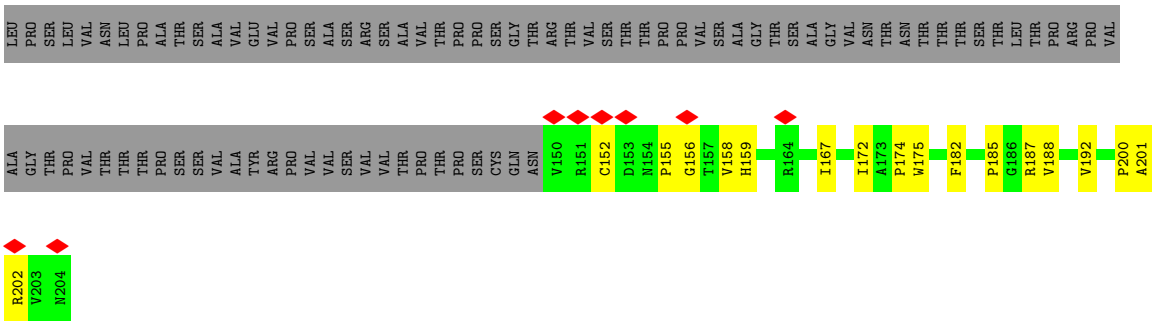
• Molecule 1: TraV

Chain A2:



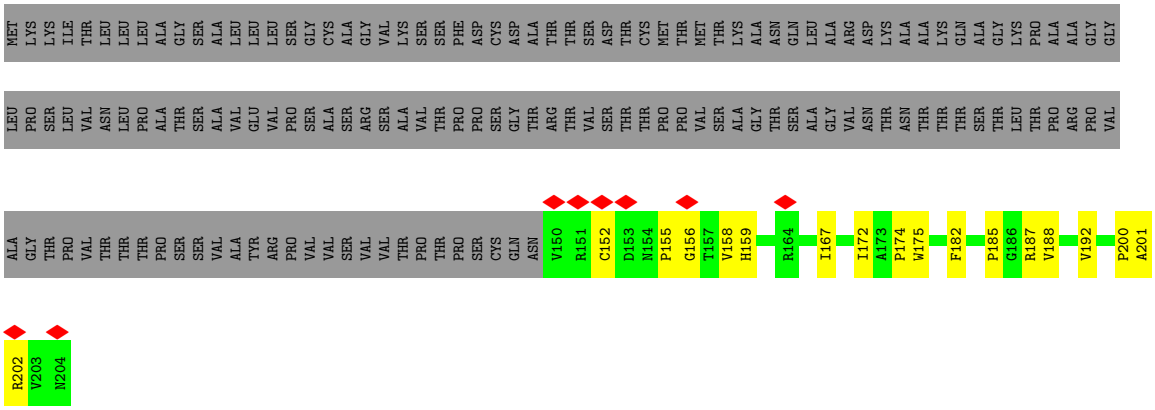
• Molecule 1: TraV

Chain A3:



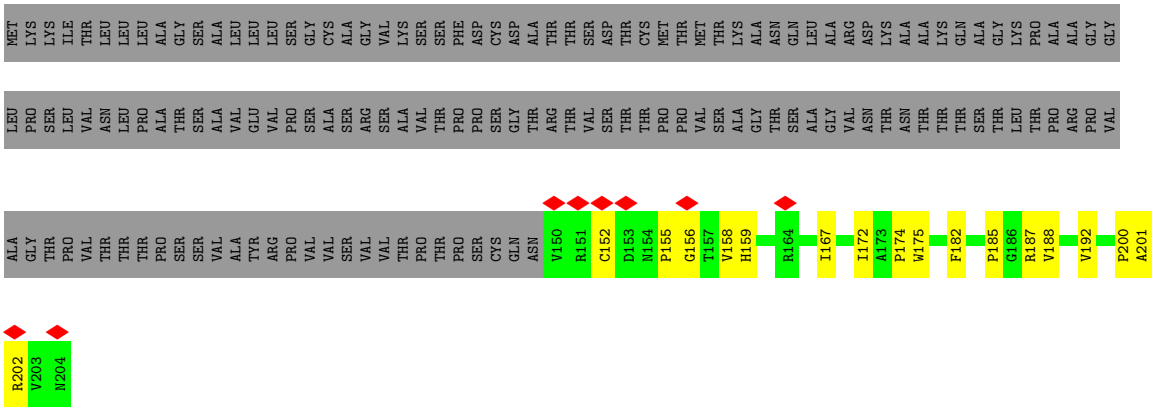
• Molecule 1: TraV

Chain A4:



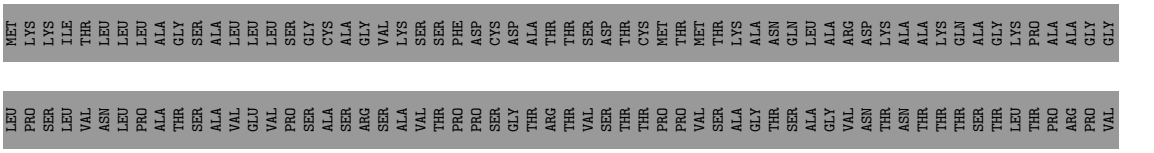
• Molecule 1: TraV

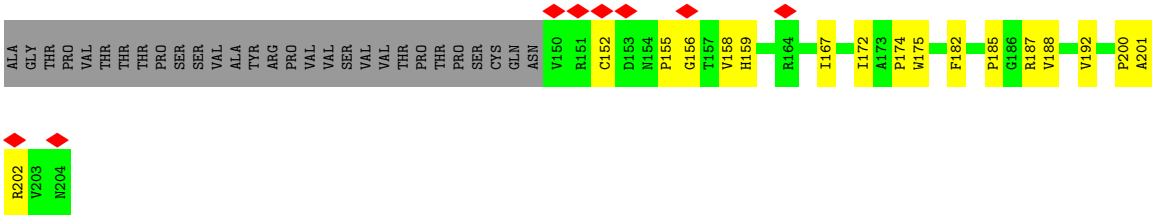
Chain A5:



• Molecule 1: TraV

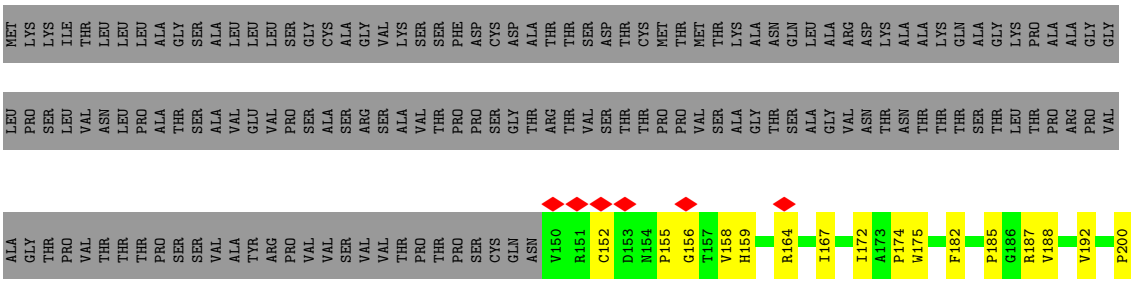
Chain A6:





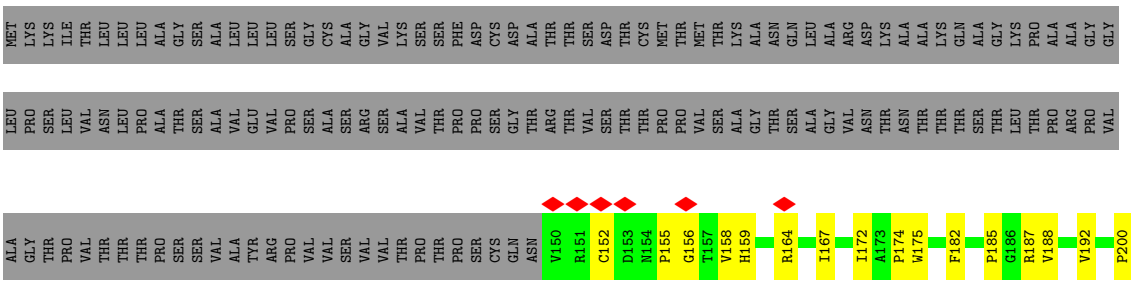
• Molecule 1: TraV

Chain A7:



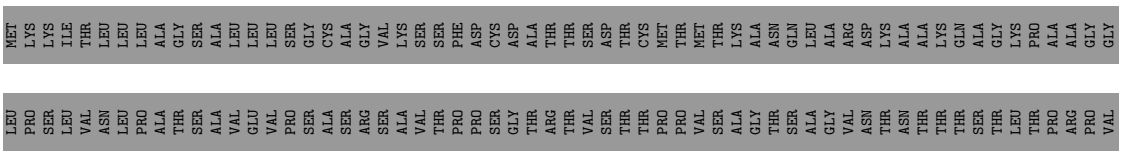
• Molecule 1: TraV

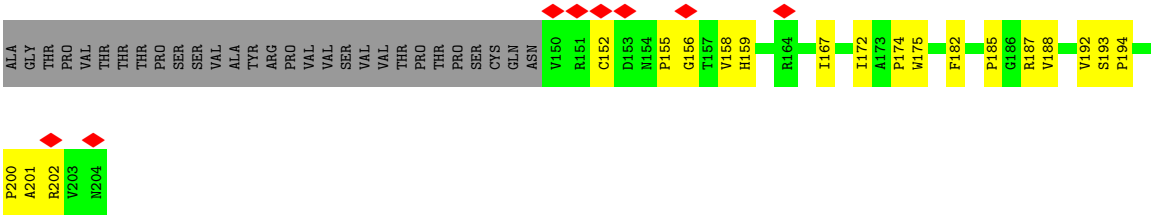
Chain A8:



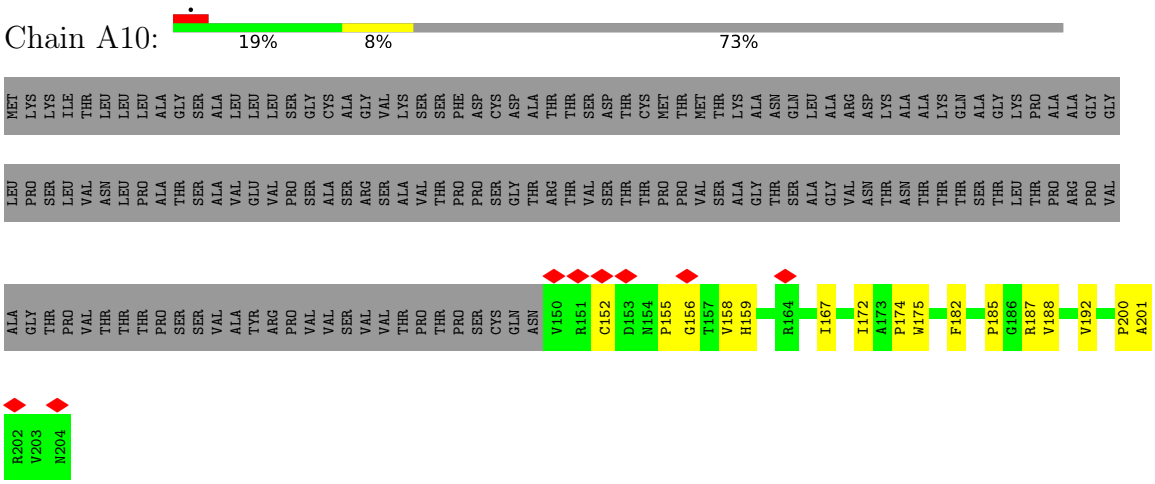
• Molecule 1: TraV

Chain A9:

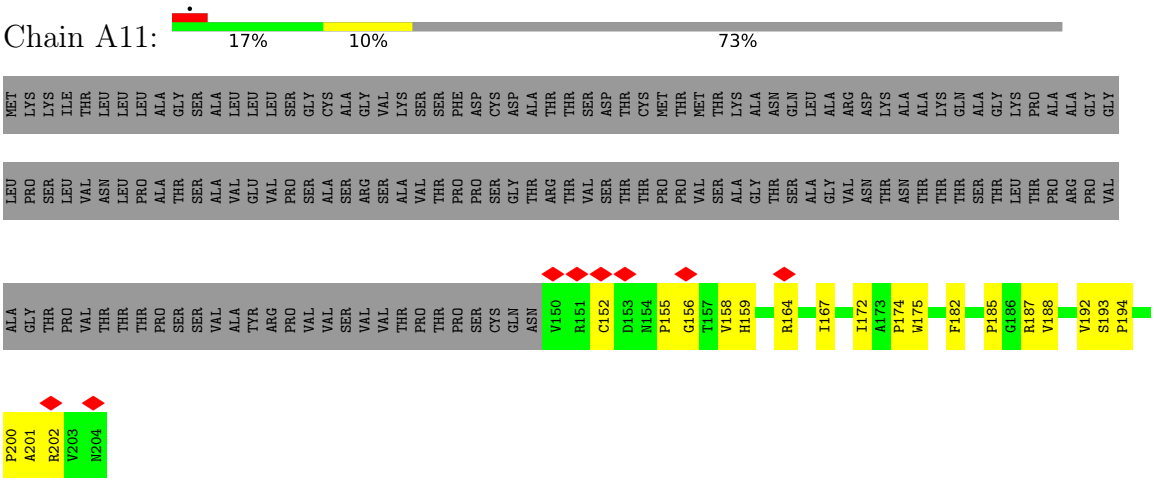




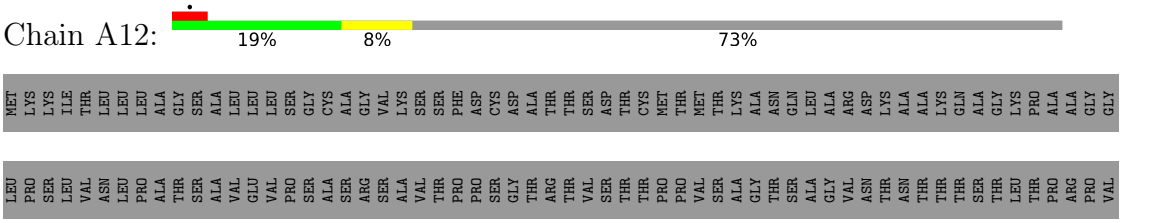
• Molecule 1: TraV

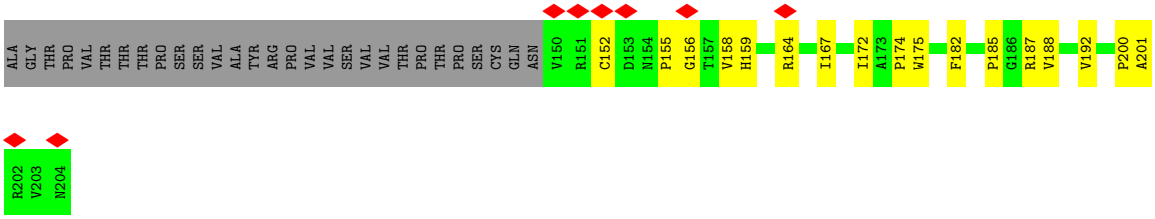


• Molecule 1: TraV



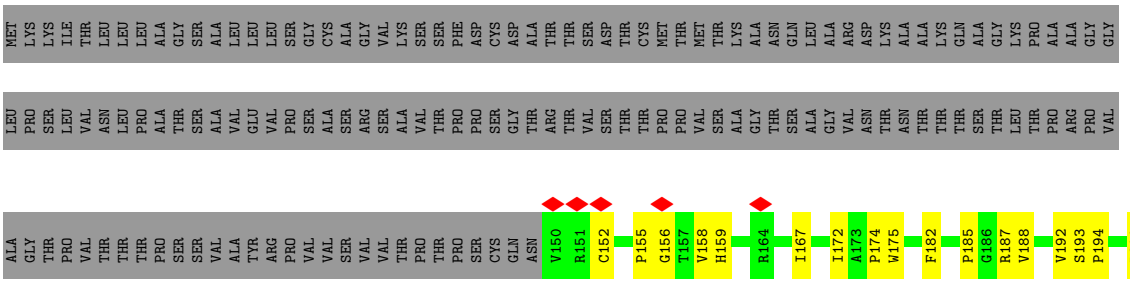
• Molecule 1: TraV





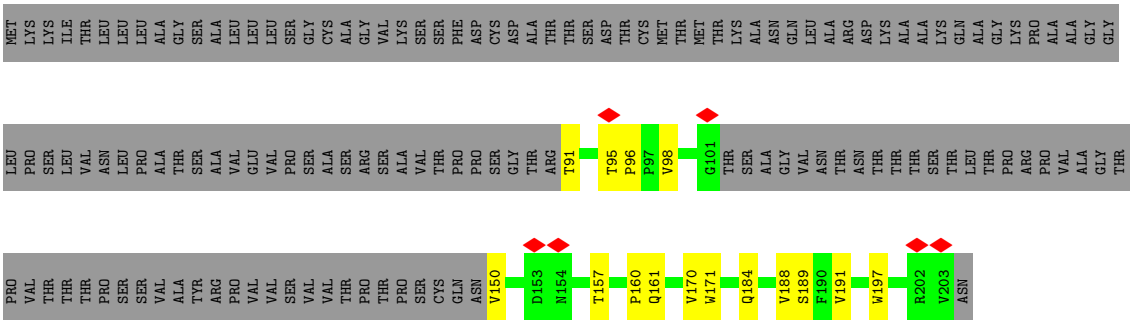
• Molecule 1: TraV

Chain A13:



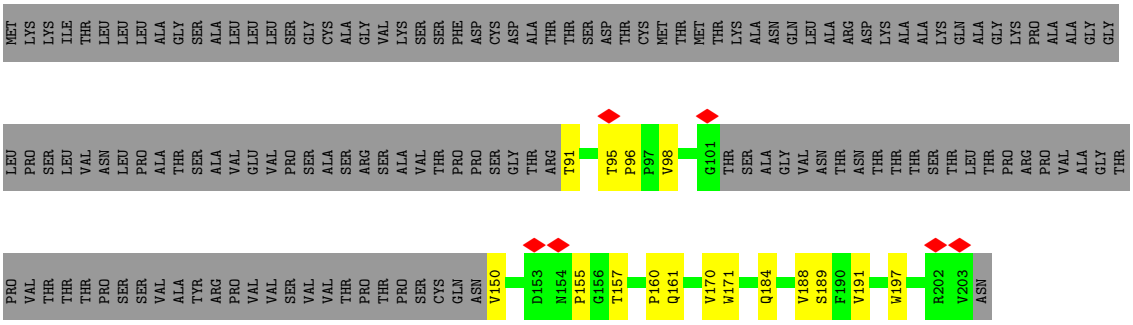
• Molecule 1: TraV

Chain B1:



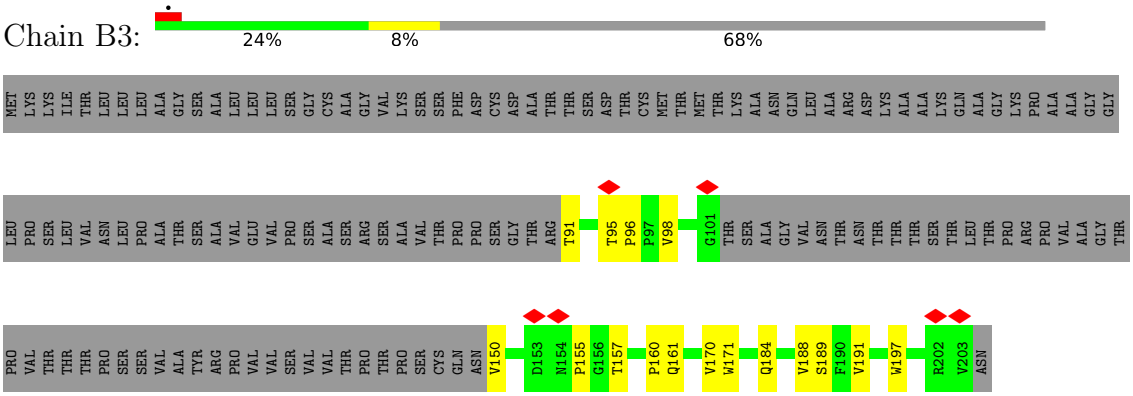
• Molecule 1: TraV

Chain B2:



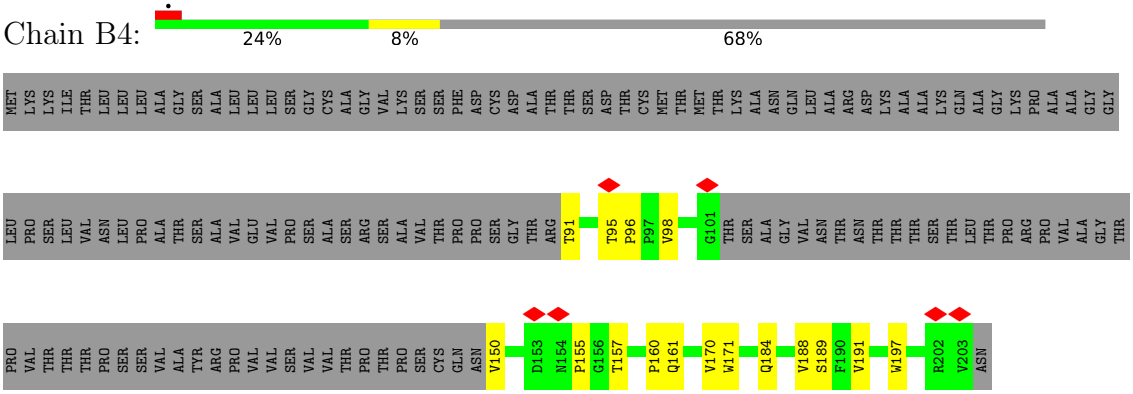
- Molecule 1: TraV

Chain B3:



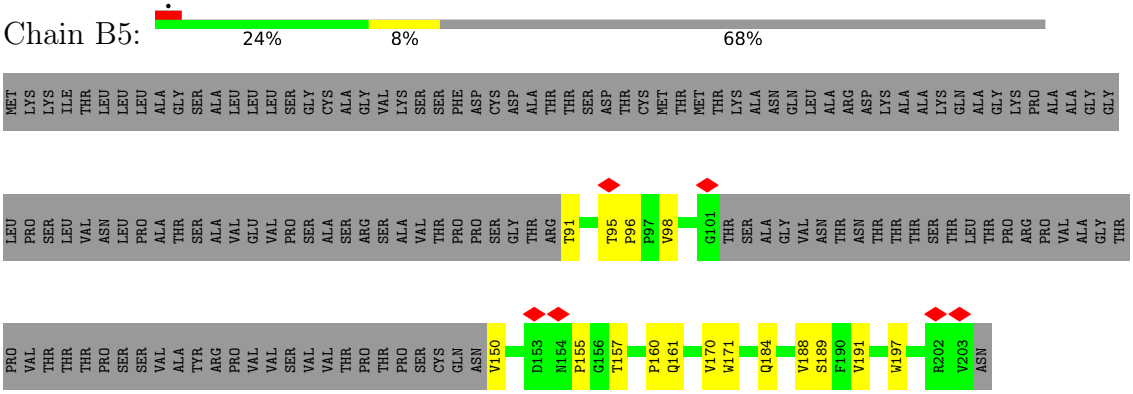
- Molecule 1: TraV

Chain B4:



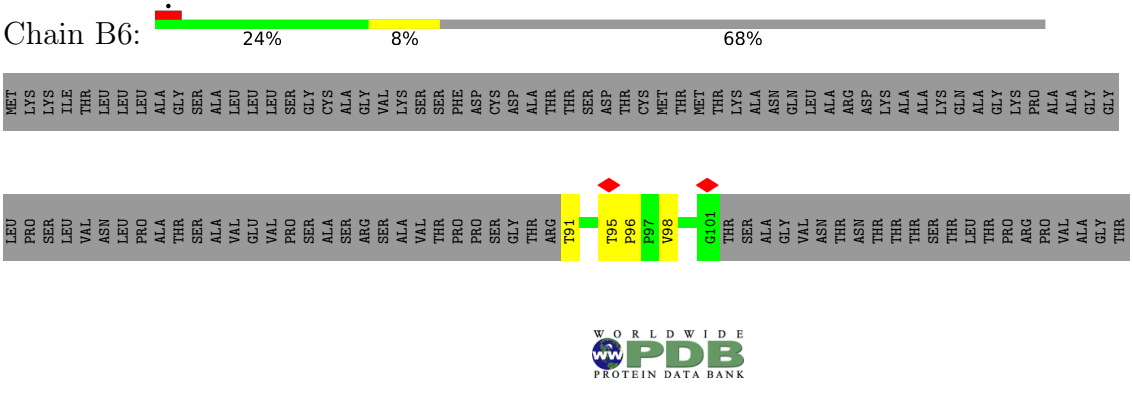
- Molecule 1: TraV

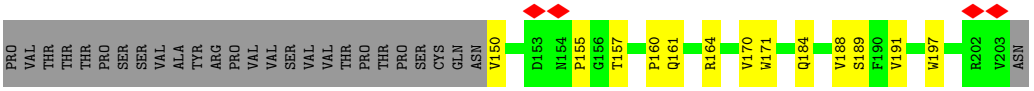
Chain B5:



- Molecule 1: TraV

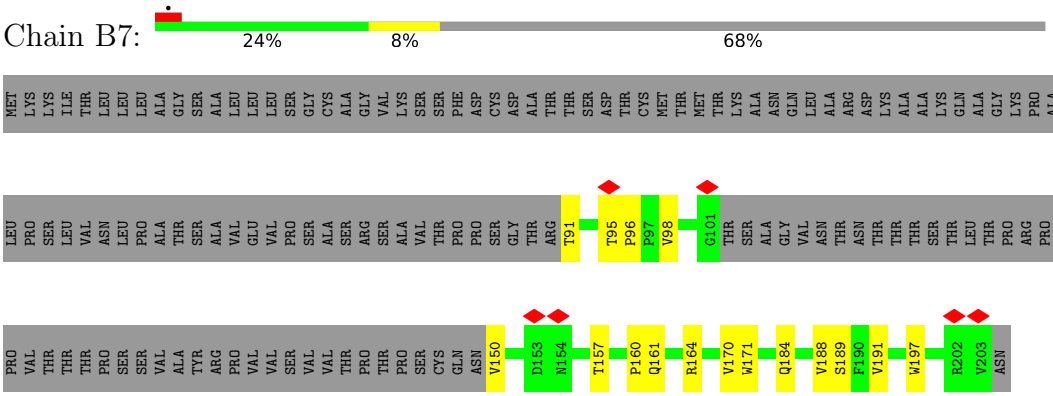
Chain B6:





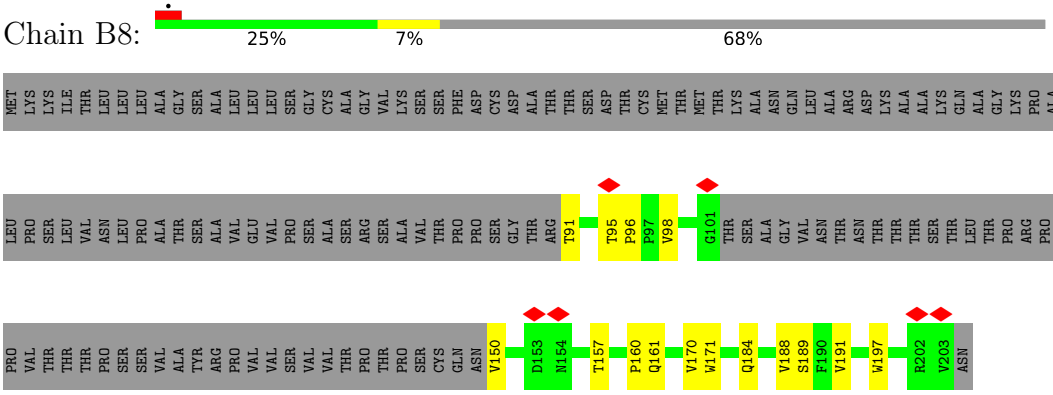
• Molecule 1: TraV

Chain B7:



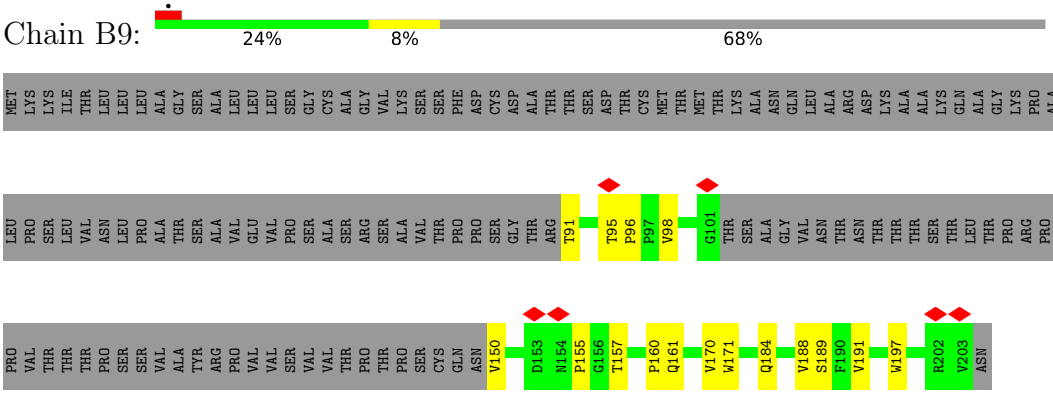
• Molecule 1: TraV

Chain B8:



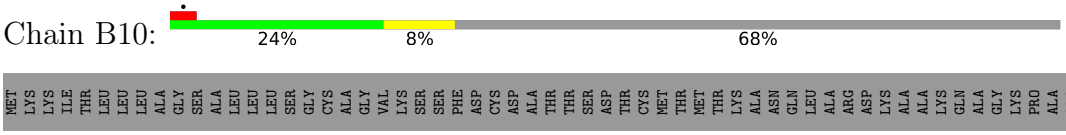
• Molecule 1: TraV

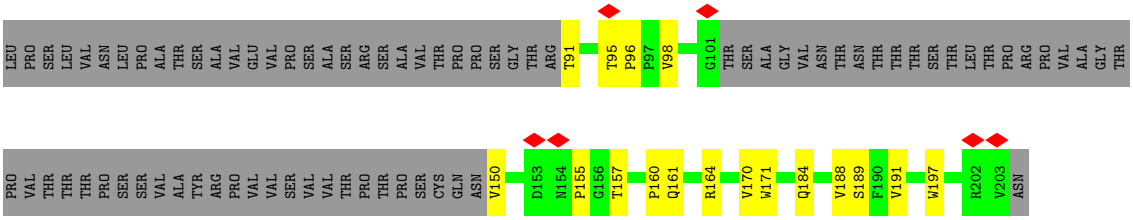
Chain B9:



• Molecule 1: TraV

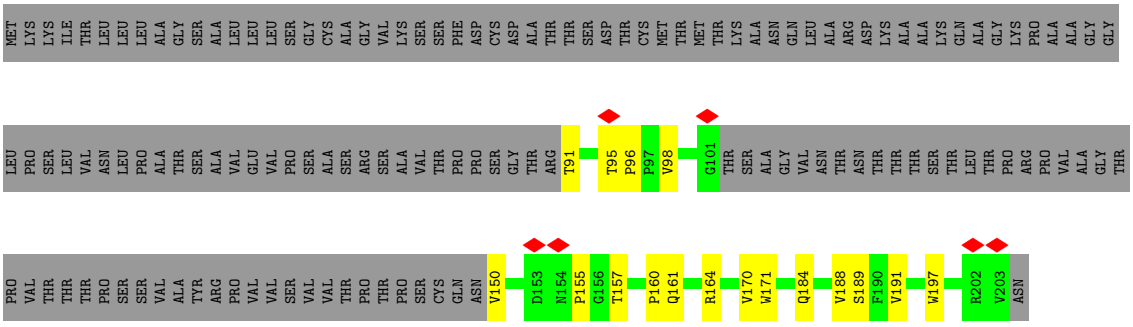
Chain B10:





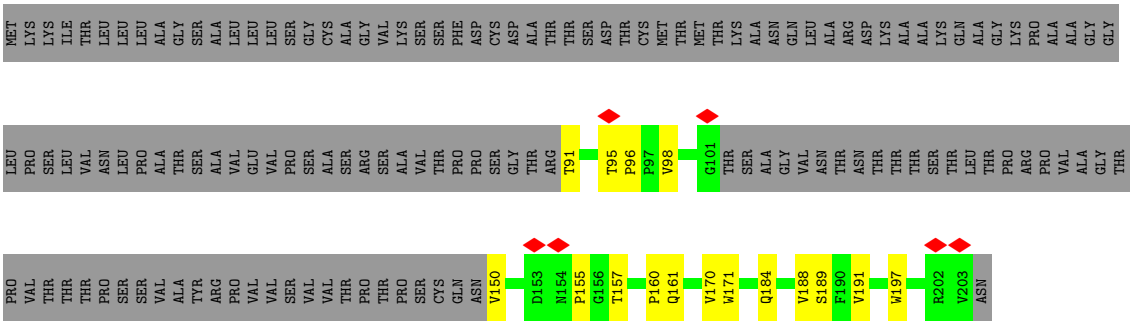
• Molecule 1: TraV

Chain B11:



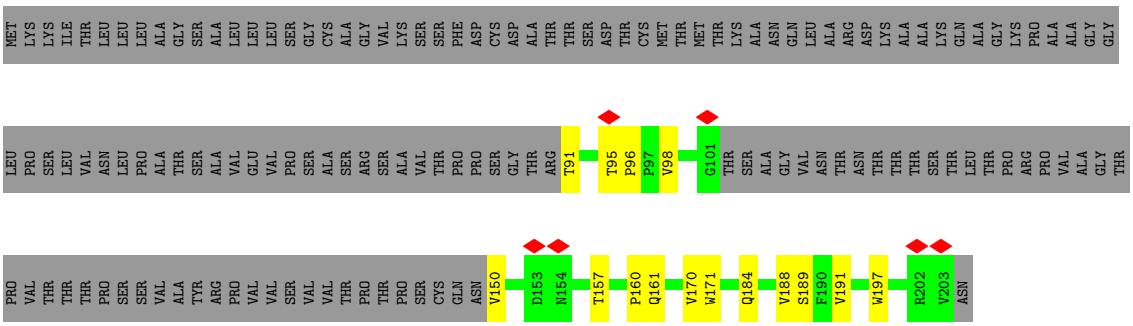
• Molecule 1: TraV

Chain B12:



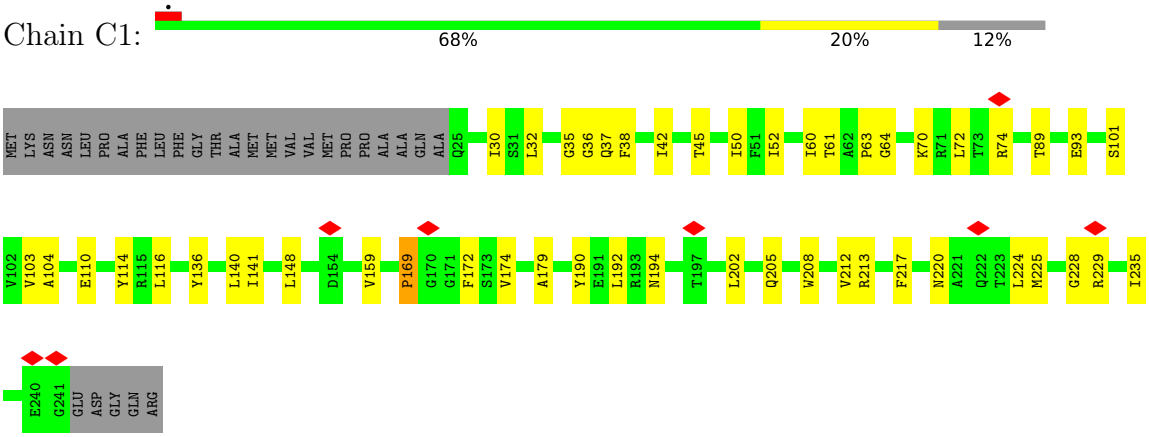
• Molecule 1: TraV

Chain B13:



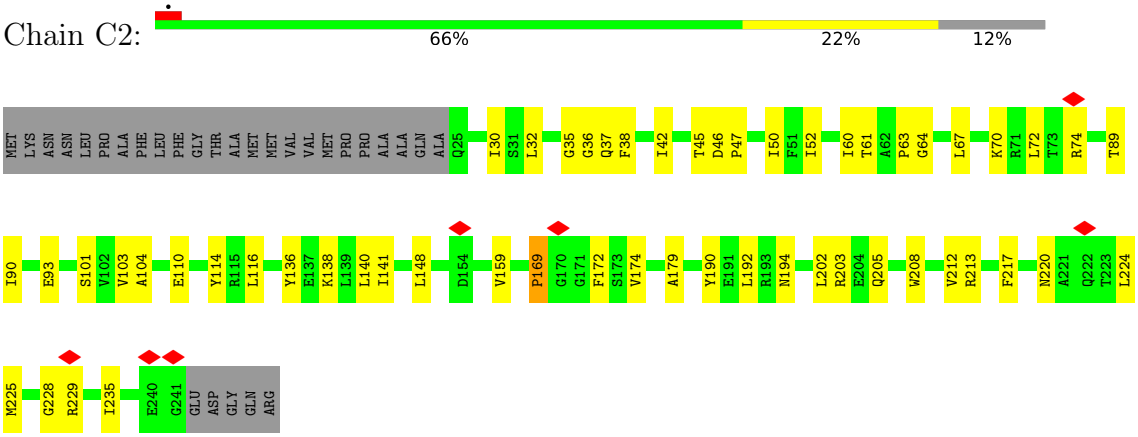
• Molecule 2: TraK

Chain C1:



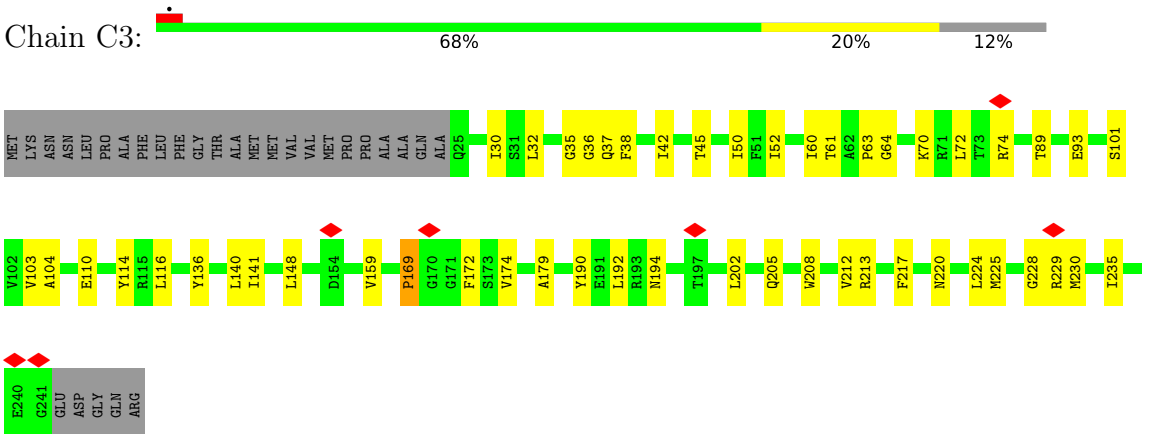
• Molecule 2: TraK

Chain C2:



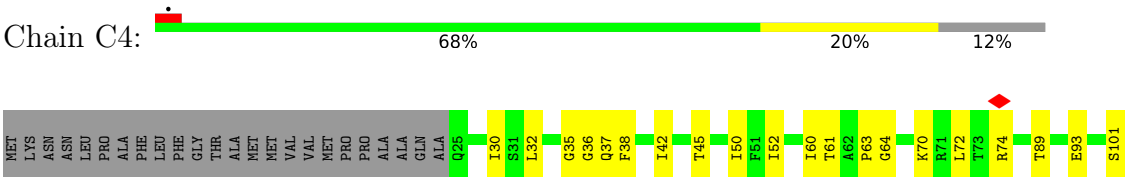
• Molecule 2: TraK

Chain C3:



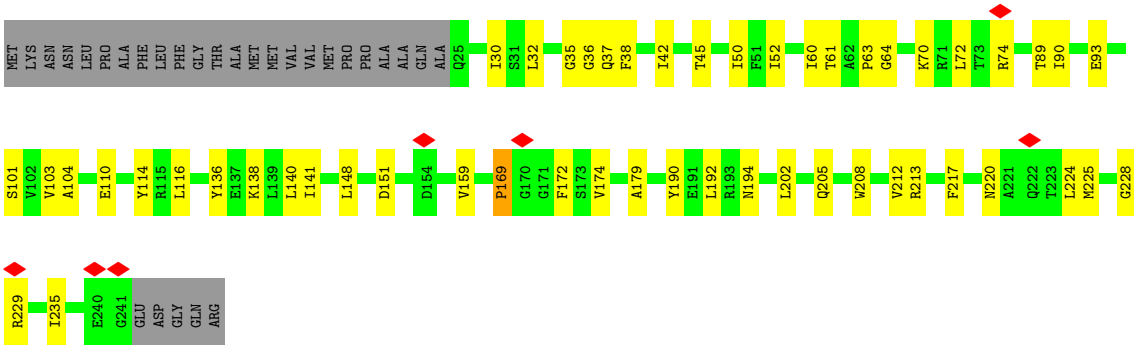
• Molecule 2: TraK

Chain C4:



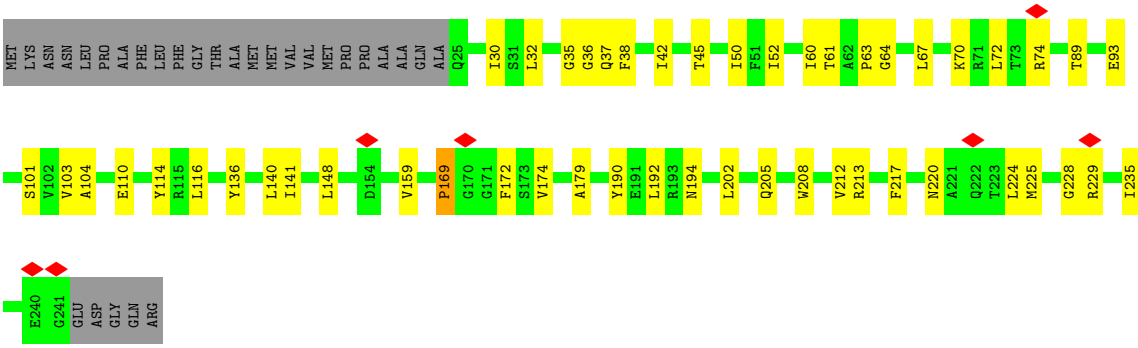
• Molecule 2: TraK

Chain C5:



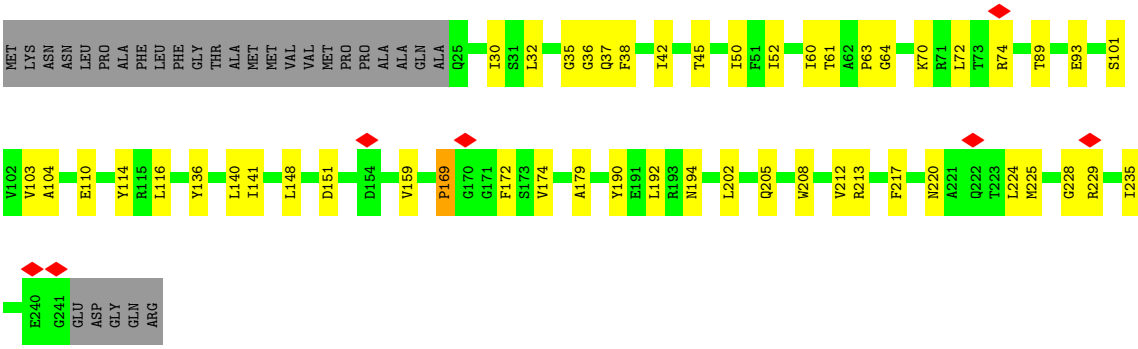
• Molecule 2: TraK

Chain C6:



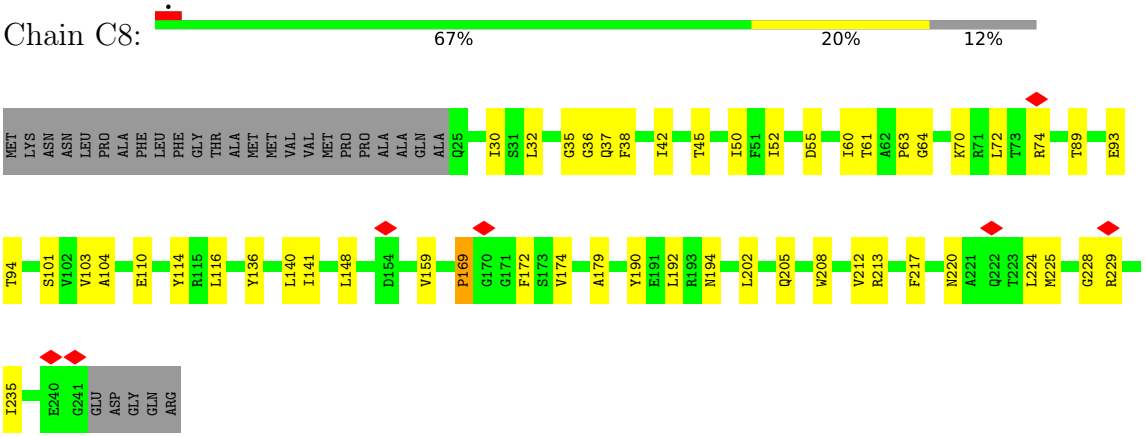
• Molecule 2: TraK

Chain C7:



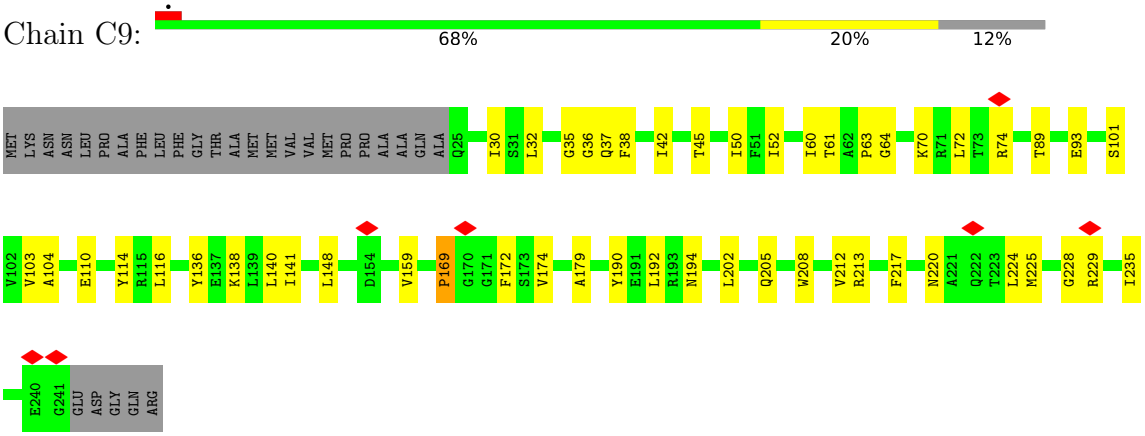
• Molecule 2: TraK

Chain C8:



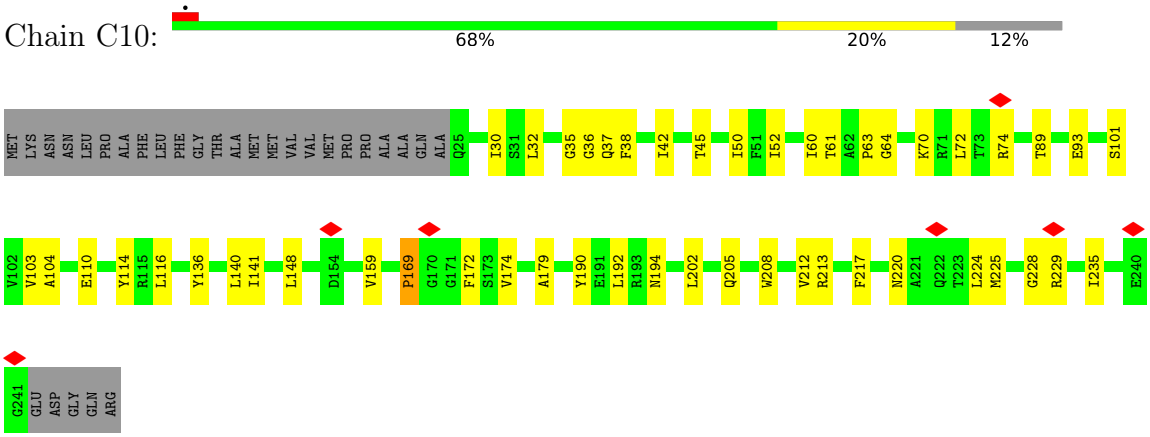
• Molecule 2: TraK

Chain C9:



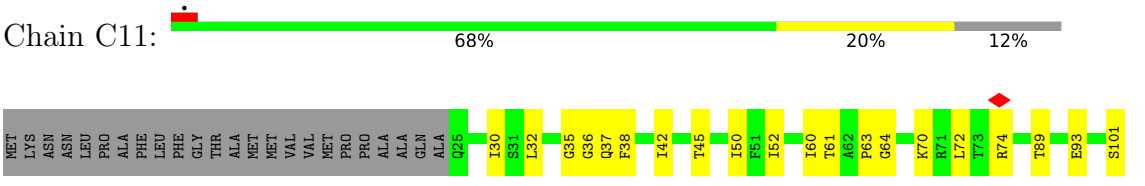
• Molecule 2: TraK

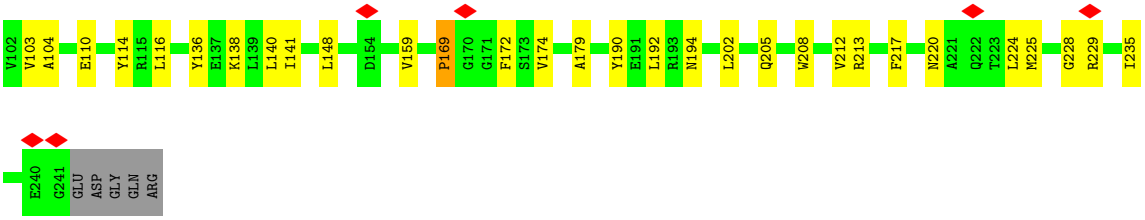
Chain C10:



• Molecule 2: TraK

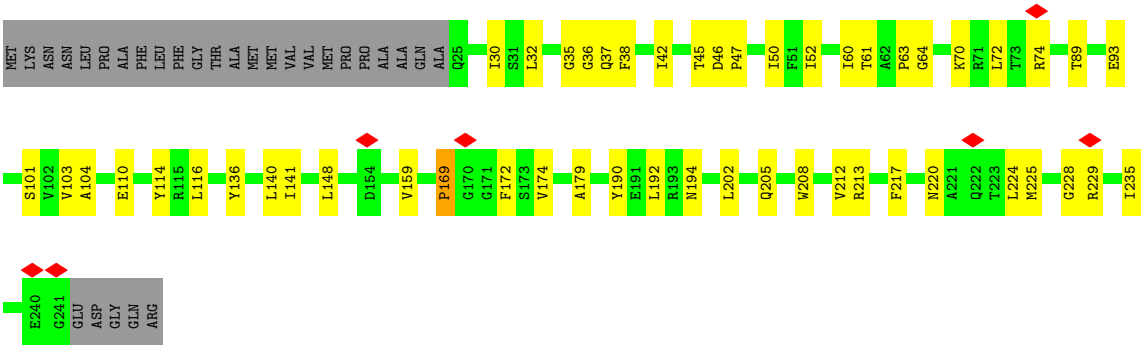
Chain C11:





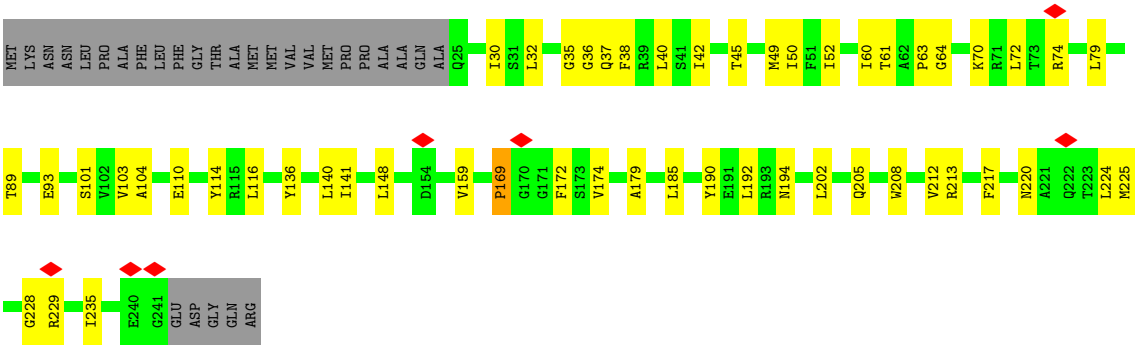
• Molecule 2: TraK

Chain C12:



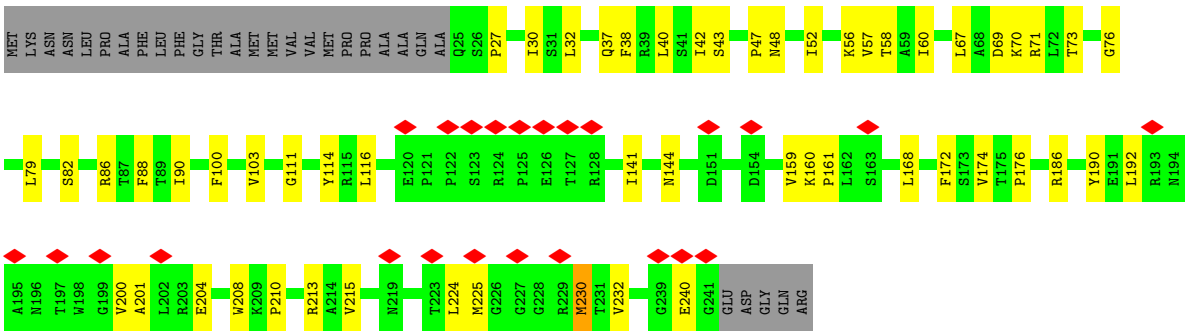
• Molecule 2: TraK

Chain C13:



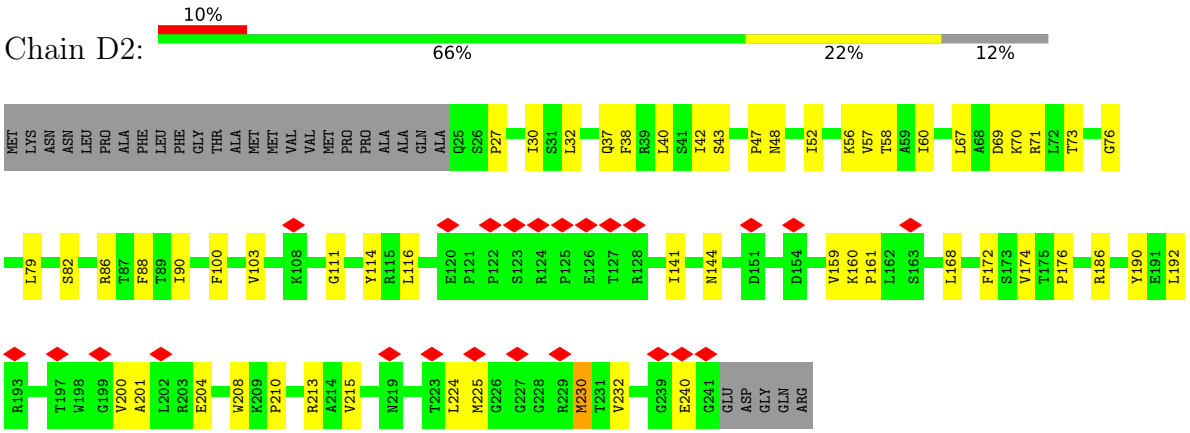
• Molecule 2: TraK

Chain D1:



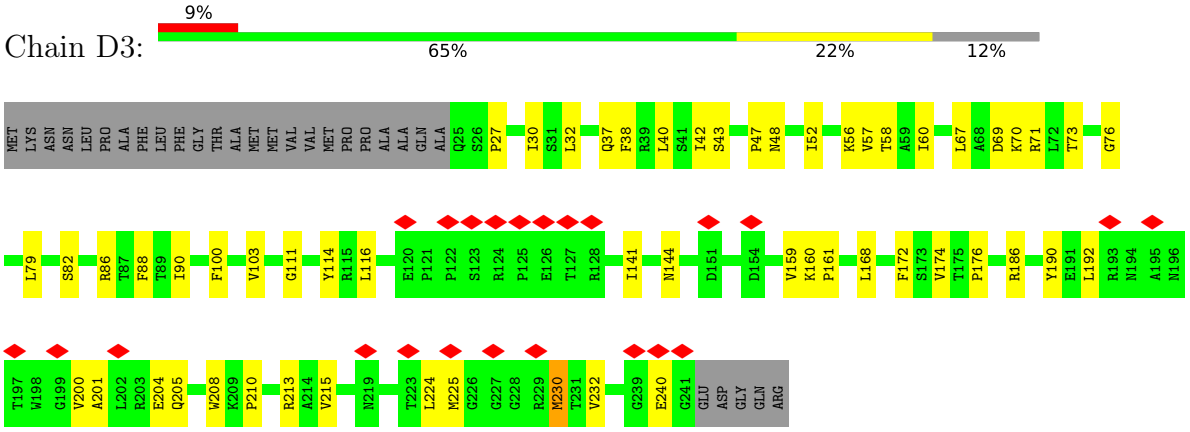
• Molecule 2: TraK

Chain D2:



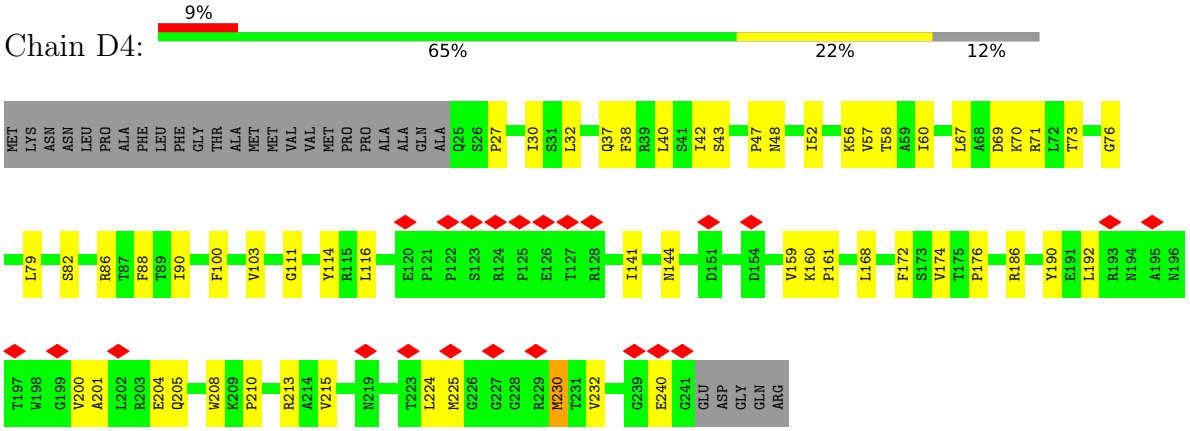
• Molecule 2: TraK

Chain D3:



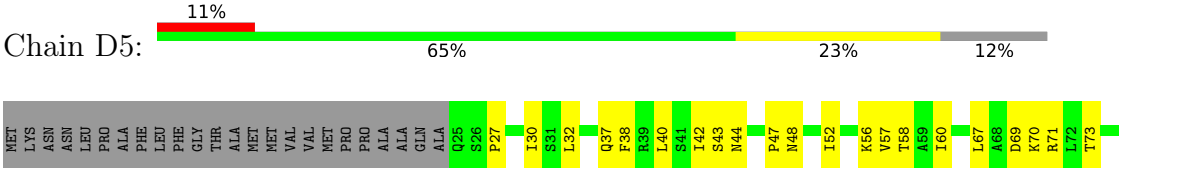
• Molecule 2: TraK

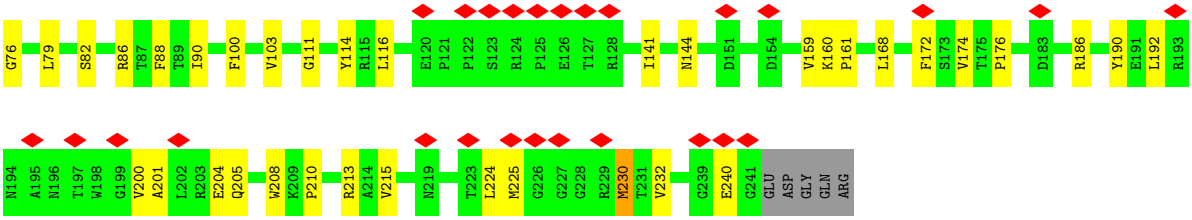
Chain D4:



• Molecule 2: TraK

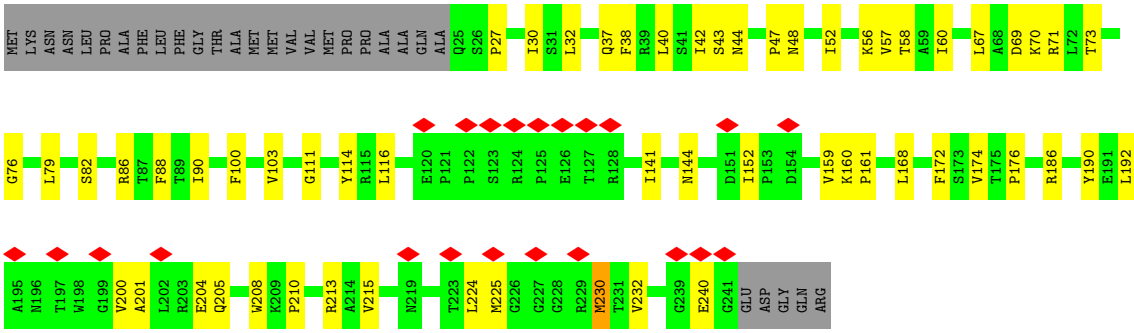
Chain D5:





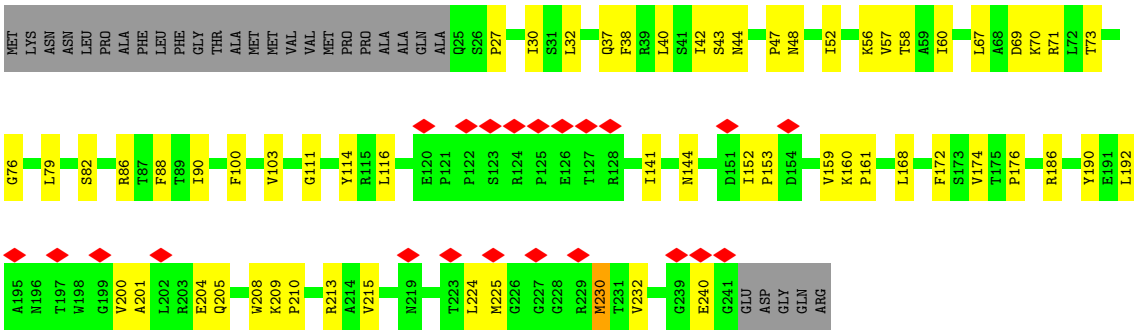
• Molecule 2: TraK

Chain D6:



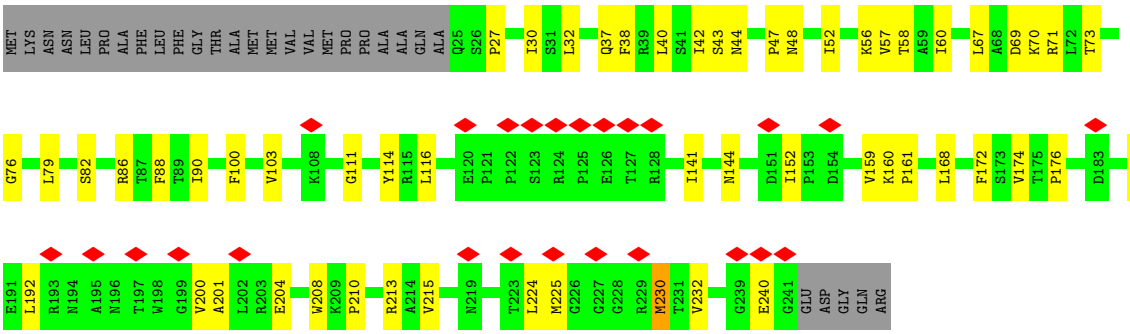
• Molecule 2: TraK

Chain D7:



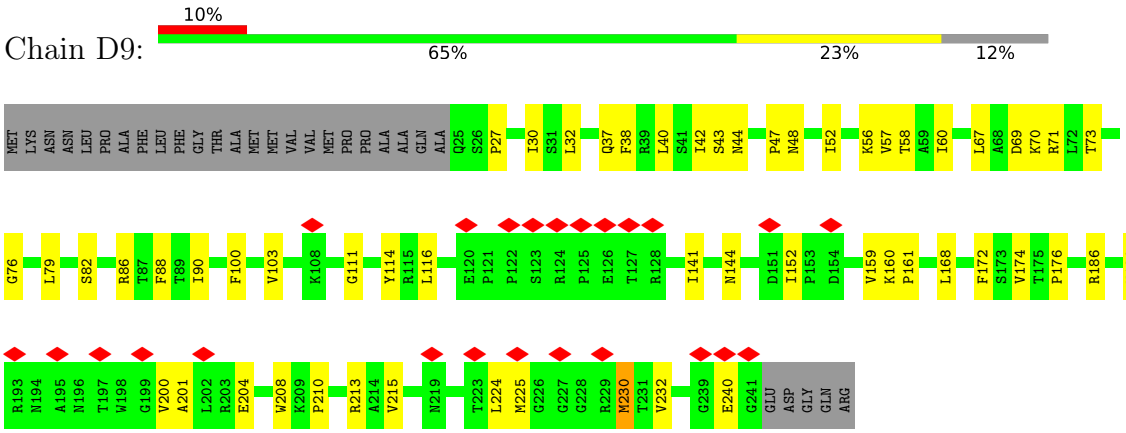
• Molecule 2: TraK

Chain D8:



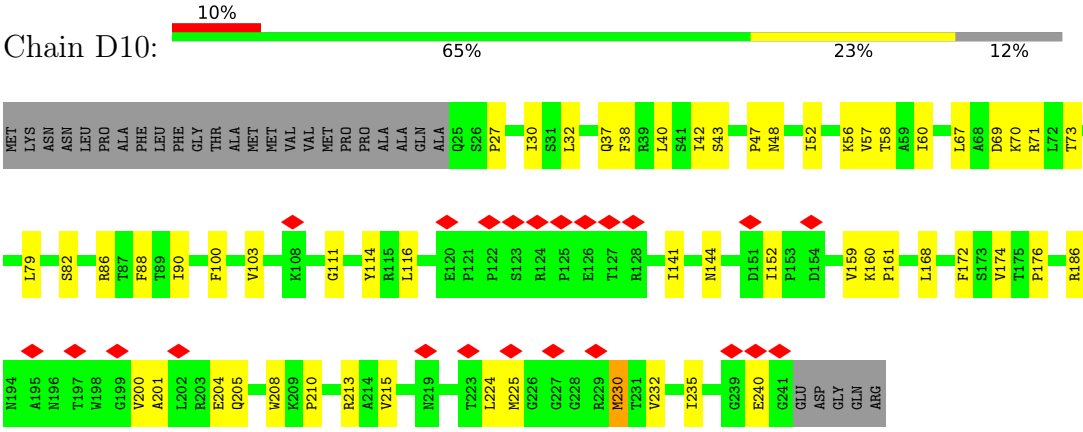
• Molecule 2: TraK

Chain D9:



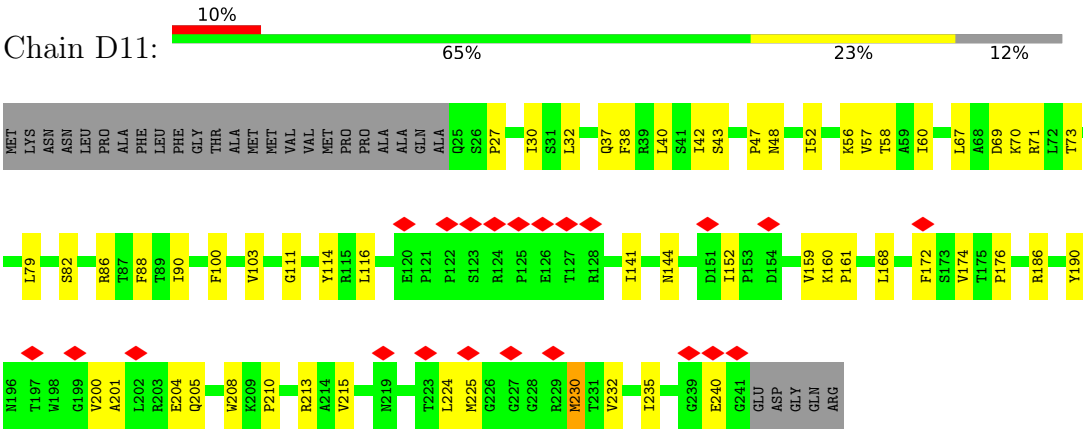
• Molecule 2: TraK

Chain D10:



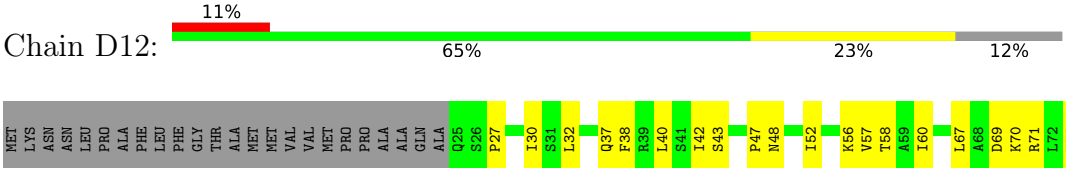
• Molecule 2: TraK

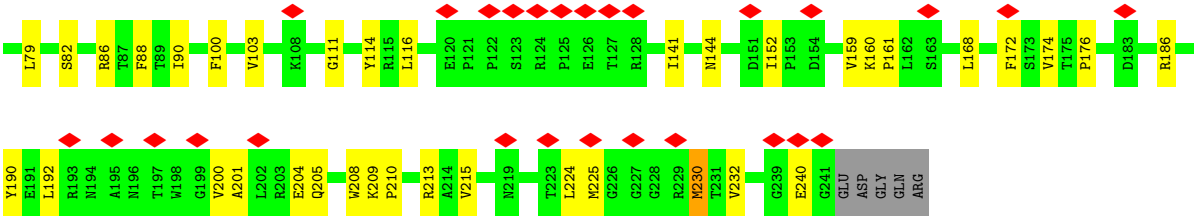
Chain D11:



• Molecule 2: TraK

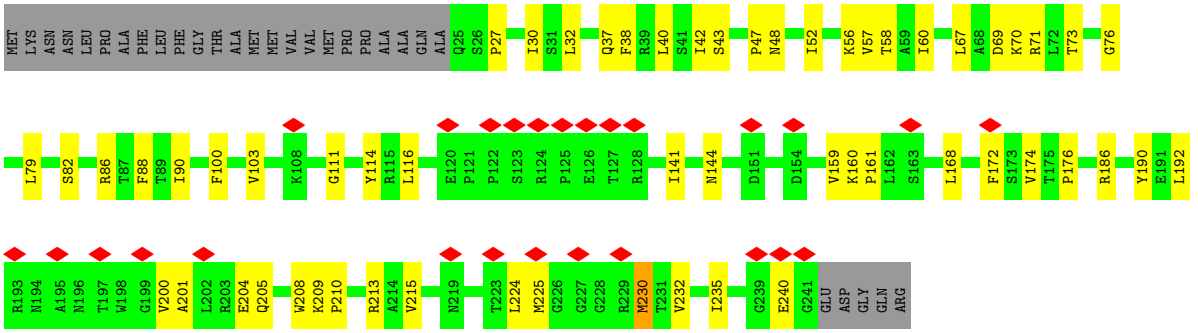
Chain D12:





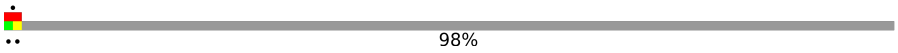
• Molecule 2: TraK

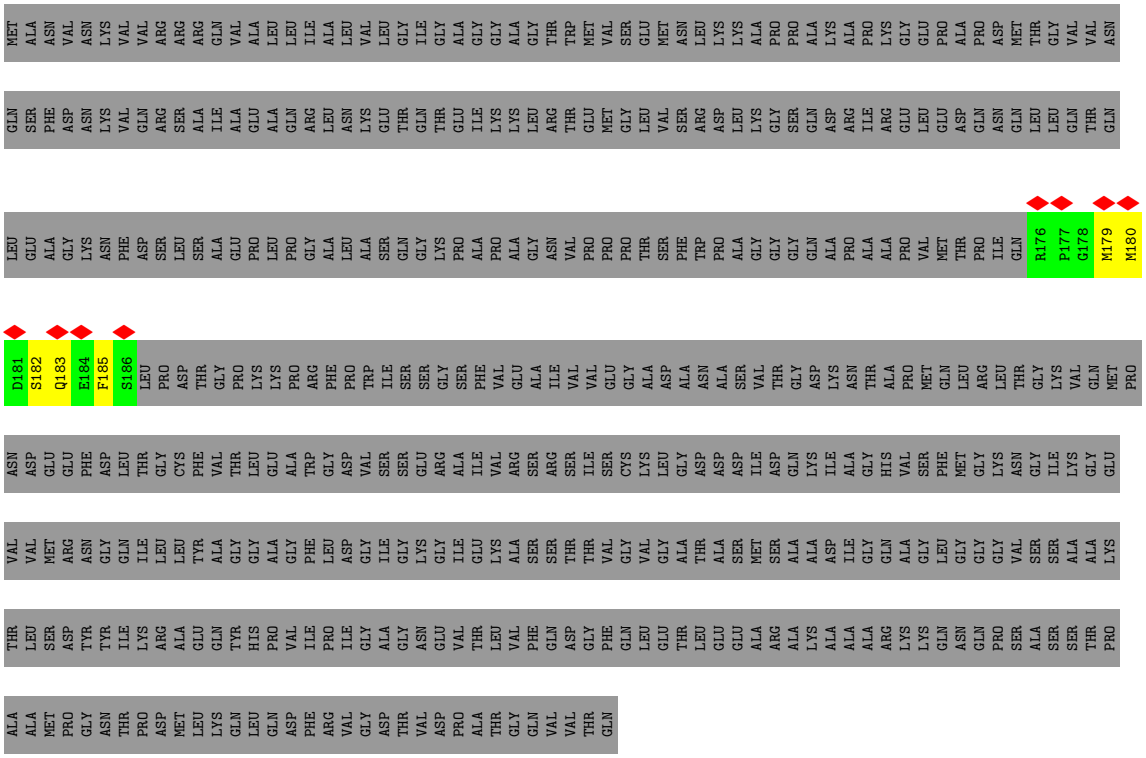
Chain D13:



• Molecule 3: TraB

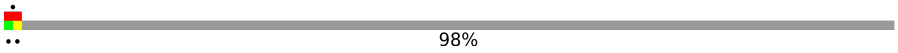
Chain E1:

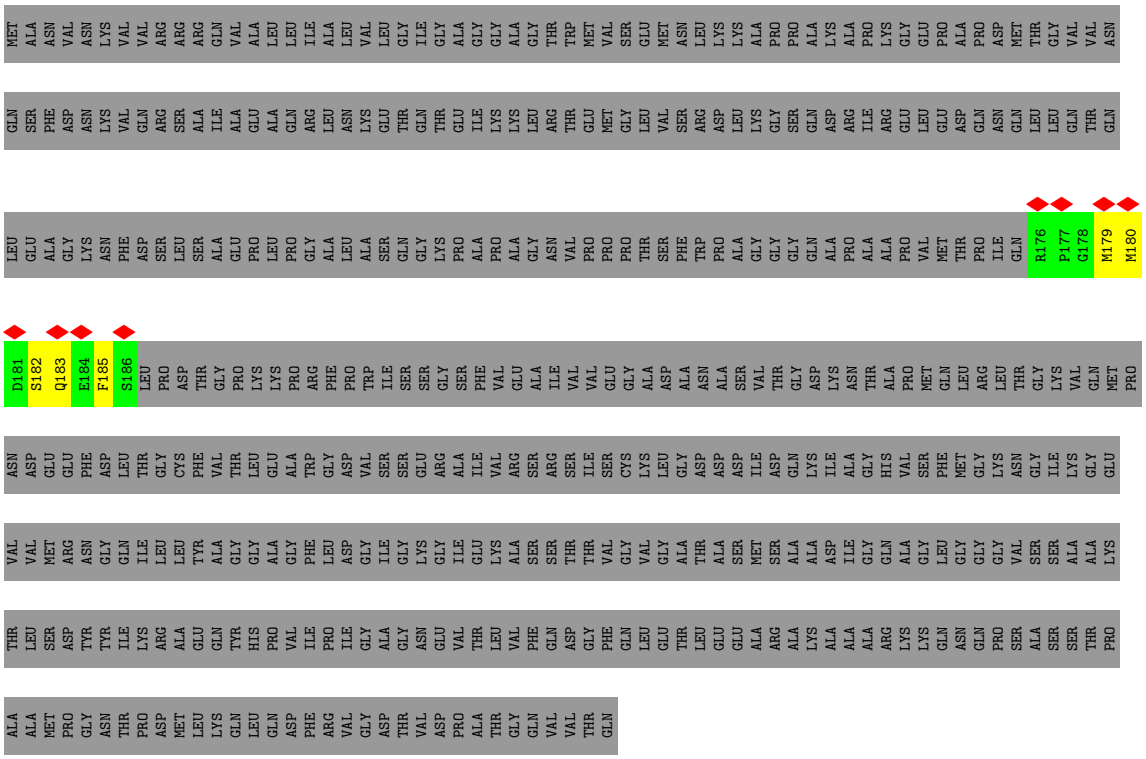




• Molecule 3: TraB

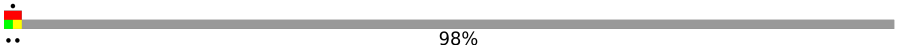
Chain E2:

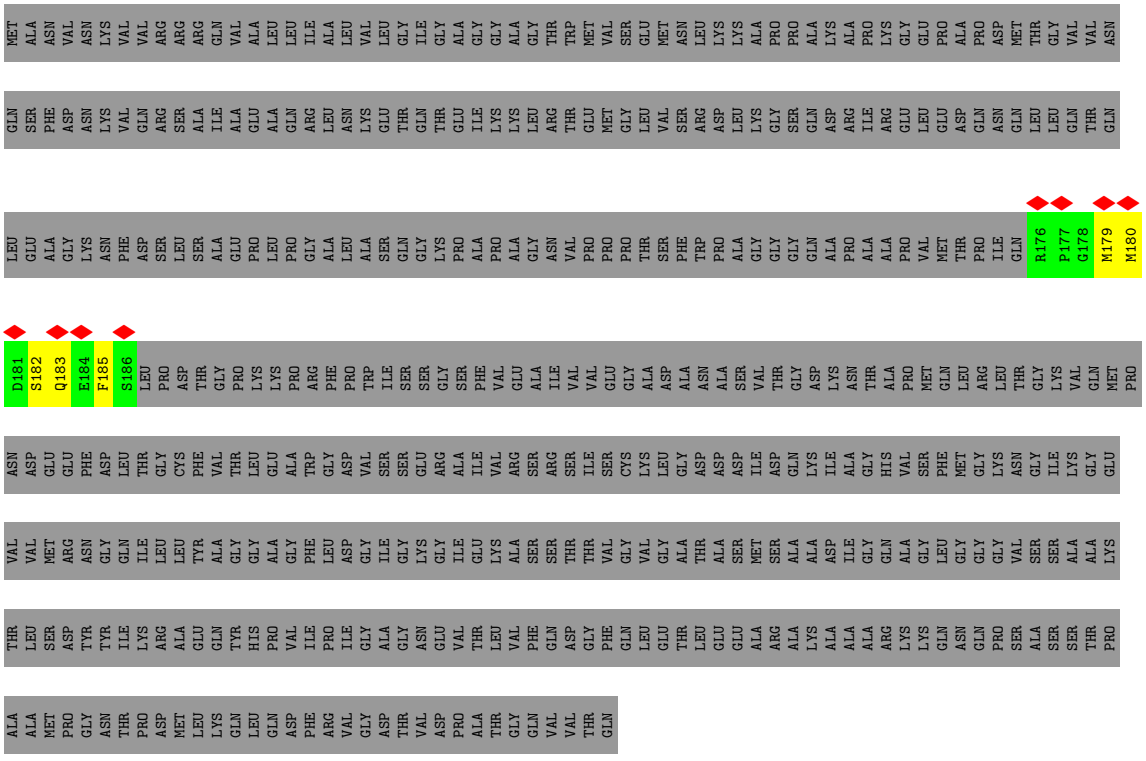




• Molecule 3: TraB

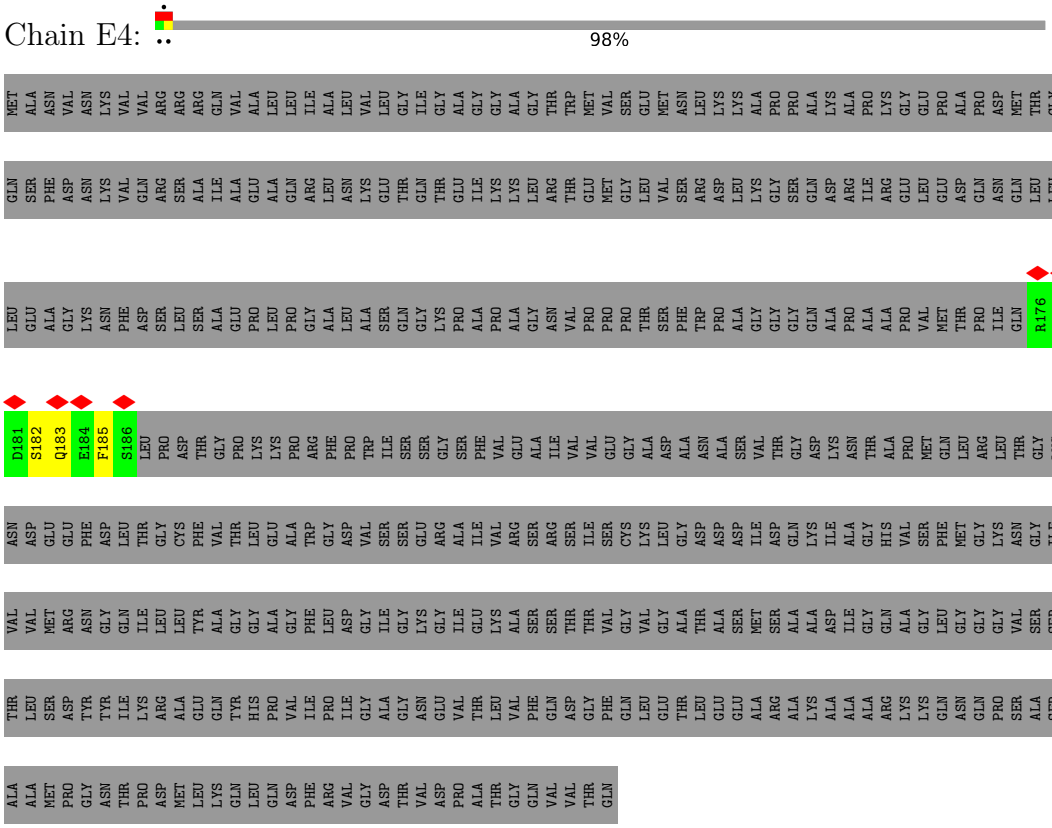
Chain E3:





• Molecule 3: TraB

Chain E4:

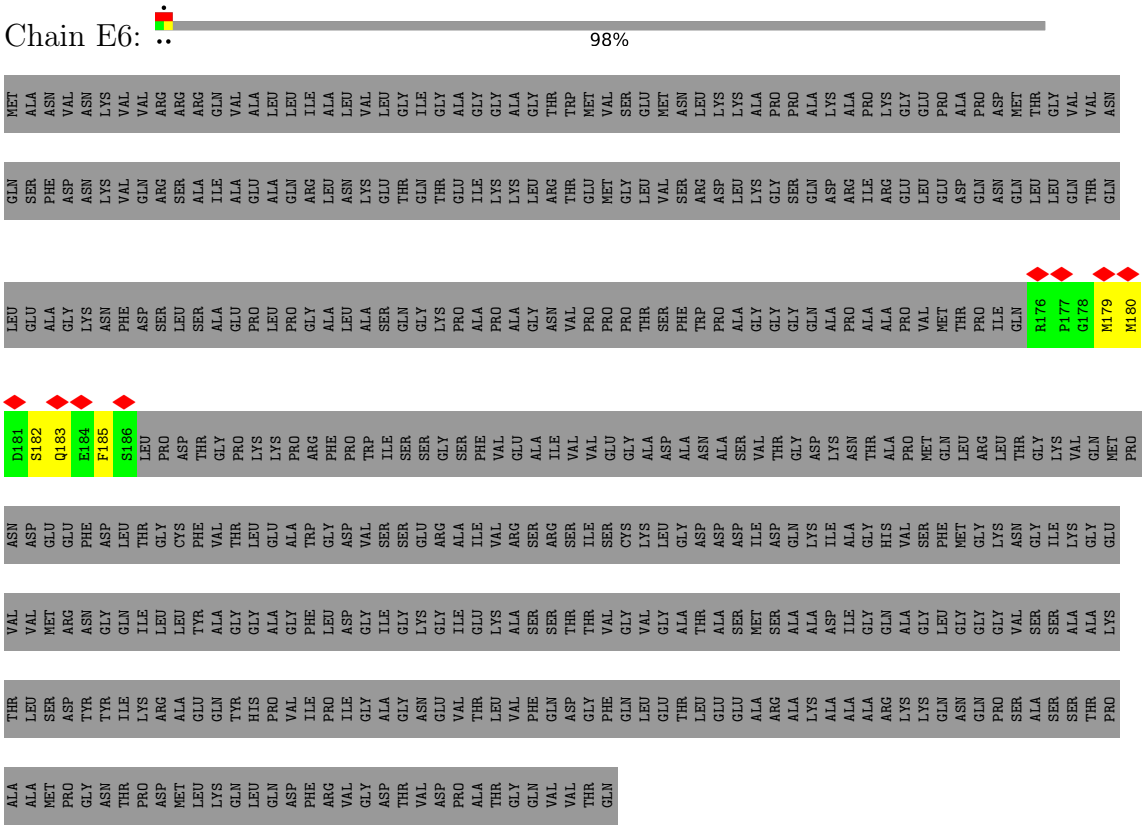


• Molecule 3: TraB

Chain E5:

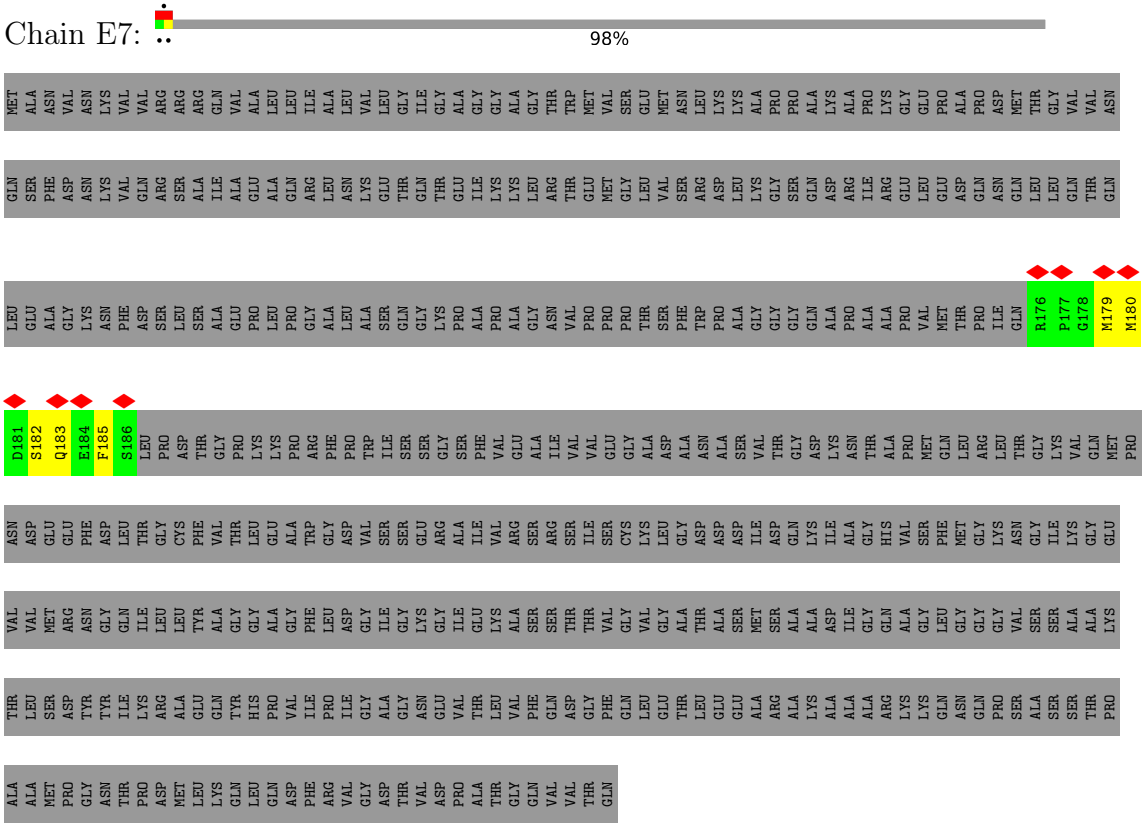
• Molecule 3: TraB

Chain E6:



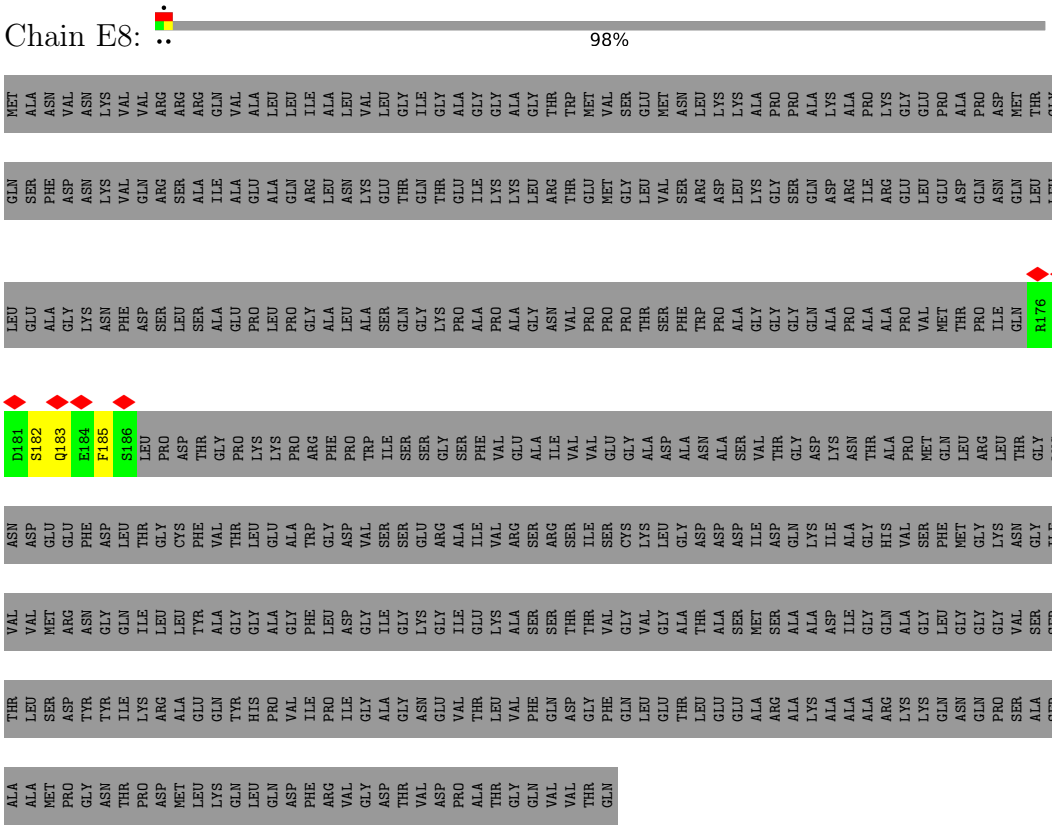
• Molecule 3: TraB

Chain E7:



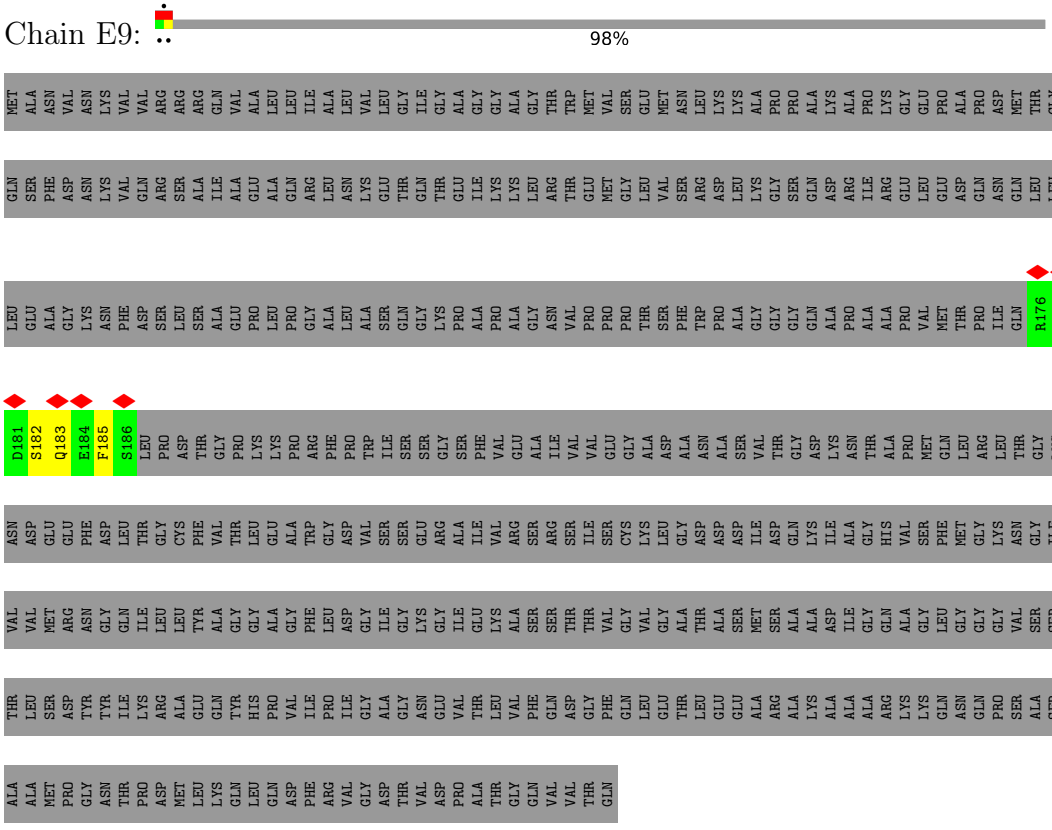
- Molecule 3: TraB

Chain E8:



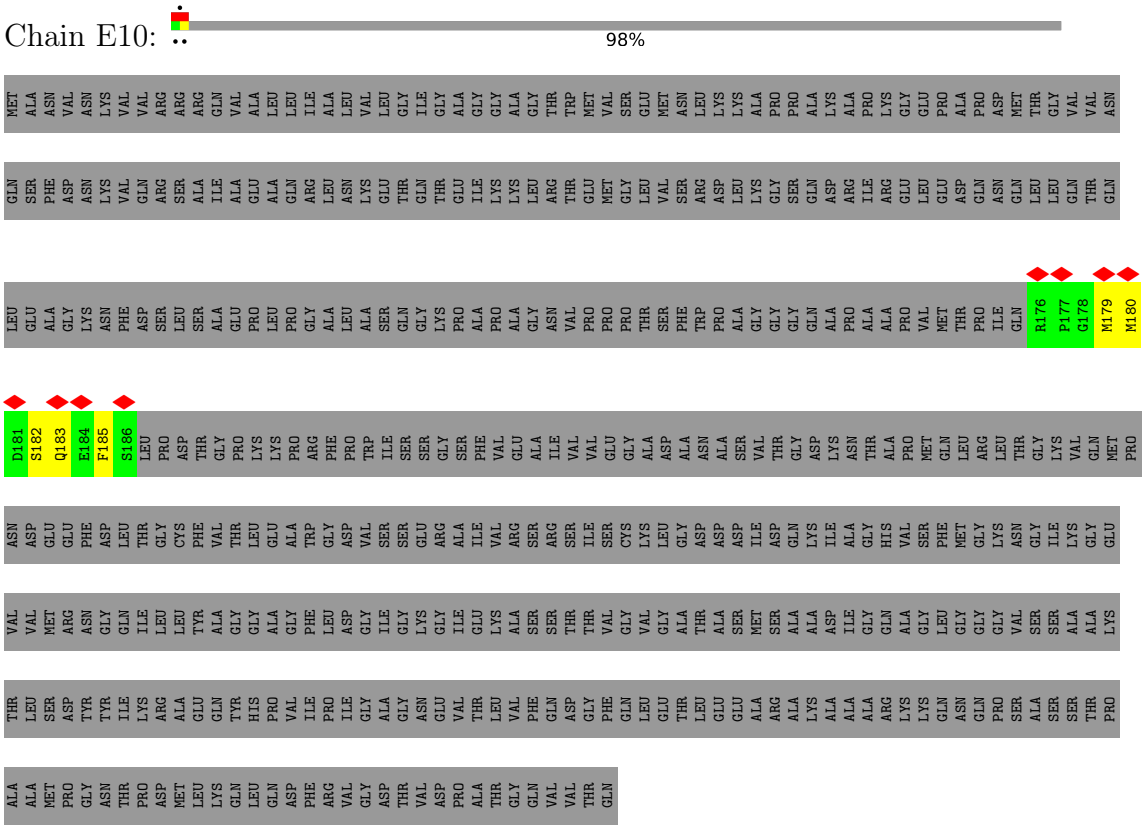
- Molecule 3: TraB

Chain E9:



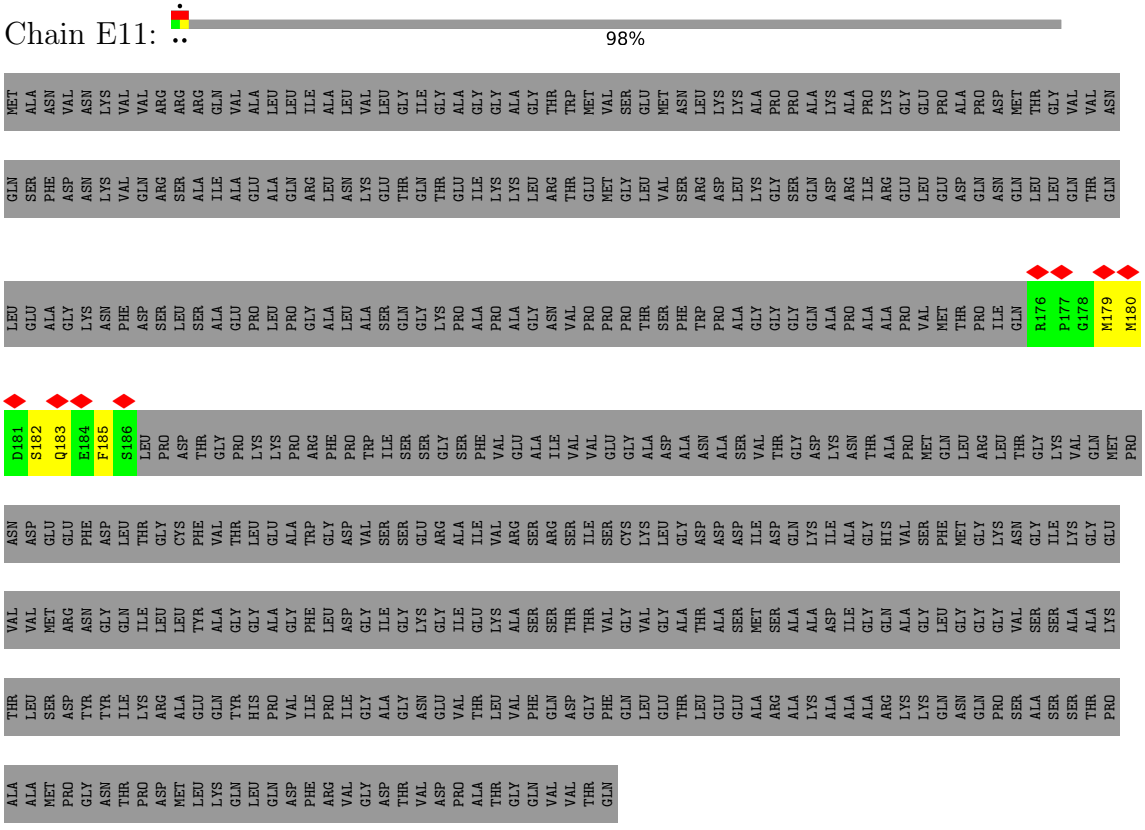
• Molecule 3: TraB

Chain E10:



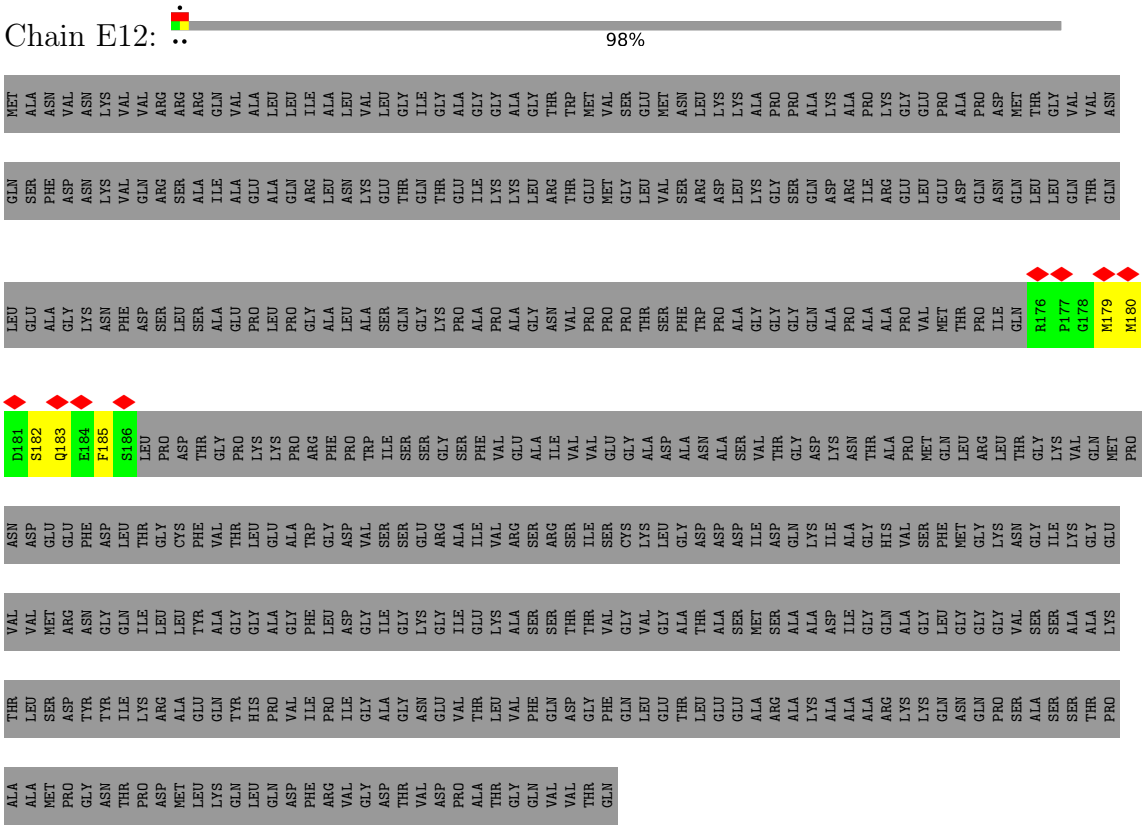
• Molecule 3: TraB

Chain E11:



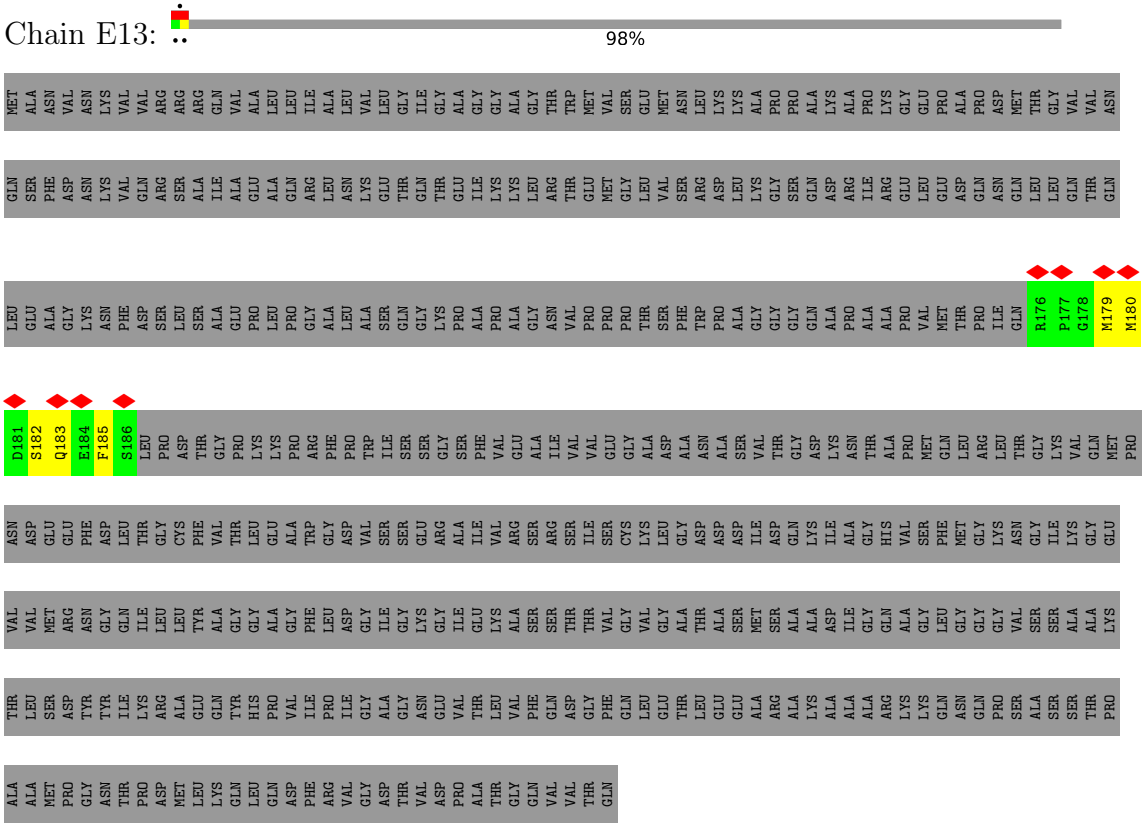
• Molecule 3: TraB

Chain E12:



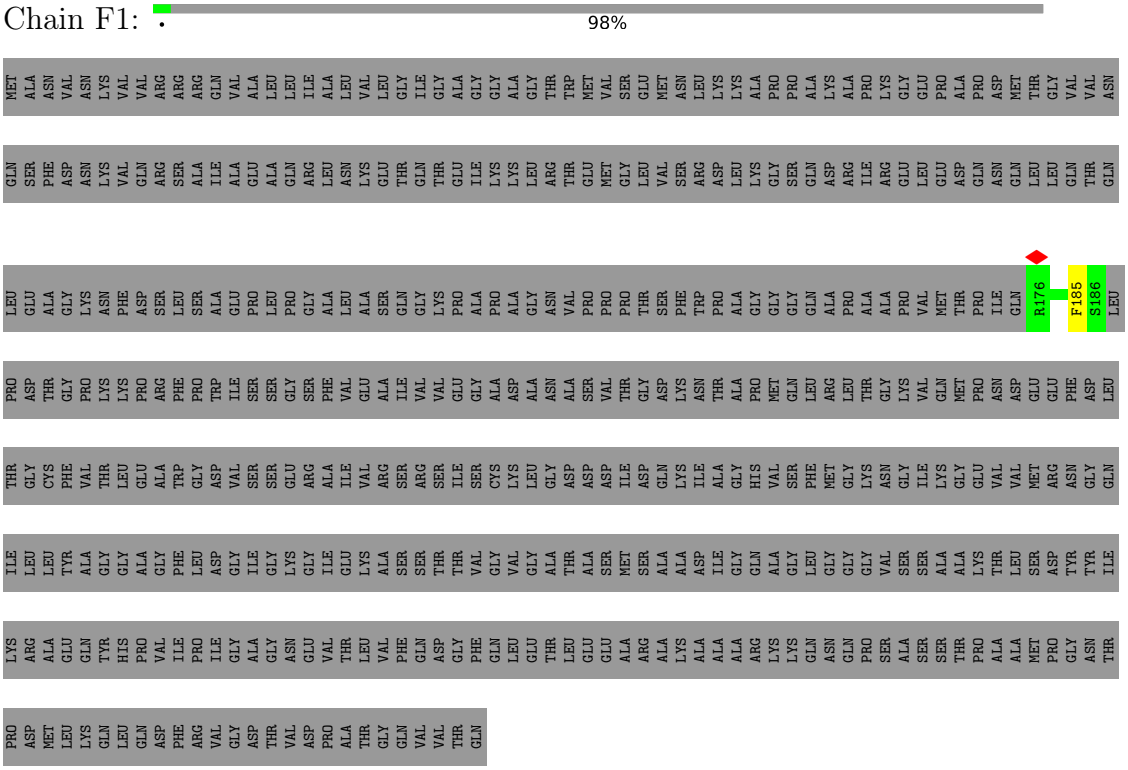
• Molecule 3: TraB

Chain E13:



• Molecule 3: TraB

Chain F1:

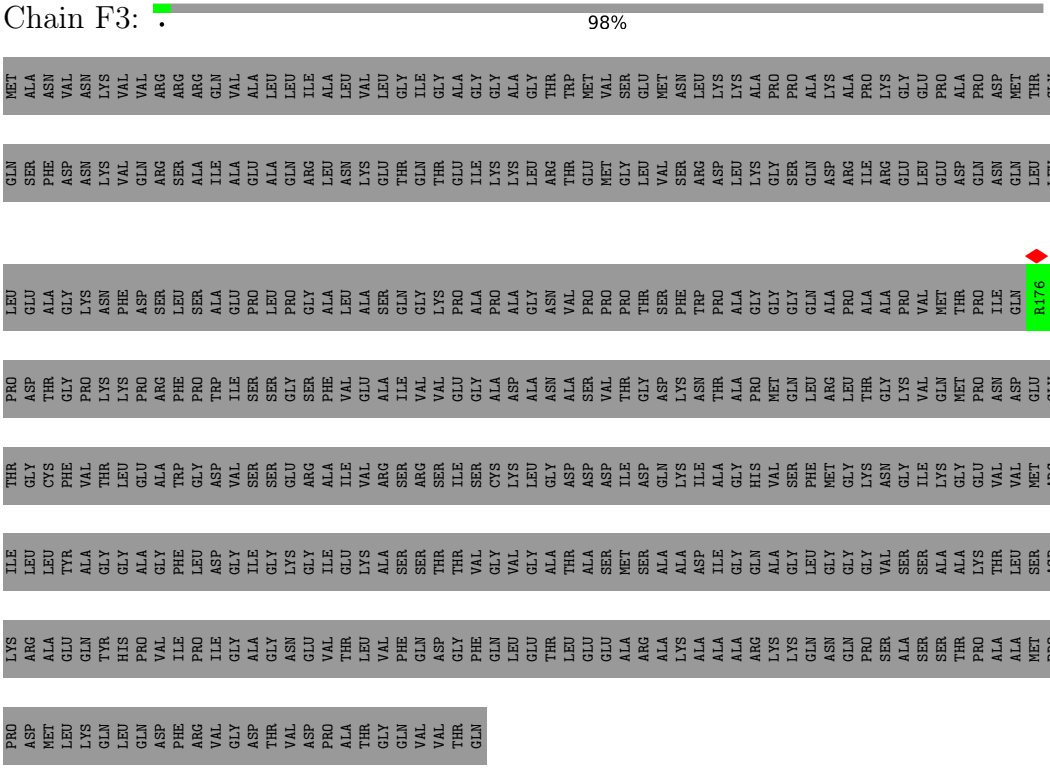


• Molecule 3: TraB

Chain F2:

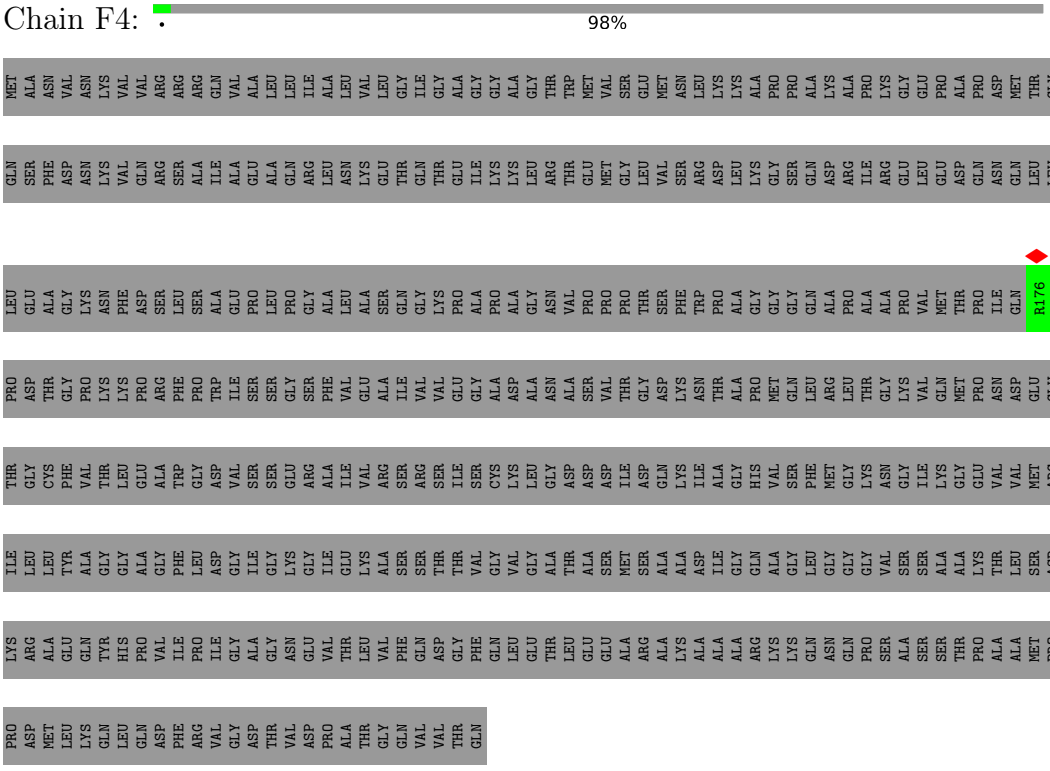
• Molecule 3: TraB

Chain F3:



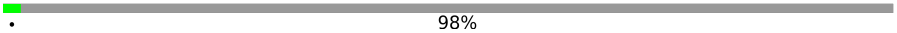
• Molecule 3: TraB

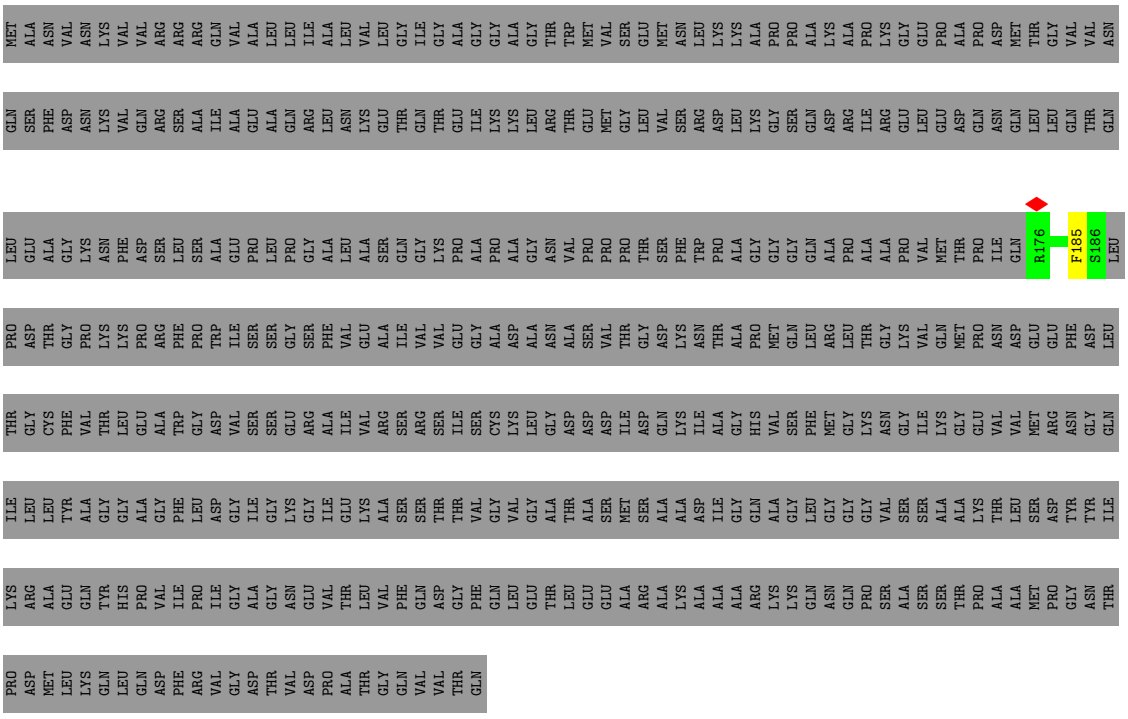
Chain F4:



• Molecule 3: TraB

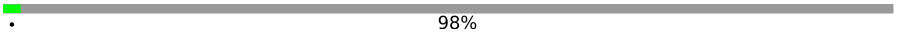
Chain F5:

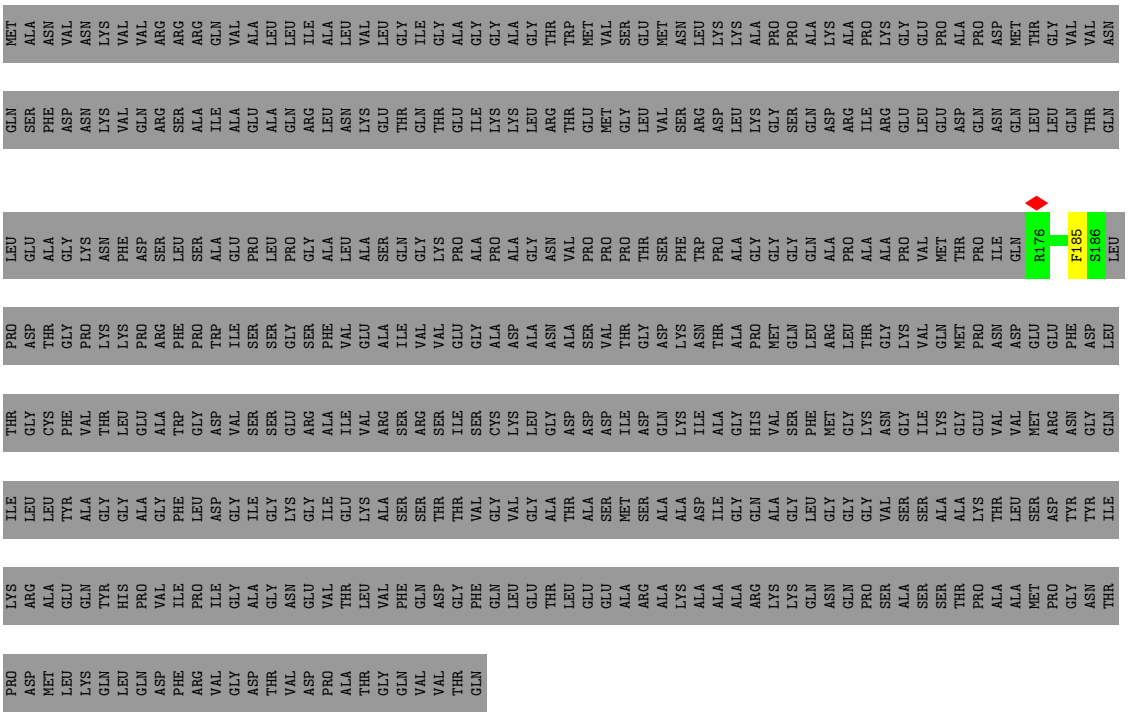




• Molecule 3: TraB

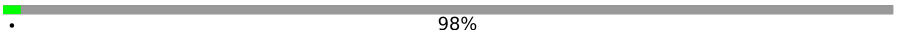
Chain F6:

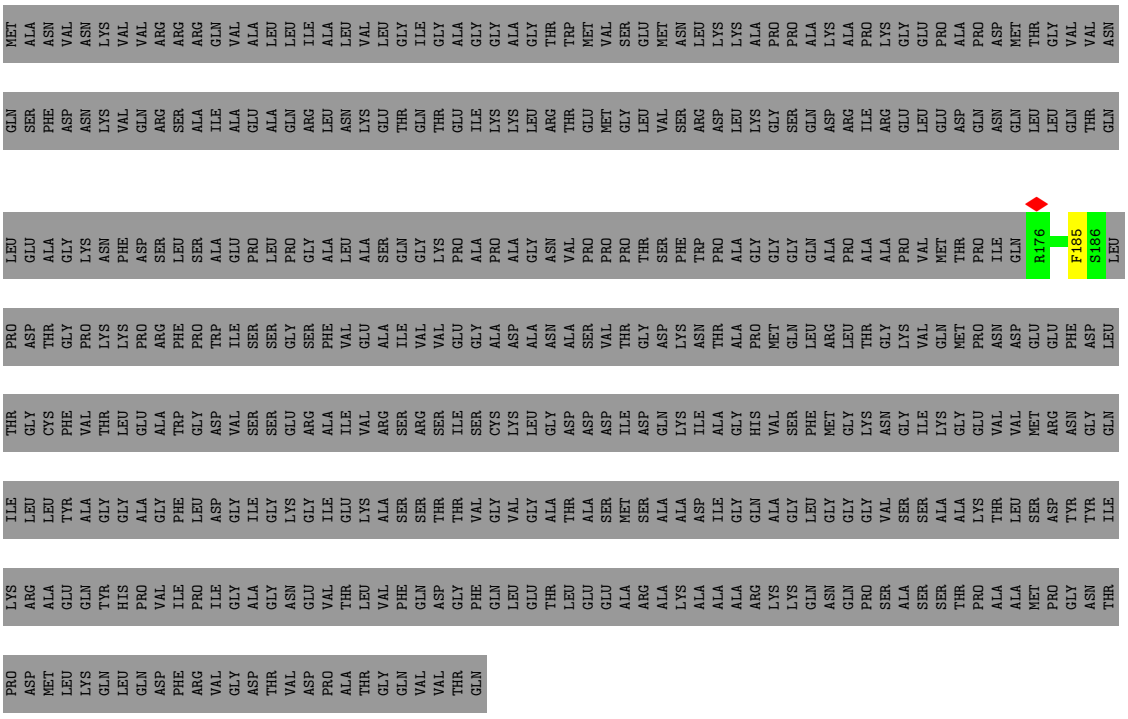




• Molecule 3: TraB

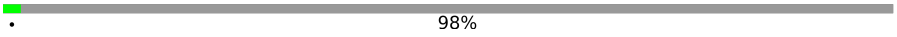
Chain F7:

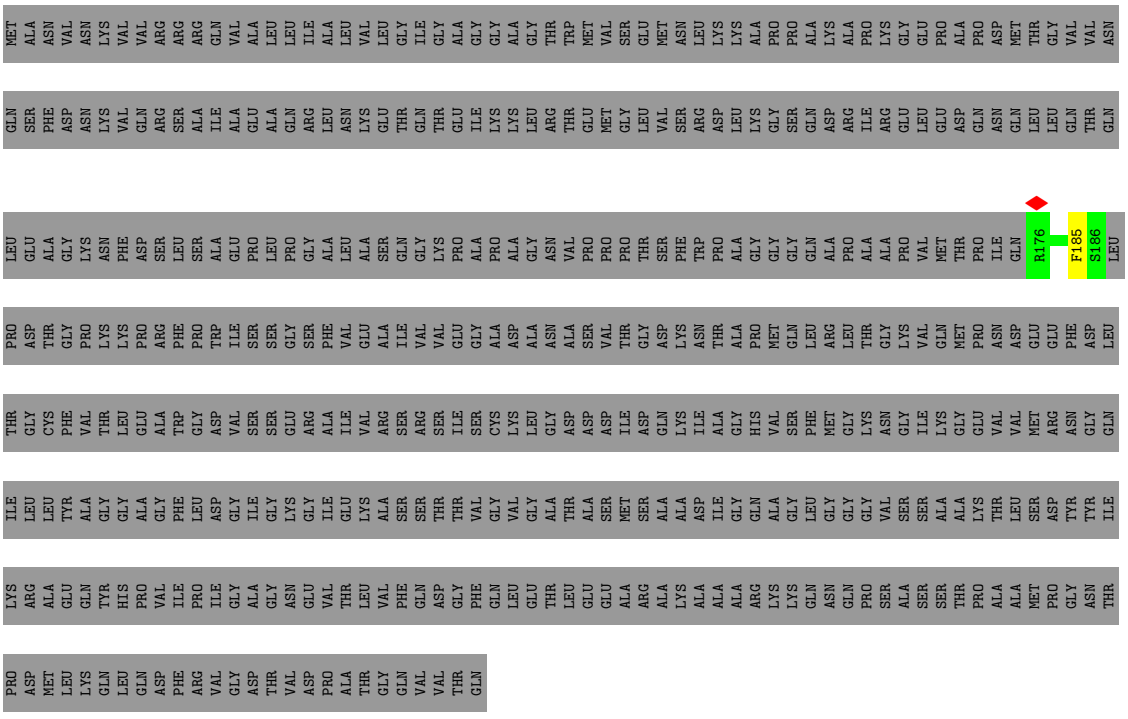




• Molecule 3: TraB

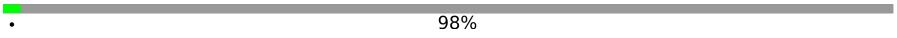
Chain F8:

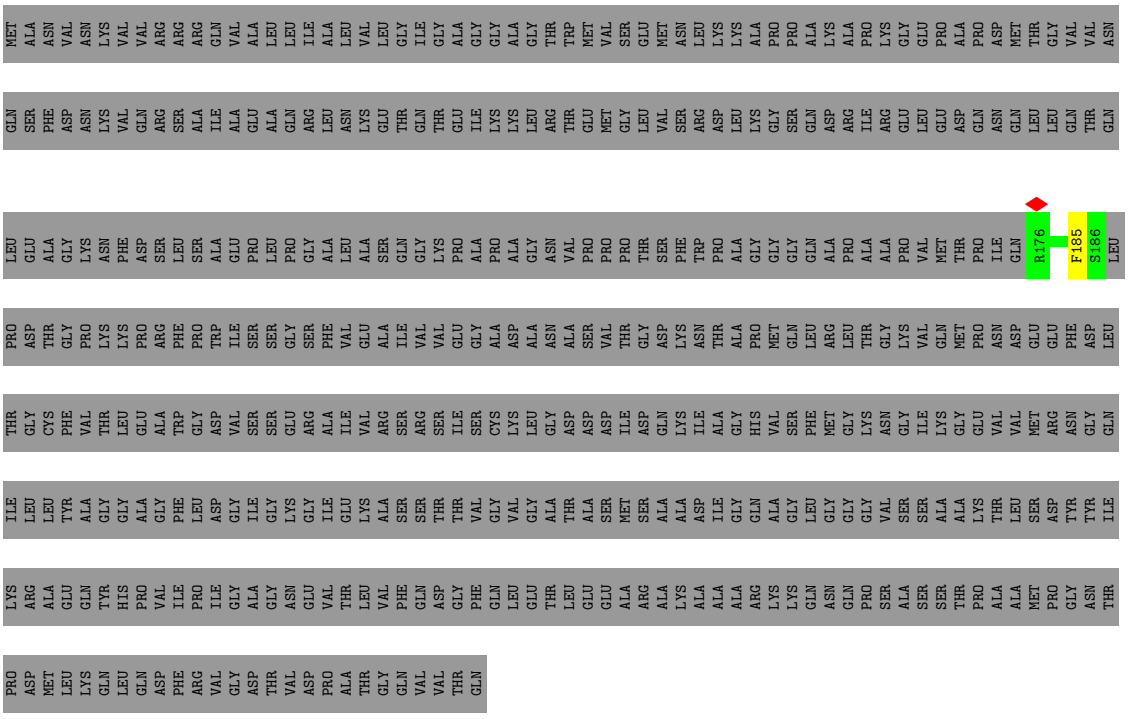




• Molecule 3: TraB

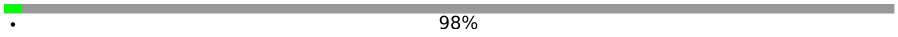
Chain F9:

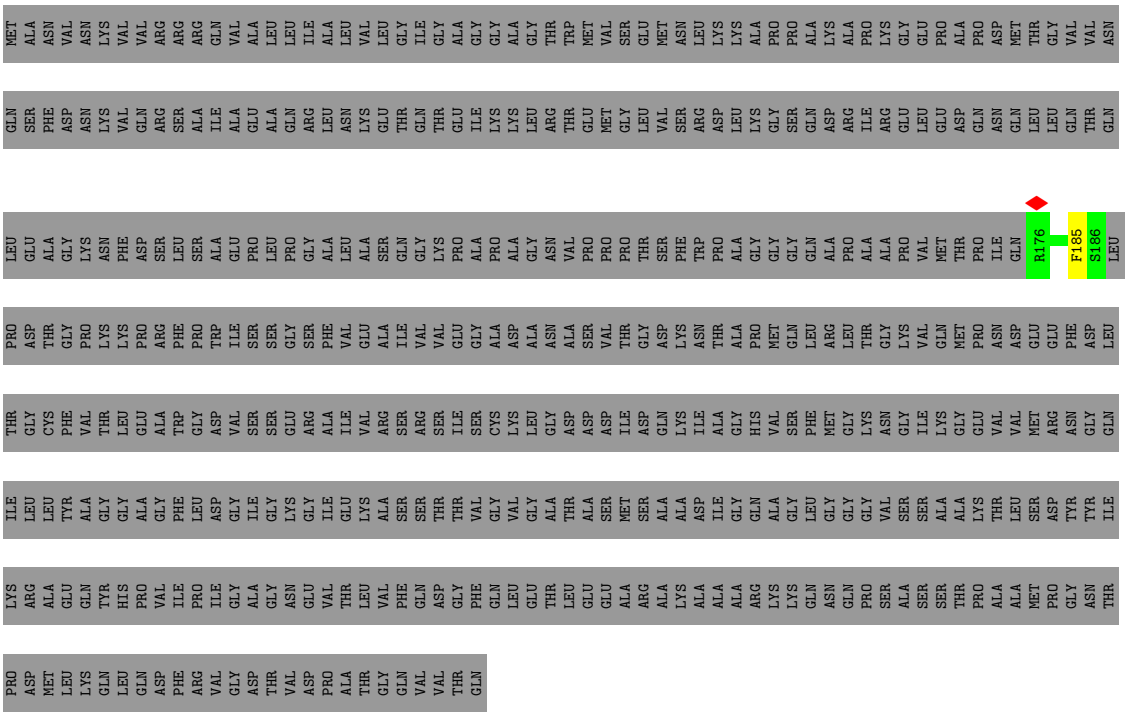




• Molecule 3: TraB

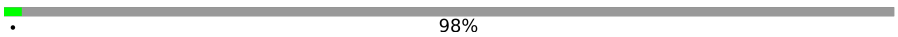
Chain F10:

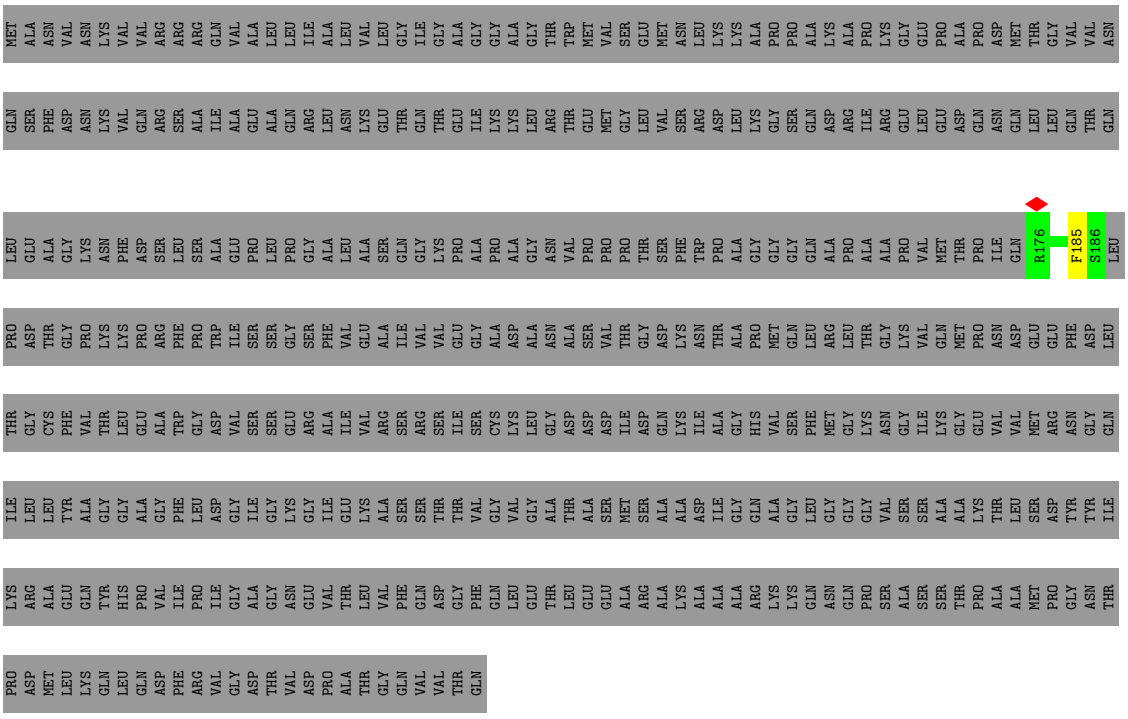




• Molecule 3: TraB

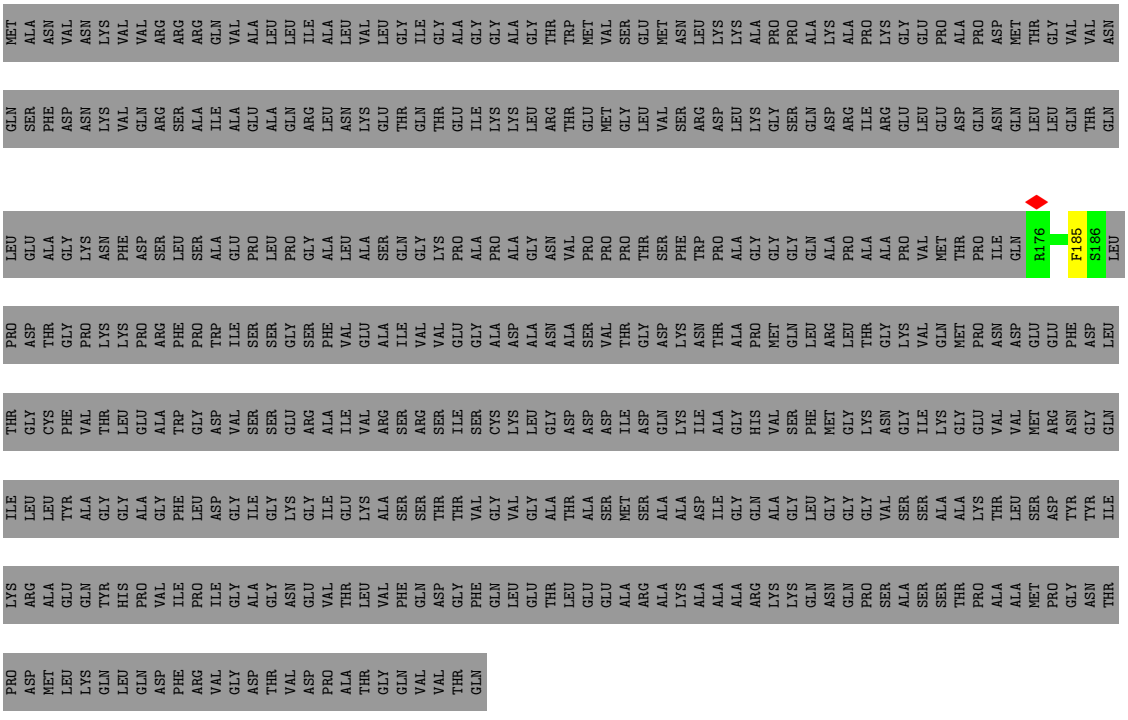
Chain F11:





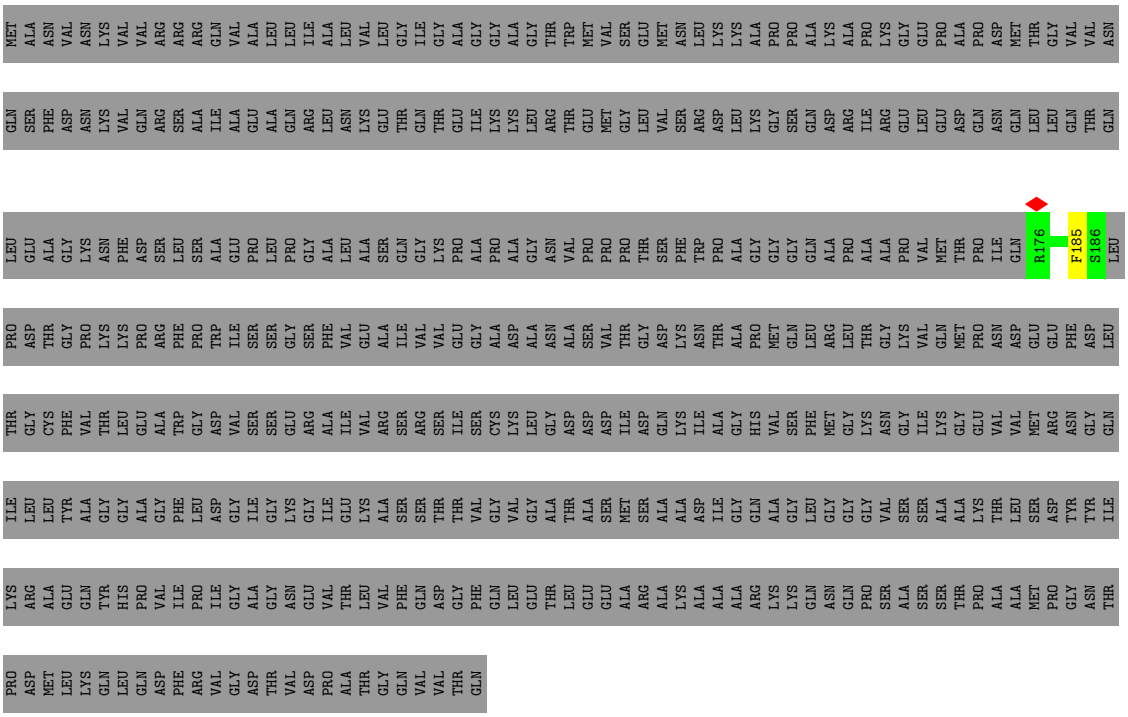
• Molecule 3: TraB

Chain F12: 98%



• Molecule 3: TraB

Chain F13: 98%


R176
F185
S186

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C13	Depositor
Number of particles used	70700	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.074	Depositor
Minimum map value	-1.310	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.072	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	426.08, 426.08, 426.08	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0652, 1.0652, 1.0652	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	A1	0.40	0/451	0.64	0/622
1	A10	0.40	0/451	0.64	0/622
1	A11	0.40	0/451	0.64	0/622
1	A12	0.40	0/451	0.64	0/622
1	A13	0.40	0/451	0.64	0/622
1	A2	0.40	0/451	0.64	0/622
1	A3	0.40	0/451	0.63	0/622
1	A4	0.40	0/451	0.64	0/622
1	A5	0.40	0/451	0.64	0/622
1	A6	0.40	0/451	0.63	0/622
1	A7	0.40	0/451	0.64	0/622
1	A8	0.40	0/451	0.64	0/622
1	A9	0.40	0/451	0.64	0/622
1	B1	0.38	0/514	0.67	0/710
1	B10	0.38	0/514	0.68	0/710
1	B11	0.38	0/514	0.67	0/710
1	B12	0.38	0/514	0.67	0/710
1	B13	0.38	0/514	0.67	0/710
1	B2	0.38	0/514	0.67	0/710
1	B3	0.38	0/514	0.67	0/710
1	B4	0.38	0/514	0.68	0/710
1	B5	0.38	0/514	0.68	0/710
1	B6	0.38	0/514	0.67	0/710
1	B7	0.38	0/514	0.68	0/710
1	B8	0.38	0/514	0.68	0/710
1	B9	0.38	0/514	0.67	0/710
2	C1	0.49	0/1688	0.68	0/2290
2	C10	0.49	0/1688	0.68	0/2290
2	C11	0.49	0/1688	0.68	0/2290
2	C12	0.49	0/1688	0.68	0/2290
2	C13	0.49	0/1688	0.68	0/2290
2	C2	0.49	0/1688	0.68	0/2290
2	C3	0.49	0/1688	0.68	0/2290
2	C4	0.49	0/1688	0.68	0/2290

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
2	C5	0.49	0/1688	0.68	0/2290
2	C6	0.49	0/1688	0.68	0/2290
2	C7	0.49	0/1688	0.68	0/2290
2	C8	0.49	0/1688	0.68	0/2290
2	C9	0.49	0/1688	0.68	0/2290
2	D1	0.47	0/1688	0.66	0/2290
2	D10	0.47	0/1688	0.66	0/2290
2	D11	0.47	0/1688	0.66	0/2290
2	D12	0.47	0/1688	0.66	0/2290
2	D13	0.47	0/1688	0.66	0/2290
2	D2	0.47	0/1688	0.66	0/2290
2	D3	0.47	0/1688	0.66	0/2290
2	D4	0.47	0/1688	0.66	0/2290
2	D5	0.47	0/1688	0.66	0/2290
2	D6	0.47	0/1688	0.66	0/2290
2	D7	0.47	0/1688	0.66	0/2290
2	D8	0.47	0/1688	0.66	0/2290
2	D9	0.47	0/1688	0.66	0/2290
3	E1	0.30	0/88	0.52	0/115
3	E10	0.30	0/88	0.52	0/115
3	E11	0.30	0/88	0.52	0/115
3	E12	0.30	0/88	0.52	0/115
3	E13	0.30	0/88	0.52	0/115
3	E2	0.30	0/88	0.52	0/115
3	E3	0.30	0/88	0.52	0/115
3	E4	0.30	0/88	0.52	0/115
3	E5	0.30	0/88	0.52	0/115
3	E6	0.30	0/88	0.52	0/115
3	E7	0.30	0/88	0.52	0/115
3	E8	0.30	0/88	0.52	0/115
3	E9	0.30	0/88	0.52	0/115
3	F1	0.36	0/88	0.62	0/115
3	F10	0.36	0/88	0.62	0/115
3	F11	0.37	0/88	0.62	0/115
3	F12	0.36	0/88	0.62	0/115
3	F13	0.37	0/88	0.62	0/115
3	F2	0.37	0/88	0.62	0/115
3	F3	0.37	0/88	0.62	0/115
3	F4	0.36	0/88	0.62	0/115
3	F5	0.36	0/88	0.62	0/115
3	F6	0.37	0/88	0.62	0/115
3	F7	0.37	0/88	0.62	0/115
3	F8	0.36	0/88	0.62	0/115

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
3	F9	0.36	0/88	0.62	0/115
All	All	0.46	0/58721	0.66	0/79846

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	A1	436	0	414	50	0
1	A10	436	0	414	48	0
1	A11	436	0	414	52	0
1	A12	436	0	414	49	0
1	A13	436	0	414	49	0
1	A2	436	0	414	48	0
1	A3	436	0	414	49	0
1	A4	436	0	414	48	0
1	A5	436	0	414	48	0
1	A6	436	0	414	50	0
1	A7	436	0	414	48	0
1	A8	436	0	414	49	0
1	A9	436	0	414	51	0
1	B1	498	0	478	54	0
1	B10	498	0	478	56	0
1	B11	498	0	478	55	0
1	B12	498	0	478	54	0
1	B13	498	0	478	54	0
1	B2	498	0	478	54	0
1	B3	498	0	478	54	0
1	B4	498	0	478	54	0
1	B5	498	0	478	56	0
1	B6	498	0	478	56	0
1	B7	498	0	478	55	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B8	498	0	478	54	0
1	B9	498	0	478	53	0
2	C1	1654	0	1664	65	0
2	C10	1654	0	1664	64	0
2	C11	1654	0	1664	69	0
2	C12	1654	0	1664	65	0
2	C13	1654	0	1664	68	0
2	C2	1654	0	1664	71	0
2	C3	1654	0	1664	68	0
2	C4	1654	0	1664	64	0
2	C5	1654	0	1664	67	0
2	C6	1654	0	1664	66	0
2	C7	1654	0	1664	67	0
2	C8	1654	0	1664	66	0
2	C9	1654	0	1664	68	0
2	D1	1654	0	1664	86	0
2	D10	1654	0	1664	86	0
2	D11	1654	0	1664	87	0
2	D12	1654	0	1664	86	0
2	D13	1654	0	1664	87	0
2	D2	1654	0	1664	82	0
2	D3	1654	0	1664	83	0
2	D4	1654	0	1664	83	0
2	D5	1654	0	1664	87	0
2	D6	1654	0	1664	85	0
2	D7	1654	0	1664	89	0
2	D8	1654	0	1664	85	0
2	D9	1654	0	1664	84	0
3	E1	87	0	77	8	0
3	E10	87	0	77	7	0
3	E11	87	0	77	9	0
3	E12	87	0	77	8	0
3	E13	87	0	77	9	0
3	E2	87	0	77	7	0
3	E3	87	0	77	9	0
3	E4	87	0	77	9	0
3	E5	87	0	77	8	0
3	E6	87	0	77	9	0
3	E7	87	0	77	8	0
3	E8	87	0	77	8	0
3	E9	87	0	77	8	0
3	F1	87	0	77	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F10	87	0	77	3	0
3	F11	87	0	77	3	0
3	F12	87	0	77	3	0
3	F13	87	0	77	3	0
3	F2	87	0	77	3	0
3	F3	87	0	77	3	0
3	F4	87	0	77	3	0
3	F5	87	0	77	3	0
3	F6	87	0	77	3	0
3	F7	87	0	77	3	0
3	F8	87	0	77	3	0
3	F9	87	0	77	3	0
All	All	57408	0	56862	2216	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 19.

All (2216) 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:B6:98:VAL:HG22	2:D7:208:TRP:CD1	1.71	1.26
1:B10:98:VAL:HG22	2:D11:208:TRP:CD1	1.71	1.26
1:B11:98:VAL:HG22	2:D12:208:TRP:CD1	1.71	1.26
1:B7:98:VAL:HG22	2:D8:208:TRP:CD1	1.71	1.26
1:B2:98:VAL:HG22	2:D3:208:TRP:CD1	1.71	1.26
1:B1:98:VAL:HG22	2:D2:208:TRP:CD1	1.71	1.25
1:B5:98:VAL:HG22	2:D6:208:TRP:CD1	1.71	1.25
1:B3:98:VAL:HG22	2:D4:208:TRP:CD1	1.71	1.25
1:B9:98:VAL:HG22	2:D10:208:TRP:CD1	1.71	1.25
1:B12:98:VAL:HG22	2:D13:208:TRP:CD1	1.71	1.25
1:B13:98:VAL:HG22	2:D1:208:TRP:CD1	1.71	1.25
1:B8:98:VAL:HG22	2:D9:208:TRP:CD1	1.71	1.24
1:B4:98:VAL:HG22	2:D5:208:TRP:CD1	1.71	1.24
1:B7:98:VAL:CG2	2:D8:208:TRP:CD1	2.24	1.21
1:B6:98:VAL:CG2	2:D7:208:TRP:CD1	2.24	1.21
1:B1:98:VAL:CG2	2:D2:208:TRP:CD1	2.24	1.20
1:B5:98:VAL:CG2	2:D6:208:TRP:CD1	2.24	1.20
1:B8:98:VAL:CG2	2:D9:208:TRP:CD1	2.24	1.20
1:B2:98:VAL:CG2	2:D3:208:TRP:CD1	2.24	1.20
1:B13:98:VAL:CG2	2:D1:208:TRP:CD1	2.24	1.20
1:B9:98:VAL:CG2	2:D10:208:TRP:CD1	2.24	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B10:98:VAL:CG2	2:D11:208:TRP:CD1	2.24	1.20
1:B3:98:VAL:CG2	2:D4:208:TRP:CD1	2.24	1.19
1:B4:98:VAL:CG2	2:D5:208:TRP:CD1	2.24	1.19
1:B12:98:VAL:CG2	2:D13:208:TRP:CD1	2.24	1.19
1:B11:98:VAL:CG2	2:D12:208:TRP:CD1	2.24	1.19
1:A12:155:PRO:HD3	1:B10:157:THR:HB	1.20	1.15
1:A1:155:PRO:HD3	1:B12:157:THR:HB	1.20	1.15
1:A2:155:PRO:HD3	1:B13:157:THR:HB	1.20	1.15
1:A11:155:PRO:HD3	1:B9:157:THR:HB	1.20	1.15
2:D5:159:VAL:HG12	2:D5:160:LYS:H	1.01	1.14
1:A13:155:PRO:HD3	1:B11:157:THR:HB	1.20	1.13
2:D3:159:VAL:HG12	2:D3:160:LYS:H	1.01	1.13
1:A3:155:PRO:HD3	1:B1:157:THR:HB	1.20	1.12
1:A10:155:PRO:HD3	1:B8:157:THR:HB	1.20	1.12
2:D11:159:VAL:HG12	2:D11:160:LYS:H	1.02	1.11
1:B13:98:VAL:CG2	2:D1:208:TRP:HD1	1.63	1.11
2:D7:159:VAL:HG12	2:D7:160:LYS:H	1.01	1.11
1:B12:98:VAL:CG2	2:D13:208:TRP:HD1	1.63	1.11
2:D12:159:VAL:HG12	2:D12:160:LYS:H	1.01	1.11
1:A5:155:PRO:HD3	1:B3:157:THR:HB	1.20	1.10
1:A8:155:PRO:HD3	1:B6:157:THR:HB	1.20	1.10
1:B1:98:VAL:CG2	2:D2:208:TRP:HD1	1.63	1.10
1:B4:98:VAL:CG2	2:D5:208:TRP:HD1	1.63	1.10
2:D6:159:VAL:HG12	2:D6:160:LYS:H	1.01	1.10
1:B3:188:VAL:HG11	2:D3:141:ILE:HD11	1.34	1.10
1:B1:188:VAL:HG11	2:D1:141:ILE:HD11	1.34	1.09
1:B5:98:VAL:CG2	2:D6:208:TRP:HD1	1.63	1.09
1:B6:188:VAL:HG11	2:D6:141:ILE:HD11	1.34	1.09
1:B11:98:VAL:CG2	2:D12:208:TRP:HD1	1.63	1.09
2:D8:159:VAL:HG12	2:D8:160:LYS:H	1.01	1.09
1:A4:155:PRO:HD3	1:B2:157:THR:HB	1.20	1.09
1:A9:155:PRO:HD3	1:B7:157:THR:HB	1.20	1.09
1:B13:188:VAL:HG11	2:D13:141:ILE:HD11	1.34	1.09
2:D9:159:VAL:HG12	2:D9:160:LYS:H	1.01	1.09
1:B11:188:VAL:HG11	2:D11:141:ILE:HD11	1.34	1.09
1:B2:98:VAL:CG2	2:D3:208:TRP:HD1	1.63	1.09
1:B4:188:VAL:HG11	2:D4:141:ILE:HD11	1.34	1.09
1:B6:98:VAL:CG2	2:D7:208:TRP:HD1	1.63	1.08
2:D1:159:VAL:HG12	2:D1:160:LYS:H	1.01	1.08
1:A7:155:PRO:HD3	1:B5:157:THR:HB	1.20	1.08
1:B7:188:VAL:HG11	2:D7:141:ILE:HD11	1.34	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B10:188:VAL:HG11	2:D10:141:ILE:HD11	1.34	1.08
1:A6:155:PRO:HD3	1:B4:157:THR:HB	1.20	1.08
1:B10:98:VAL:CG2	2:D11:208:TRP:HD1	1.63	1.08
2:D2:159:VAL:HG12	2:D2:160:LYS:H	1.01	1.08
2:D4:159:VAL:HG12	2:D4:160:LYS:H	1.01	1.08
1:B7:98:VAL:CG2	2:D8:208:TRP:HD1	1.63	1.08
1:B8:98:VAL:CG2	2:D9:208:TRP:HD1	1.63	1.07
2:D13:159:VAL:HG12	2:D13:160:LYS:H	1.02	1.07
1:B3:98:VAL:CG2	2:D4:208:TRP:HD1	1.63	1.07
1:B9:98:VAL:CG2	2:D10:208:TRP:HD1	1.63	1.07
2:D10:159:VAL:HG12	2:D10:160:LYS:H	1.01	1.07
1:B5:188:VAL:HG11	2:D5:141:ILE:HD11	1.34	1.06
1:B9:188:VAL:HG11	2:D9:141:ILE:HD11	1.34	1.05
1:B12:188:VAL:HG11	2:D12:141:ILE:HD11	1.34	1.05
2:D5:159:VAL:HG12	2:D5:160:LYS:N	1.72	1.05
1:B8:188:VAL:HG11	2:D8:141:ILE:HD11	1.34	1.05
1:B2:188:VAL:HG11	2:D2:141:ILE:HD11	1.34	1.04
2:D6:159:VAL:HG12	2:D6:160:LYS:N	1.72	1.04
1:B11:188:VAL:CG1	2:D11:141:ILE:HD11	1.88	1.03
2:D7:159:VAL:HG12	2:D7:160:LYS:N	1.72	1.03
1:B9:188:VAL:CG1	2:D9:141:ILE:HD11	1.88	1.03
1:B10:188:VAL:CG1	2:D10:141:ILE:HD11	1.88	1.03
1:B12:188:VAL:CG1	2:D12:141:ILE:HD11	1.88	1.03
1:B13:188:VAL:CG1	2:D13:141:ILE:HD11	1.88	1.03
1:B1:188:VAL:CG1	2:D1:141:ILE:HD11	1.88	1.03
1:B2:188:VAL:CG1	2:D2:141:ILE:HD11	1.88	1.03
1:B8:188:VAL:CG1	2:D8:141:ILE:HD11	1.88	1.03
1:B3:188:VAL:CG1	2:D3:141:ILE:HD11	1.88	1.02
1:B4:188:VAL:CG1	2:D4:141:ILE:HD11	1.88	1.02
1:B7:188:VAL:CG1	2:D7:141:ILE:HD11	1.88	1.02
1:B5:188:VAL:CG1	2:D5:141:ILE:HD11	1.88	1.02
1:B6:188:VAL:CG1	2:D6:141:ILE:HD11	1.88	1.02
2:D13:159:VAL:HG12	2:D13:160:LYS:N	1.72	1.02
2:D8:159:VAL:HG12	2:D8:160:LYS:N	1.72	1.02
2:D1:159:VAL:HG12	2:D1:160:LYS:N	1.72	1.01
2:D11:159:VAL:HG12	2:D11:160:LYS:N	1.72	1.01
2:D12:159:VAL:HG12	2:D12:160:LYS:N	1.72	1.01
2:D10:159:VAL:HG12	2:D10:160:LYS:N	1.72	1.01
2:C1:202:LEU:HD13	2:C1:217:PHE:CZ	1.96	1.00
2:C2:202:LEU:HD13	2:C2:217:PHE:CZ	1.96	1.00
2:C7:202:LEU:HD13	2:C7:217:PHE:CZ	1.96	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C8:202:LEU:HD13	2:C8:217:PHE:CZ	1.96	1.00
2:C9:202:LEU:HD13	2:C9:217:PHE:CZ	1.96	1.00
2:C3:202:LEU:HD13	2:C3:217:PHE:CZ	1.96	1.00
2:C13:202:LEU:HD13	2:C13:217:PHE:CZ	1.96	1.00
2:C6:202:LEU:HD13	2:C6:217:PHE:CZ	1.96	1.00
2:D9:159:VAL:HG12	2:D9:160:LYS:N	1.72	1.00
2:C12:202:LEU:HD13	2:C12:217:PHE:CZ	1.96	0.99
2:C4:202:LEU:HD13	2:C4:217:PHE:CZ	1.96	0.99
2:C10:202:LEU:HD13	2:C10:217:PHE:CZ	1.96	0.99
2:D2:159:VAL:HG12	2:D2:160:LYS:N	1.72	0.99
2:C5:202:LEU:HD13	2:C5:217:PHE:CZ	1.96	0.99
2:C11:202:LEU:HD13	2:C11:217:PHE:CZ	1.96	0.98
2:D3:159:VAL:HG12	2:D3:160:LYS:N	1.72	0.97
2:D3:159:VAL:CG1	2:D3:160:LYS:H	1.78	0.97
2:D8:159:VAL:CG1	2:D8:160:LYS:H	1.78	0.97
2:D1:159:VAL:CG1	2:D1:160:LYS:H	1.78	0.97
2:D11:159:VAL:CG1	2:D11:160:LYS:H	1.78	0.97
2:D6:159:VAL:CG1	2:D6:160:LYS:H	1.78	0.97
2:D10:159:VAL:CG1	2:D10:160:LYS:H	1.78	0.97
2:D13:159:VAL:CG1	2:D13:160:LYS:H	1.78	0.96
2:D4:159:VAL:CG1	2:D4:160:LYS:H	1.78	0.96
1:A3:172:ILE:HD12	2:C3:140:LEU:HD12	1.48	0.96
1:A12:172:ILE:HD12	2:C12:140:LEU:HD12	1.48	0.96
2:D5:159:VAL:CG1	2:D5:160:LYS:H	1.78	0.96
2:D9:159:VAL:CG1	2:D9:160:LYS:H	1.78	0.96
1:A6:172:ILE:HD12	2:C6:140:LEU:HD12	1.48	0.96
1:A11:172:ILE:HD12	2:C11:140:LEU:HD12	1.48	0.96
1:A2:172:ILE:HD12	2:C2:140:LEU:HD12	1.48	0.96
1:A9:155:PRO:CD	1:B7:157:THR:HB	1.96	0.96
1:A9:172:ILE:HD12	2:C9:140:LEU:HD12	1.48	0.96
1:A10:155:PRO:CD	1:B8:157:THR:HB	1.96	0.96
1:A8:155:PRO:CD	1:B6:157:THR:HB	1.96	0.95
2:D7:159:VAL:CG1	2:D7:160:LYS:H	1.78	0.95
2:D12:159:VAL:CG1	2:D12:160:LYS:H	1.78	0.95
1:A11:155:PRO:CD	1:B9:157:THR:HB	1.96	0.95
2:D2:159:VAL:CG1	2:D2:160:LYS:H	1.78	0.95
1:A7:155:PRO:CD	1:B5:157:THR:HB	1.96	0.95
1:A3:155:PRO:CD	1:B1:157:THR:HB	1.96	0.95
1:A4:155:PRO:CD	1:B2:157:THR:HB	1.96	0.95
1:A8:172:ILE:HD12	2:C8:140:LEU:HD12	1.48	0.95
2:D4:159:VAL:HG12	2:D4:160:LYS:N	1.72	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A2:155:PRO:CD	1:B13:157:THR:HB	1.96	0.95
1:A5:155:PRO:CD	1:B3:157:THR:HB	1.96	0.95
1:A5:172:ILE:HD12	2:C5:140:LEU:HD12	1.48	0.95
1:A6:155:PRO:CD	1:B4:157:THR:HB	1.96	0.95
1:A12:155:PRO:CD	1:B10:157:THR:HB	1.96	0.95
1:A4:172:ILE:HD12	2:C4:140:LEU:HD12	1.48	0.94
1:A13:172:ILE:HD12	2:C13:140:LEU:HD12	1.48	0.94
1:A1:155:PRO:CD	1:B12:157:THR:HB	1.96	0.94
1:A13:155:PRO:CD	1:B11:157:THR:HB	1.96	0.94
2:D3:43:SER:H	2:D3:48:ASN:HD21	1.16	0.94
2:D1:43:SER:H	2:D1:48:ASN:HD21	1.16	0.94
2:D12:43:SER:H	2:D12:48:ASN:HD21	1.16	0.94
1:A1:172:ILE:HD12	2:C1:140:LEU:HD12	1.48	0.94
2:D5:43:SER:H	2:D5:48:ASN:HD21	1.16	0.94
1:A7:172:ILE:HD12	2:C7:140:LEU:HD12	1.48	0.93
1:A5:192:VAL:HG13	2:C5:148:LEU:HD23	1.50	0.93
2:D11:43:SER:H	2:D11:48:ASN:HD21	1.16	0.93
2:D13:43:SER:H	2:D13:48:ASN:HD21	1.16	0.93
1:A6:192:VAL:HG13	2:C6:148:LEU:HD23	1.50	0.93
1:A10:172:ILE:HD12	2:C10:140:LEU:HD12	1.48	0.93
2:D2:43:SER:H	2:D2:48:ASN:HD21	1.16	0.93
2:D4:43:SER:H	2:D4:48:ASN:HD21	1.16	0.93
1:A4:192:VAL:HG13	2:C4:148:LEU:HD23	1.50	0.93
1:A7:192:VAL:HG13	2:C7:148:LEU:HD23	1.50	0.93
1:A13:192:VAL:HG13	2:C13:148:LEU:HD23	1.50	0.93
2:D10:43:SER:H	2:D10:48:ASN:HD21	1.16	0.93
1:A1:192:VAL:HG13	2:C1:148:LEU:HD23	1.50	0.92
2:D9:43:SER:H	2:D9:48:ASN:HD21	1.16	0.92
1:B7:98:VAL:HG21	2:D8:208:TRP:HD1	1.33	0.92
1:B8:98:VAL:HG21	2:D9:208:TRP:HD1	1.33	0.92
1:B13:98:VAL:HG21	2:D1:208:TRP:HD1	1.33	0.92
2:D6:43:SER:H	2:D6:48:ASN:HD21	1.16	0.92
1:A12:192:VAL:HG13	2:C12:148:LEU:HD23	1.50	0.92
1:A8:192:VAL:HG13	2:C8:148:LEU:HD23	1.50	0.92
1:B1:98:VAL:HG21	2:D2:208:TRP:HD1	1.33	0.92
1:A3:192:VAL:HG13	2:C3:148:LEU:HD23	1.50	0.92
1:B9:98:VAL:HG21	2:D10:208:TRP:HD1	1.33	0.92
1:B12:98:VAL:HG21	2:D13:208:TRP:HD1	1.33	0.92
2:D8:43:SER:H	2:D8:48:ASN:HD21	1.16	0.92
1:A2:192:VAL:HG13	2:C2:148:LEU:HD23	1.50	0.91
1:B6:98:VAL:HG21	2:D7:208:TRP:HD1	1.33	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D7:43:SER:H	2:D7:48:ASN:HD21	1.16	0.91
1:B2:98:VAL:HG21	2:D3:208:TRP:HD1	1.33	0.91
1:A11:192:VAL:HG13	2:C11:148:LEU:HD23	1.50	0.91
1:B11:98:VAL:HG21	2:D12:208:TRP:HD1	1.33	0.91
1:A9:192:VAL:HG13	2:C9:148:LEU:HD23	1.50	0.90
1:B3:98:VAL:HG21	2:D4:208:TRP:HD1	1.33	0.90
1:B4:98:VAL:HG21	2:D5:208:TRP:HD1	1.33	0.90
1:B10:98:VAL:HG21	2:D11:208:TRP:HD1	1.33	0.90
1:A5:155:PRO:HD3	1:B3:157:THR:CB	2.02	0.90
1:A7:155:PRO:HD3	1:B5:157:THR:CB	2.02	0.90
1:A10:155:PRO:HD3	1:B8:157:THR:CB	2.02	0.90
1:A8:155:PRO:HD3	1:B6:157:THR:CB	2.02	0.90
2:D8:168:LEU:HD21	2:D8:174:VAL:CG2	2.02	0.90
1:A4:155:PRO:HD3	1:B2:157:THR:CB	2.02	0.89
1:B5:98:VAL:HG21	2:D6:208:TRP:HD1	1.33	0.89
2:D12:168:LEU:HD21	2:D12:174:VAL:CG2	2.02	0.89
1:A10:192:VAL:HG13	2:C10:148:LEU:HD23	1.50	0.89
1:A11:155:PRO:HD3	1:B9:157:THR:CB	2.02	0.89
2:D9:168:LEU:HD21	2:D9:174:VAL:CG2	2.02	0.89
1:A1:155:PRO:HD3	1:B12:157:THR:CB	2.02	0.89
1:A2:155:PRO:HD3	1:B13:157:THR:CB	2.02	0.89
2:D7:168:LEU:HD21	2:D7:174:VAL:CG2	2.02	0.89
2:D11:168:LEU:HD21	2:D11:174:VAL:CG2	2.02	0.89
1:A13:192:VAL:CG1	2:C13:148:LEU:HD23	2.03	0.89
1:A1:192:VAL:CG1	2:C1:148:LEU:HD23	2.03	0.89
1:A12:192:VAL:CG1	2:C12:148:LEU:HD23	2.03	0.89
2:D13:168:LEU:HD21	2:D13:174:VAL:CG2	2.02	0.89
1:A6:192:VAL:CG1	2:C6:148:LEU:HD23	2.03	0.89
1:A9:155:PRO:HD3	1:B7:157:THR:CB	2.02	0.89
1:A6:155:PRO:HD3	1:B4:157:THR:CB	2.02	0.89
1:A5:192:VAL:CG1	2:C5:148:LEU:HD23	2.03	0.88
1:A7:192:VAL:CG1	2:C7:148:LEU:HD23	2.03	0.88
1:A11:192:VAL:CG1	2:C11:148:LEU:HD23	2.03	0.88
1:A13:155:PRO:HD3	1:B11:157:THR:CB	2.02	0.88
2:C6:74:ARG:NH1	2:D5:58:THR:HG21	1.88	0.88
2:C11:74:ARG:NH1	2:D10:58:THR:HG21	1.88	0.88
2:C5:74:ARG:NH1	2:D4:58:THR:HG21	1.88	0.88
2:C10:74:ARG:NH1	2:D9:58:THR:HG21	1.88	0.88
1:A2:192:VAL:CG1	2:C2:148:LEU:HD23	2.03	0.88
1:A8:192:VAL:CG1	2:C8:148:LEU:HD23	2.03	0.88
2:D10:168:LEU:HD21	2:D10:174:VAL:CG2	2.02	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A10:192:VAL:CG1	2:C10:148:LEU:HD23	2.03	0.88
2:C9:74:ARG:NH1	2:D8:58:THR:HG21	1.88	0.88
2:D1:168:LEU:HD21	2:D1:174:VAL:CG2	2.02	0.88
2:D4:168:LEU:HD21	2:D4:174:VAL:CG2	2.02	0.88
1:A3:155:PRO:HD3	1:B1:157:THR:CB	2.02	0.88
2:D3:168:LEU:HD21	2:D3:174:VAL:CG2	2.02	0.88
1:A4:192:VAL:CG1	2:C4:148:LEU:HD23	2.03	0.88
2:D6:168:LEU:HD21	2:D6:174:VAL:CG2	2.02	0.88
1:A12:155:PRO:HD3	1:B10:157:THR:CB	2.02	0.88
2:C2:74:ARG:NH1	2:D1:58:THR:HG21	1.88	0.88
2:D5:168:LEU:HD21	2:D5:174:VAL:CG2	2.02	0.88
2:C1:74:ARG:NH1	2:D13:58:THR:HG21	1.88	0.87
2:C1:202:LEU:CD1	2:C1:217:PHE:CE2	2.57	0.87
2:C2:202:LEU:CD1	2:C2:217:PHE:CE2	2.57	0.87
2:D2:168:LEU:HD21	2:D2:174:VAL:CG2	2.02	0.87
1:A9:192:VAL:CG1	2:C9:148:LEU:HD23	2.03	0.87
2:C3:202:LEU:CD1	2:C3:217:PHE:CE2	2.58	0.87
2:C8:74:ARG:NH1	2:D7:58:THR:HG21	1.88	0.87
1:A3:192:VAL:CG1	2:C3:148:LEU:HD23	2.03	0.87
2:C4:74:ARG:NH1	2:D3:58:THR:HG21	1.88	0.87
2:C7:74:ARG:NH1	2:D6:58:THR:HG21	1.88	0.87
2:C12:74:ARG:NH1	2:D11:58:THR:HG21	1.88	0.87
2:C4:202:LEU:CD1	2:C4:217:PHE:CE2	2.57	0.87
2:C13:202:LEU:CD1	2:C13:217:PHE:CE2	2.57	0.87
2:C9:202:LEU:CD1	2:C9:217:PHE:CE2	2.57	0.87
2:C11:202:LEU:CD1	2:C11:217:PHE:CE2	2.57	0.87
2:C3:74:ARG:NH1	2:D2:58:THR:HG21	1.88	0.86
2:C12:202:LEU:CD1	2:C12:217:PHE:CE2	2.57	0.86
2:D9:42:ILE:HB	2:D9:48:ASN:ND2	1.90	0.86
2:D10:42:ILE:HB	2:D10:48:ASN:ND2	1.90	0.86
2:D3:42:ILE:HB	2:D3:48:ASN:ND2	1.90	0.86
2:D4:42:ILE:HB	2:D4:48:ASN:ND2	1.90	0.86
2:D11:42:ILE:HB	2:D11:48:ASN:ND2	1.90	0.86
2:D12:42:ILE:HB	2:D12:48:ASN:ND2	1.90	0.86
2:C6:202:LEU:CD1	2:C6:217:PHE:CE2	2.57	0.86
2:C7:202:LEU:CD1	2:C7:217:PHE:CE2	2.57	0.86
2:C8:202:LEU:CD1	2:C8:217:PHE:CE2	2.58	0.86
2:C10:202:LEU:CD1	2:C10:217:PHE:CE2	2.57	0.86
2:C5:202:LEU:CD1	2:C5:217:PHE:CE2	2.57	0.86
2:C13:74:ARG:NH1	2:D12:58:THR:HG21	1.88	0.86
2:D5:42:ILE:HB	2:D5:48:ASN:ND2	1.90	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D8:42:ILE:HB	2:D8:48:ASN:ND2	1.90	0.86
2:D2:42:ILE:HB	2:D2:48:ASN:ND2	1.90	0.86
2:D13:42:ILE:HB	2:D13:48:ASN:ND2	1.90	0.86
2:D6:42:ILE:HB	2:D6:48:ASN:ND2	1.90	0.85
2:D7:42:ILE:HB	2:D7:48:ASN:ND2	1.90	0.85
2:C6:35:GLY:HA3	2:D6:27:PRO:HG3	1.59	0.85
2:D1:42:ILE:HB	2:D1:48:ASN:ND2	1.90	0.85
2:C2:35:GLY:HA3	2:D2:27:PRO:HG3	1.59	0.85
2:C5:35:GLY:HA3	2:D5:27:PRO:HG3	1.59	0.85
2:C7:35:GLY:HA3	2:D7:27:PRO:HG3	1.59	0.85
2:C3:35:GLY:HA3	2:D3:27:PRO:HG3	1.59	0.85
2:C8:202:LEU:HD13	2:C8:217:PHE:CE2	2.12	0.85
2:C9:202:LEU:HD13	2:C9:217:PHE:CE2	2.12	0.85
2:C1:35:GLY:HA3	2:D1:27:PRO:HG3	1.59	0.84
2:C5:35:GLY:HA3	2:D5:27:PRO:CG	2.07	0.84
2:C4:35:GLY:HA3	2:D4:27:PRO:HG3	1.59	0.84
2:C8:35:GLY:HA3	2:D8:27:PRO:HG3	1.59	0.84
2:C10:35:GLY:HA3	2:D10:27:PRO:CG	2.08	0.84
2:C11:35:GLY:HA3	2:D11:27:PRO:CG	2.08	0.84
2:C4:35:GLY:HA3	2:D4:27:PRO:CG	2.07	0.84
2:C7:202:LEU:HD13	2:C7:217:PHE:CE2	2.12	0.84
2:C10:202:LEU:HD13	2:C10:217:PHE:CE2	2.12	0.84
2:C4:202:LEU:HD13	2:C4:217:PHE:CE2	2.12	0.84
2:C6:35:GLY:HA3	2:D6:27:PRO:CG	2.07	0.84
2:C12:35:GLY:HA3	2:D12:27:PRO:CG	2.07	0.84
2:C13:35:GLY:HA3	2:D13:27:PRO:HG3	1.59	0.84
2:C1:202:LEU:HD13	2:C1:217:PHE:CE2	2.12	0.84
2:C5:202:LEU:HD13	2:C5:217:PHE:CE2	2.12	0.84
2:C9:35:GLY:HA3	2:D9:27:PRO:CG	2.07	0.84
2:C13:202:LEU:HD13	2:C13:217:PHE:CE2	2.12	0.84
2:C3:202:LEU:HD13	2:C3:217:PHE:CE2	2.12	0.84
2:C9:35:GLY:HA3	2:D9:27:PRO:HG3	1.59	0.83
2:C13:35:GLY:HA3	2:D13:27:PRO:CG	2.07	0.83
2:C1:35:GLY:HA3	2:D1:27:PRO:CG	2.08	0.83
2:C8:35:GLY:HA3	2:D8:27:PRO:CG	2.07	0.83
2:C12:35:GLY:HA3	2:D12:27:PRO:HG3	1.59	0.83
2:C2:202:LEU:HD13	2:C2:217:PHE:CE2	2.12	0.83
2:C10:35:GLY:HA3	2:D10:27:PRO:HG3	1.59	0.83
2:C6:202:LEU:HD13	2:C6:217:PHE:CE2	2.12	0.83
2:D7:42:ILE:HB	2:D7:48:ASN:HD22	1.44	0.83
2:D8:42:ILE:HB	2:D8:48:ASN:HD22	1.44	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:35:GLY:HA3	2:D2:27:PRO:CG	2.08	0.83
2:C3:35:GLY:HA3	2:D3:27:PRO:CG	2.08	0.83
2:C11:35:GLY:HA3	2:D11:27:PRO:HG3	1.59	0.83
2:D3:42:ILE:HB	2:D3:48:ASN:HD22	1.44	0.83
2:C11:202:LEU:HD13	2:C11:217:PHE:CE2	2.12	0.83
2:D2:42:ILE:HB	2:D2:48:ASN:HD22	1.44	0.83
2:D6:42:ILE:HB	2:D6:48:ASN:HD22	1.44	0.83
2:C7:35:GLY:HA3	2:D7:27:PRO:CG	2.08	0.83
2:C12:202:LEU:HD13	2:C12:217:PHE:CE2	2.12	0.83
2:D4:42:ILE:HB	2:D4:48:ASN:HD22	1.44	0.83
2:D5:42:ILE:HB	2:D5:48:ASN:HD22	1.44	0.83
2:D9:42:ILE:HB	2:D9:48:ASN:HD22	1.44	0.82
2:D1:42:ILE:HB	2:D1:48:ASN:HD22	1.44	0.82
2:D5:168:LEU:CD2	2:D5:174:VAL:HG23	2.11	0.81
2:D6:168:LEU:CD2	2:D6:174:VAL:HG23	2.11	0.81
2:D10:42:ILE:HB	2:D10:48:ASN:HD22	1.44	0.81
2:D11:168:LEU:CD2	2:D11:174:VAL:HG23	2.11	0.81
2:D12:168:LEU:CD2	2:D12:174:VAL:HG23	2.11	0.81
2:D7:168:LEU:CD2	2:D7:174:VAL:HG23	2.11	0.81
2:D4:168:LEU:CD2	2:D4:174:VAL:HG23	2.11	0.81
2:D13:42:ILE:HB	2:D13:48:ASN:HD22	1.44	0.81
2:D13:168:LEU:CD2	2:D13:174:VAL:HG23	2.11	0.81
2:D12:42:ILE:HB	2:D12:48:ASN:HD22	1.44	0.81
2:D9:168:LEU:CD2	2:D9:174:VAL:HG23	2.11	0.81
2:D10:168:LEU:CD2	2:D10:174:VAL:HG23	2.11	0.81
2:D3:168:LEU:CD2	2:D3:174:VAL:HG23	2.11	0.81
2:D8:168:LEU:CD2	2:D8:174:VAL:HG23	2.11	0.81
2:D8:174:VAL:HG13	2:D8:190:TYR:HB3	1.63	0.80
1:B9:98:VAL:CG1	2:D10:208:TRP:CD1	2.65	0.80
2:D9:174:VAL:HG13	2:D9:190:TYR:HB3	1.63	0.80
2:D1:168:LEU:CD2	2:D1:174:VAL:HG23	2.11	0.80
1:B3:98:VAL:CG1	2:D4:208:TRP:CD1	2.65	0.80
2:C5:60:ILE:HG22	3:E5:185:PHE:HE2	1.47	0.80
1:B5:98:VAL:CG1	2:D6:208:TRP:CD1	2.65	0.80
2:D2:168:LEU:CD2	2:D2:174:VAL:HG23	2.11	0.80
1:B2:98:VAL:CG1	2:D3:208:TRP:CD1	2.65	0.80
1:B7:98:VAL:CG1	2:D8:208:TRP:CD1	2.65	0.80
1:B9:98:VAL:HG21	2:D10:208:TRP:CD1	2.12	0.80
2:D7:174:VAL:HG13	2:D7:190:TYR:HB3	1.63	0.80
1:B12:98:VAL:CG1	2:D13:208:TRP:CD1	2.65	0.80
2:D10:174:VAL:HG13	2:D10:190:TYR:HB3	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B10:98:VAL:CG1	2:D11:208:TRP:CD1	2.65	0.80
1:B13:98:VAL:CG1	2:D1:208:TRP:CD1	2.65	0.79
2:C6:60:ILE:HG22	3:E6:185:PHE:HE2	1.47	0.79
2:C4:60:ILE:HG22	3:E4:185:PHE:HE2	1.47	0.79
2:C7:60:ILE:HG22	3:E7:185:PHE:HE2	1.47	0.79
2:D11:42:ILE:HB	2:D11:48:ASN:HD22	1.44	0.79
1:B4:98:VAL:CG1	2:D5:208:TRP:CD1	2.65	0.79
1:B8:98:VAL:CG1	2:D9:208:TRP:CD1	2.65	0.79
2:C12:60:ILE:HG22	3:E12:185:PHE:HE2	1.47	0.79
1:B4:98:VAL:HG21	2:D5:208:TRP:CD1	2.12	0.79
1:B11:98:VAL:CG1	2:D12:208:TRP:CD1	2.65	0.79
2:D1:174:VAL:HG13	2:D1:190:TYR:HB3	1.63	0.79
1:B6:98:VAL:CG1	2:D7:208:TRP:CD1	2.65	0.79
2:C13:60:ILE:HG22	3:E13:185:PHE:HE2	1.47	0.79
2:D6:174:VAL:HG13	2:D6:190:TYR:HB3	1.63	0.79
2:C11:60:ILE:HG22	3:E11:185:PHE:HE2	1.47	0.79
2:D2:174:VAL:HG13	2:D2:190:TYR:HB3	1.63	0.79
1:B10:98:VAL:HG21	2:D11:208:TRP:CD1	2.12	0.79
2:C8:60:ILE:HG22	3:E8:185:PHE:HE2	1.47	0.79
2:D13:174:VAL:HG13	2:D13:190:TYR:HB3	1.63	0.79
1:B1:98:VAL:CG1	2:D2:208:TRP:CD1	2.65	0.79
2:D11:174:VAL:HG13	2:D11:190:TYR:HB3	1.63	0.78
1:B1:98:VAL:HG22	2:D2:208:TRP:NE1	1.99	0.78
1:B13:98:VAL:HG22	2:D1:208:TRP:NE1	1.99	0.78
2:C1:60:ILE:HG22	3:E1:185:PHE:HE2	1.47	0.78
2:D3:174:VAL:HG13	2:D3:190:TYR:HB3	1.63	0.78
1:A10:187:ARG:HD2	1:B10:184:GLN:OE1	1.84	0.78
1:B4:98:VAL:HG22	2:D5:208:TRP:NE1	1.98	0.78
1:B9:98:VAL:HG22	2:D10:208:TRP:NE1	1.99	0.78
1:B10:98:VAL:HG22	2:D11:208:TRP:NE1	1.99	0.78
1:A4:187:ARG:HD2	1:B4:184:GLN:OE1	1.84	0.78
1:B5:98:VAL:HG22	2:D6:208:TRP:NE1	1.99	0.78
1:A5:187:ARG:HD2	1:B5:184:GLN:OE1	1.84	0.78
2:C3:194:ASN:OD1	2:C3:224:LEU:HD23	1.84	0.78
2:C8:194:ASN:OD1	2:C8:224:LEU:HD23	1.84	0.78
2:C10:60:ILE:HG22	3:E10:185:PHE:HE2	1.47	0.78
1:A11:187:ARG:CG	1:B11:184:GLN:OE1	2.32	0.78
1:A11:187:ARG:HD2	1:B11:184:GLN:OE1	1.84	0.78
2:D12:174:VAL:HG13	2:D12:190:TYR:HB3	1.63	0.78
2:D4:174:VAL:HG13	2:D4:190:TYR:HB3	1.63	0.78
1:A1:187:ARG:HD2	1:B1:184:GLN:OE1	1.84	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A9:187:ARG:HD2	1:B9:184:GLN:OE1	1.84	0.78
1:B12:98:VAL:HG22	2:D13:208:TRP:NE1	1.99	0.78
2:C3:60:ILE:HG22	3:E3:185:PHE:HE2	1.47	0.78
2:C6:194:ASN:OD1	2:C6:224:LEU:HD23	1.84	0.78
1:A2:187:ARG:HD2	1:B2:184:GLN:OE1	1.84	0.78
1:B8:98:VAL:HG22	2:D9:208:TRP:NE1	1.99	0.78
2:C9:60:ILE:HG22	3:E9:185:PHE:HE2	1.47	0.78
2:C9:194:ASN:OD1	2:C9:224:LEU:HD23	1.84	0.78
1:A7:187:ARG:CG	1:B7:184:GLN:OE1	2.32	0.77
1:A8:187:ARG:CG	1:B8:184:GLN:OE1	2.32	0.77
1:A12:187:ARG:HD2	1:B12:184:GLN:OE1	1.84	0.77
1:B3:98:VAL:HG22	2:D4:208:TRP:NE1	1.98	0.77
2:C2:194:ASN:OD1	2:C2:224:LEU:HD23	1.84	0.77
2:C5:194:ASN:OD1	2:C5:224:LEU:HD23	1.84	0.77
2:C12:194:ASN:OD1	2:C12:224:LEU:HD23	1.84	0.77
2:D5:174:VAL:HG13	2:D5:190:TYR:HB3	1.63	0.77
1:A10:187:ARG:CG	1:B10:184:GLN:OE1	2.32	0.77
1:B2:98:VAL:HG22	2:D3:208:TRP:NE1	1.99	0.77
2:C2:60:ILE:HG22	3:E2:185:PHE:HE2	1.47	0.77
2:C11:194:ASN:OD1	2:C11:224:LEU:HD23	1.84	0.77
1:A4:187:ARG:CG	1:B4:184:GLN:OE1	2.32	0.77
1:A5:187:ARG:CG	1:B5:184:GLN:OE1	2.32	0.77
1:B6:98:VAL:HG22	2:D7:208:TRP:NE1	1.98	0.77
2:C7:194:ASN:OD1	2:C7:224:LEU:HD23	1.84	0.77
1:A2:187:ARG:CG	1:B2:184:GLN:OE1	2.32	0.77
1:A3:187:ARG:CG	1:B3:184:GLN:OE1	2.32	0.77
1:A12:187:ARG:CG	1:B12:184:GLN:OE1	2.32	0.77
1:A1:187:ARG:CG	1:B1:184:GLN:OE1	2.32	0.77
1:A6:187:ARG:HD2	1:B6:184:GLN:OE1	1.84	0.77
1:A13:187:ARG:CG	1:B13:184:GLN:OE1	2.32	0.77
1:B11:98:VAL:HG22	2:D12:208:TRP:NE1	1.99	0.77
1:A6:187:ARG:CG	1:B6:184:GLN:OE1	2.32	0.77
1:A13:187:ARG:HD2	1:B13:184:GLN:OE1	1.84	0.77
1:A7:187:ARG:HD2	1:B7:184:GLN:OE1	1.84	0.77
1:A8:187:ARG:HD2	1:B8:184:GLN:OE1	1.84	0.77
2:C13:194:ASN:OD1	2:C13:224:LEU:HD23	1.84	0.77
2:C4:194:ASN:OD1	2:C4:224:LEU:HD23	1.84	0.77
2:C1:194:ASN:OD1	2:C1:224:LEU:HD23	1.84	0.77
1:A3:187:ARG:HD2	1:B3:184:GLN:OE1	1.84	0.76
1:A1:155:PRO:CD	1:B12:157:THR:CB	2.63	0.76
1:A13:155:PRO:CD	1:B11:157:THR:CB	2.63	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A2:155:PRO:CD	1:B13:157:THR:CB	2.63	0.76
1:A9:187:ARG:CG	1:B9:184:GLN:OE1	2.32	0.76
1:B7:98:VAL:HG22	2:D8:208:TRP:NE1	1.99	0.76
2:C10:194:ASN:OD1	2:C10:224:LEU:HD23	1.84	0.76
1:A7:152:CYS:SG	1:B5:150:VAL:HG13	2.26	0.76
1:A9:152:CYS:SG	1:B7:150:VAL:HG13	2.26	0.76
1:A1:152:CYS:SG	1:B12:150:VAL:HG13	2.26	0.76
1:A5:152:CYS:SG	1:B3:150:VAL:HG13	2.26	0.76
1:A7:155:PRO:CD	1:B5:157:THR:CB	2.63	0.76
1:A2:152:CYS:SG	1:B13:150:VAL:HG13	2.26	0.76
1:A3:155:PRO:CD	1:B1:157:THR:CB	2.63	0.76
1:A11:152:CYS:SG	1:B9:150:VAL:HG13	2.26	0.76
2:D8:168:LEU:HD21	2:D8:174:VAL:HG21	1.68	0.75
2:D9:168:LEU:HD21	2:D9:174:VAL:HG21	1.68	0.75
1:A4:152:CYS:SG	1:B2:150:VAL:HG13	2.26	0.75
2:D7:168:LEU:HD21	2:D7:174:VAL:HG21	1.68	0.75
1:A10:152:CYS:SG	1:B8:150:VAL:HG13	2.26	0.75
1:A13:152:CYS:SG	1:B11:150:VAL:HG13	2.26	0.75
1:B1:98:VAL:HG21	2:D2:208:TRP:CD1	2.12	0.75
2:D10:168:LEU:HD21	2:D10:174:VAL:HG21	1.68	0.75
1:B3:98:VAL:HG21	2:D4:208:TRP:CD1	2.12	0.75
2:D2:168:LEU:HD21	2:D2:174:VAL:HG21	1.68	0.75
1:A6:152:CYS:SG	1:B4:150:VAL:HG13	2.26	0.75
1:A12:152:CYS:SG	1:B10:150:VAL:HG13	2.26	0.75
1:A3:152:CYS:SG	1:B1:150:VAL:HG13	2.26	0.75
1:A8:155:PRO:CD	1:B6:157:THR:CB	2.63	0.75
2:D1:168:LEU:HD21	2:D1:174:VAL:HG21	1.68	0.75
2:D3:168:LEU:HD21	2:D3:174:VAL:HG21	1.68	0.75
2:D6:168:LEU:HD21	2:D6:174:VAL:HG21	1.68	0.75
2:D11:168:LEU:HD21	2:D11:174:VAL:HG21	1.68	0.75
1:A4:155:PRO:CD	1:B2:157:THR:CB	2.63	0.74
2:D9:40:LEU:HD13	2:D9:114:TYR:CE2	2.23	0.74
2:D10:40:LEU:HD13	2:D10:114:TYR:CE2	2.23	0.74
2:D11:40:LEU:HD13	2:D11:114:TYR:CE2	2.23	0.74
1:A8:152:CYS:SG	1:B6:150:VAL:HG13	2.26	0.74
1:B2:98:VAL:HG13	2:D3:208:TRP:CD1	2.23	0.74
1:B12:98:VAL:HG13	2:D13:208:TRP:CD1	2.23	0.74
2:D8:40:LEU:HD13	2:D8:114:TYR:CE2	2.23	0.74
2:D13:168:LEU:HD21	2:D13:174:VAL:HG21	1.68	0.74
1:B6:98:VAL:HG21	2:D7:208:TRP:CD1	2.12	0.74
2:D4:168:LEU:HD21	2:D4:174:VAL:HG21	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D12:40:LEU:HD13	2:D12:114:TYR:CE2	2.23	0.74
2:C10:30:ILE:HD11	2:C10:116:LEU:HD13	1.70	0.74
2:D7:40:LEU:HD13	2:D7:114:TYR:CE2	2.23	0.74
1:B10:98:VAL:HG13	2:D11:208:TRP:CD1	2.23	0.74
1:B13:98:VAL:HG21	2:D1:208:TRP:CD1	2.12	0.74
2:C6:30:ILE:HD11	2:C6:116:LEU:HD13	1.70	0.74
2:D2:168:LEU:CD2	2:D2:174:VAL:CG2	2.66	0.74
1:A11:155:PRO:CD	1:B9:157:THR:CB	2.63	0.73
1:B7:98:VAL:HG13	2:D8:208:TRP:CD1	2.23	0.73
1:B13:98:VAL:HG13	2:D1:208:TRP:CD1	2.23	0.73
2:C3:30:ILE:HD11	2:C3:116:LEU:HD13	1.70	0.73
2:D1:37:GLN:HE22	2:D1:103:VAL:HG23	1.54	0.73
2:D12:168:LEU:HD21	2:D12:174:VAL:HG21	1.68	0.73
1:B3:98:VAL:HG13	2:D4:208:TRP:CD1	2.23	0.73
2:D2:37:GLN:HE22	2:D2:103:VAL:HG23	1.53	0.73
2:D3:168:LEU:CD2	2:D3:174:VAL:CG2	2.66	0.73
2:D13:40:LEU:HD13	2:D13:114:TYR:CE2	2.23	0.73
1:B6:98:VAL:HG13	2:D7:208:TRP:CD1	2.23	0.73
2:D9:37:GLN:HE22	2:D9:103:VAL:HG23	1.54	0.73
2:D9:168:LEU:CD2	2:D9:174:VAL:CG2	2.66	0.73
1:A6:155:PRO:CD	1:B4:157:THR:CB	2.63	0.73
1:A9:155:PRO:CD	1:B7:157:THR:CB	2.63	0.73
1:B5:98:VAL:HG13	2:D6:208:TRP:CD1	2.23	0.73
2:C13:30:ILE:HD11	2:C13:116:LEU:HD13	1.70	0.73
2:D6:40:LEU:HD13	2:D6:114:TYR:CE2	2.23	0.73
2:D10:168:LEU:CD2	2:D10:174:VAL:CG2	2.66	0.73
2:D13:37:GLN:HE22	2:D13:103:VAL:HG23	1.53	0.73
1:B1:98:VAL:HG13	2:D2:208:TRP:CD1	2.23	0.73
1:B4:98:VAL:HG13	2:D5:208:TRP:CD1	2.23	0.73
2:C5:30:ILE:HD11	2:C5:116:LEU:HD13	1.70	0.73
2:C7:30:ILE:HD11	2:C7:116:LEU:HD13	1.70	0.73
2:C9:30:ILE:HD11	2:C9:116:LEU:HD13	1.70	0.73
2:D5:168:LEU:HD21	2:D5:174:VAL:HG21	1.68	0.73
2:D11:37:GLN:HE22	2:D11:103:VAL:HG23	1.53	0.73
2:D11:168:LEU:CD2	2:D11:174:VAL:CG2	2.66	0.73
2:D12:37:GLN:HE22	2:D12:103:VAL:HG23	1.53	0.73
1:B9:170:VAL:HG11	2:D9:144:ASN:ND2	2.04	0.73
2:C11:30:ILE:HD11	2:C11:116:LEU:HD13	1.70	0.73
2:D4:168:LEU:CD2	2:D4:174:VAL:CG2	2.66	0.73
2:D6:37:GLN:HE22	2:D6:103:VAL:HG23	1.54	0.73
2:D8:168:LEU:CD2	2:D8:174:VAL:CG2	2.66	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B11:98:VAL:HG13	2:D12:208:TRP:CD1	2.23	0.73
2:D3:40:LEU:HD13	2:D3:114:TYR:CE2	2.23	0.73
2:D8:37:GLN:HE22	2:D8:103:VAL:HG23	1.54	0.73
1:B6:170:VAL:HG11	2:D6:144:ASN:ND2	2.04	0.73
1:B7:170:VAL:HG11	2:D7:144:ASN:ND2	2.04	0.73
1:B10:170:VAL:HG11	2:D10:144:ASN:ND2	2.04	0.73
2:C2:30:ILE:HD11	2:C2:116:LEU:HD13	1.70	0.73
2:D3:37:GLN:HE22	2:D3:103:VAL:HG23	1.54	0.73
1:B5:170:VAL:HG11	2:D5:144:ASN:ND2	2.04	0.73
1:B11:170:VAL:HG11	2:D11:144:ASN:ND2	2.04	0.73
2:D1:40:LEU:HD13	2:D1:114:TYR:CE2	2.23	0.73
2:D5:40:LEU:HD13	2:D5:114:TYR:CE2	2.23	0.73
2:D4:40:LEU:HD13	2:D4:114:TYR:CE2	2.22	0.72
2:D7:168:LEU:CD2	2:D7:174:VAL:CG2	2.66	0.72
1:A5:155:PRO:CD	1:B3:157:THR:CB	2.63	0.72
1:B9:98:VAL:HG13	2:D10:208:TRP:CD1	2.23	0.72
2:C12:30:ILE:HD11	2:C12:116:LEU:HD13	1.70	0.72
2:D12:168:LEU:CD2	2:D12:174:VAL:CG2	2.66	0.72
1:B8:98:VAL:HG13	2:D9:208:TRP:CD1	2.23	0.72
2:C4:30:ILE:HD11	2:C4:116:LEU:HD13	1.70	0.72
1:B12:98:VAL:HG21	2:D13:208:TRP:CD1	2.12	0.72
2:D2:40:LEU:HD13	2:D2:114:TYR:CE2	2.23	0.72
2:C1:30:ILE:HD11	2:C1:116:LEU:HD13	1.70	0.72
1:B2:170:VAL:HG11	2:D2:144:ASN:ND2	2.04	0.72
2:D4:37:GLN:HE22	2:D4:103:VAL:HG23	1.54	0.72
1:B12:170:VAL:HG11	2:D12:144:ASN:ND2	2.04	0.72
2:D5:168:LEU:CD2	2:D5:174:VAL:CG2	2.66	0.72
1:A10:155:PRO:CD	1:B8:157:THR:CB	2.63	0.72
2:C8:30:ILE:HD11	2:C8:116:LEU:HD13	1.70	0.72
2:D7:37:GLN:HE22	2:D7:103:VAL:HG23	1.54	0.72
1:B4:170:VAL:HG11	2:D4:144:ASN:ND2	2.04	0.71
2:D6:168:LEU:CD2	2:D6:174:VAL:CG2	2.66	0.71
2:D10:37:GLN:HE22	2:D10:103:VAL:HG23	1.54	0.71
1:B8:170:VAL:HG11	2:D8:144:ASN:ND2	2.04	0.71
1:B13:170:VAL:HG11	2:D13:144:ASN:ND2	2.04	0.71
2:D13:168:LEU:CD2	2:D13:174:VAL:CG2	2.66	0.71
1:B3:170:VAL:HG11	2:D3:144:ASN:ND2	2.04	0.71
2:D5:37:GLN:HE22	2:D5:103:VAL:HG23	1.54	0.71
1:B1:170:VAL:HG11	2:D1:144:ASN:ND2	2.04	0.71
1:A5:188:VAL:CG1	2:C5:141:ILE:HD11	2.21	0.71
2:D12:174:VAL:CG1	2:D12:190:TYR:HB3	2.21	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D13:174:VAL:CG1	2:D13:190:TYR:HB3	2.21	0.71
1:A4:188:VAL:CG1	2:C4:141:ILE:HD11	2.21	0.71
1:A6:188:VAL:CG1	2:C6:141:ILE:HD11	2.21	0.71
1:B11:98:VAL:HG21	2:D12:208:TRP:CD1	2.12	0.71
2:D1:174:VAL:CG1	2:D1:190:TYR:HB3	2.21	0.71
2:D11:174:VAL:CG1	2:D11:190:TYR:HB3	2.21	0.71
2:D2:174:VAL:CG1	2:D2:190:TYR:HB3	2.21	0.71
2:D3:174:VAL:CG1	2:D3:190:TYR:HB3	2.21	0.71
1:A7:188:VAL:CG1	2:C7:141:ILE:HD11	2.21	0.71
1:A3:188:VAL:CG1	2:C3:141:ILE:HD11	2.21	0.70
2:D7:67:LEU:HD23	2:D7:82:SER:HB3	1.73	0.70
2:D10:174:VAL:CG1	2:D10:190:TYR:HB3	2.21	0.70
2:D4:174:VAL:CG1	2:D4:190:TYR:HB3	2.21	0.70
2:D1:168:LEU:CD2	2:D1:174:VAL:CG2	2.66	0.70
2:D8:67:LEU:HD23	2:D8:82:SER:HB3	1.73	0.70
1:A8:188:VAL:CG1	2:C8:141:ILE:HD11	2.21	0.70
1:A10:188:VAL:CG1	2:C10:141:ILE:HD11	2.21	0.70
1:A13:188:VAL:CG1	2:C13:141:ILE:HD11	2.21	0.70
1:B2:98:VAL:HG21	2:D3:208:TRP:CD1	2.12	0.70
2:D9:174:VAL:CG1	2:D9:190:TYR:HB3	2.21	0.70
1:A2:188:VAL:CG1	2:C2:141:ILE:HD11	2.21	0.70
2:D5:174:VAL:CG1	2:D5:190:TYR:HB3	2.21	0.70
2:D11:67:LEU:HD23	2:D11:82:SER:HB3	1.73	0.70
2:C1:35:GLY:HA3	2:D1:27:PRO:HD3	1.74	0.70
1:A11:188:VAL:CG1	2:C11:141:ILE:HD11	2.21	0.70
1:A12:155:PRO:CD	1:B10:157:THR:CB	2.63	0.70
1:A1:188:VAL:CG1	2:C1:141:ILE:HD11	2.21	0.70
1:A9:188:VAL:CG1	2:C9:141:ILE:HD11	2.21	0.70
1:B13:171:TRP:HB2	2:D13:204:GLU:OE1	1.92	0.70
2:C3:35:GLY:HA3	2:D3:27:PRO:HD3	1.74	0.70
2:C12:35:GLY:HA3	2:D12:27:PRO:HD3	1.74	0.70
2:D8:174:VAL:CG1	2:D8:190:TYR:HB3	2.21	0.70
1:B9:171:TRP:HB2	2:D9:204:GLU:OE1	1.92	0.70
2:C2:35:GLY:HA3	2:D2:27:PRO:HD3	1.74	0.70
2:C13:35:GLY:HA3	2:D13:27:PRO:HD3	1.74	0.70
1:B2:171:TRP:HB2	2:D2:204:GLU:OE1	1.92	0.70
1:B7:171:TRP:HB2	2:D7:204:GLU:OE1	1.92	0.70
2:C11:35:GLY:HA3	2:D11:27:PRO:HD3	1.74	0.70
1:B3:171:TRP:HB2	2:D3:204:GLU:OE1	1.92	0.69
1:B11:171:TRP:HB2	2:D11:204:GLU:OE1	1.92	0.69
1:B5:98:VAL:HG21	2:D6:208:TRP:CD1	2.12	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B6:171:TRP:HB2	2:D6:204:GLU:OE1	1.92	0.69
2:D10:67:LEU:HD23	2:D10:82:SER:HB3	1.73	0.69
2:D11:168:LEU:HD21	2:D11:174:VAL:HG23	1.73	0.69
1:A12:188:VAL:CG1	2:C12:141:ILE:HD11	2.21	0.69
1:B1:188:VAL:HG13	2:D1:141:ILE:HD11	1.75	0.69
2:D4:67:LEU:HD23	2:D4:82:SER:HB3	1.73	0.69
2:D6:67:LEU:HD23	2:D6:82:SER:HB3	1.73	0.69
2:D6:174:VAL:CG1	2:D6:190:TYR:HB3	2.21	0.69
2:D7:174:VAL:CG1	2:D7:190:TYR:HB3	2.21	0.69
1:B4:171:TRP:HB2	2:D4:204:GLU:OE1	1.92	0.69
1:B8:171:TRP:HB2	2:D8:204:GLU:OE1	1.92	0.69
2:D12:67:LEU:HD23	2:D12:82:SER:HB3	1.73	0.69
2:C4:35:GLY:HA3	2:D4:27:PRO:HD3	1.74	0.69
2:D9:67:LEU:HD23	2:D9:82:SER:HB3	1.73	0.69
1:B10:188:VAL:HG13	2:D10:141:ILE:HD11	1.75	0.69
2:C5:35:GLY:HA3	2:D5:27:PRO:HD3	1.74	0.69
1:B13:188:VAL:HG13	2:D13:141:ILE:HD11	1.75	0.69
2:D5:67:LEU:HD23	2:D5:82:SER:HB3	1.73	0.69
1:B5:171:TRP:HB2	2:D5:204:GLU:OE1	1.92	0.69
1:B9:188:VAL:HG13	2:D9:141:ILE:HD11	1.75	0.69
2:C6:74:ARG:NH1	2:D5:58:THR:CG2	2.56	0.69
2:C9:74:ARG:NH1	2:D8:58:THR:CG2	2.56	0.69
2:C10:35:GLY:HA3	2:D10:27:PRO:HD3	1.74	0.69
2:C12:74:ARG:NH1	2:D11:58:THR:CG2	2.56	0.69
2:C13:202:LEU:CD1	2:C13:217:PHE:CZ	2.76	0.69
2:D1:67:LEU:HD23	2:D1:82:SER:HB3	1.73	0.69
1:A2:167:ILE:HG22	1:B1:197:TRP:HH2	1.58	0.69
1:A4:167:ILE:HG22	1:B3:197:TRP:HH2	1.58	0.69
1:B1:171:TRP:CB	2:D1:204:GLU:OE1	2.41	0.69
2:C5:35:GLY:HA3	2:D5:27:PRO:CD	2.23	0.69
2:C6:35:GLY:HA3	2:D6:27:PRO:CD	2.23	0.69
1:B2:171:TRP:CB	2:D2:204:GLU:OE1	2.41	0.69
1:B10:171:TRP:CB	2:D10:204:GLU:OE1	2.41	0.69
1:B12:171:TRP:CB	2:D12:204:GLU:OE1	2.41	0.69
2:C4:74:ARG:NH1	2:D3:58:THR:CG2	2.56	0.69
2:C7:74:ARG:NH1	2:D6:58:THR:CG2	2.56	0.69
1:B1:171:TRP:HB2	2:D1:204:GLU:OE1	1.92	0.68
1:B5:188:VAL:HG13	2:D5:141:ILE:HD11	1.75	0.68
1:B13:171:TRP:CB	2:D13:204:GLU:OE1	2.41	0.68
2:C4:35:GLY:HA3	2:D4:27:PRO:CD	2.23	0.68
2:C9:35:GLY:HA3	2:D9:27:PRO:HD3	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C10:74:ARG:NH1	2:D9:58:THR:CG2	2.56	0.68
1:A7:167:ILE:HG22	1:B6:197:TRP:HH2	1.58	0.68
1:B3:171:TRP:CB	2:D3:204:GLU:OE1	2.41	0.68
1:A13:167:ILE:HG22	1:B12:197:TRP:HH2	1.58	0.68
1:B8:171:TRP:CB	2:D8:204:GLU:OE1	2.41	0.68
1:B10:171:TRP:HB2	2:D10:204:GLU:OE1	1.92	0.68
2:C6:35:GLY:HA3	2:D6:27:PRO:HD3	1.74	0.68
2:C9:35:GLY:HA3	2:D9:27:PRO:CD	2.23	0.68
2:D1:60:ILE:HG22	3:F1:185:PHE:HE2	1.59	0.68
1:B7:171:TRP:CB	2:D7:204:GLU:OE1	2.41	0.68
1:B9:171:TRP:CB	2:D9:204:GLU:OE1	2.41	0.68
2:C1:74:ARG:NH1	2:D13:58:THR:CG2	2.56	0.68
2:C8:74:ARG:NH1	2:D7:58:THR:CG2	2.56	0.68
2:C10:35:GLY:HA3	2:D10:27:PRO:CD	2.23	0.68
2:C11:74:ARG:NH1	2:D10:58:THR:CG2	2.56	0.68
2:D2:67:LEU:HD23	2:D2:82:SER:HB3	1.73	0.68
2:D10:168:LEU:HD21	2:D10:174:VAL:HG23	1.73	0.68
2:D11:60:ILE:HG22	3:F11:185:PHE:HE2	1.59	0.68
1:B4:171:TRP:CB	2:D4:204:GLU:OE1	2.41	0.68
1:B6:171:TRP:CB	2:D6:204:GLU:OE1	2.41	0.68
2:C7:35:GLY:HA3	2:D7:27:PRO:HD3	1.74	0.68
1:A6:167:ILE:HG22	1:B5:197:TRP:HH2	1.58	0.68
1:A12:167:ILE:HG22	1:B11:197:TRP:HH2	1.58	0.68
1:B5:171:TRP:CB	2:D5:204:GLU:OE1	2.41	0.68
1:B6:188:VAL:HG13	2:D6:141:ILE:HD11	1.75	0.68
1:B12:171:TRP:HB2	2:D12:204:GLU:OE1	1.92	0.68
1:A5:167:ILE:HG22	1:B4:197:TRP:HH2	1.58	0.68
1:A10:167:ILE:HG22	1:B9:197:TRP:HH2	1.58	0.68
1:B4:188:VAL:HG13	2:D4:141:ILE:HD11	1.75	0.68
2:C2:74:ARG:NH1	2:D1:58:THR:CG2	2.56	0.68
2:D3:67:LEU:HD23	2:D3:82:SER:HB3	1.73	0.68
2:D6:60:ILE:HG22	3:F6:185:PHE:HE2	1.59	0.68
2:D8:60:ILE:HG22	3:F8:185:PHE:HE2	1.59	0.68
2:D13:67:LEU:HD23	2:D13:82:SER:HB3	1.73	0.68
2:C3:74:ARG:NH1	2:D2:58:THR:CG2	2.56	0.68
2:C7:35:GLY:HA3	2:D7:27:PRO:CD	2.23	0.68
2:C8:35:GLY:HA3	2:D8:27:PRO:HD3	1.74	0.68
2:C13:74:ARG:NH1	2:D12:58:THR:CG2	2.56	0.68
1:A11:167:ILE:HG22	1:B10:197:TRP:HH2	1.58	0.68
1:B12:188:VAL:HG13	2:D12:141:ILE:HD11	1.75	0.68
2:C2:35:GLY:HA3	2:D2:27:PRO:CD	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C3:35:GLY:HA3	2:D3:27:PRO:CD	2.23	0.68
2:C1:35:GLY:HA3	2:D1:27:PRO:CD	2.23	0.68
2:C8:35:GLY:HA3	2:D8:27:PRO:CD	2.23	0.68
2:D3:60:ILE:HG22	3:F3:185:PHE:HE2	1.59	0.68
2:D9:60:ILE:HG22	3:F9:185:PHE:HE2	1.59	0.68
1:B11:171:TRP:CB	2:D11:204:GLU:OE1	2.41	0.67
2:C5:74:ARG:NH1	2:D4:58:THR:CG2	2.56	0.67
1:A3:167:ILE:HG22	1:B2:197:TRP:HH2	1.58	0.67
1:A9:167:ILE:HG22	1:B8:197:TRP:HH2	1.58	0.67
1:B8:188:VAL:HG13	2:D8:141:ILE:HD11	1.75	0.67
2:C11:35:GLY:HA3	2:D11:27:PRO:CD	2.23	0.67
2:D5:60:ILE:HG22	3:F5:185:PHE:HE2	1.59	0.67
2:D6:168:LEU:HD21	2:D6:174:VAL:HG23	1.73	0.67
1:A1:167:ILE:HG22	1:B13:197:TRP:HH2	1.58	0.67
2:C9:32:LEU:HD21	2:C9:38:PHE:HB2	1.77	0.67
2:C10:32:LEU:HD21	2:C10:38:PHE:HB2	1.77	0.67
2:D4:60:ILE:HG22	3:F4:185:PHE:HE2	1.59	0.67
2:C11:32:LEU:HD21	2:C11:38:PHE:HB2	1.77	0.67
2:C13:32:LEU:HD21	2:C13:38:PHE:HB2	1.77	0.67
2:D12:60:ILE:HG22	3:F12:185:PHE:HE2	1.59	0.67
2:C1:32:LEU:HD21	2:C1:38:PHE:HB2	1.77	0.67
2:C1:35:GLY:C	2:D1:27:PRO:HD3	2.15	0.67
2:C10:35:GLY:C	2:D10:27:PRO:HD3	2.15	0.67
2:C13:35:GLY:HA3	2:D13:27:PRO:CD	2.23	0.67
2:C9:35:GLY:C	2:D9:27:PRO:HD3	2.15	0.67
2:D13:60:ILE:HG22	3:F13:185:PHE:HE2	1.59	0.67
2:C7:32:LEU:HD21	2:C7:38:PHE:HB2	1.77	0.67
2:C8:32:LEU:HD21	2:C8:38:PHE:HB2	1.77	0.67
2:C12:32:LEU:HD21	2:C12:38:PHE:HB2	1.77	0.67
2:C13:35:GLY:C	2:D13:27:PRO:HD3	2.15	0.67
1:B7:188:VAL:HG13	2:D7:141:ILE:HD11	1.75	0.67
2:C2:35:GLY:C	2:D2:27:PRO:HD3	2.15	0.67
2:C4:35:GLY:C	2:D4:27:PRO:HD3	2.15	0.67
2:D2:60:ILE:HG22	3:F2:185:PHE:HE2	1.59	0.67
2:C7:35:GLY:C	2:D7:27:PRO:HD3	2.15	0.67
2:C12:35:GLY:C	2:D12:27:PRO:HD3	2.15	0.67
1:B3:188:VAL:HG13	2:D3:141:ILE:HD11	1.75	0.66
2:C2:32:LEU:HD21	2:C2:38:PHE:HB2	1.77	0.66
2:C3:35:GLY:C	2:D3:27:PRO:HD3	2.15	0.66
2:C11:35:GLY:C	2:D11:27:PRO:HD3	2.15	0.66
2:D5:168:LEU:HD21	2:D5:174:VAL:HG23	1.73	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A8:167:ILE:HG22	1:B7:197:TRP:HH2	1.58	0.66
2:C3:32:LEU:HD21	2:C3:38:PHE:HB2	1.77	0.66
2:C12:35:GLY:HA3	2:D12:27:PRO:CD	2.23	0.66
1:A11:155:PRO:HG2	1:B9:157:THR:CG2	2.25	0.66
2:C5:32:LEU:HD21	2:C5:38:PHE:HB2	1.77	0.66
2:C6:35:GLY:C	2:D6:27:PRO:HD3	2.15	0.66
2:D10:60:ILE:HG22	3:F10:185:PHE:HE2	1.59	0.66
1:A10:155:PRO:HG2	1:B8:157:THR:CG2	2.25	0.66
2:D7:60:ILE:HG22	3:F7:185:PHE:HE2	1.59	0.66
1:A6:187:ARG:CD	1:B6:184:GLN:OE1	2.44	0.66
1:A7:187:ARG:CD	1:B7:184:GLN:OE1	2.44	0.66
2:C6:32:LEU:HD21	2:C6:38:PHE:HB2	1.77	0.66
1:A8:187:ARG:CD	1:B8:184:GLN:OE1	2.44	0.66
1:A3:155:PRO:HG2	1:B1:157:THR:CG2	2.25	0.66
1:A4:155:PRO:HG2	1:B2:157:THR:CG2	2.25	0.66
1:A9:187:ARG:CD	1:B9:184:GLN:OE1	2.44	0.66
2:C5:35:GLY:C	2:D5:27:PRO:HD3	2.15	0.66
2:D10:168:LEU:HD22	2:D10:174:VAL:HG23	1.77	0.66
1:A2:155:PRO:HG2	1:B13:157:THR:CG2	2.25	0.66
1:A5:187:ARG:CD	1:B5:184:GLN:OE1	2.44	0.66
1:A12:155:PRO:HG2	1:B10:157:THR:CG2	2.25	0.66
2:C4:32:LEU:HD21	2:C4:38:PHE:HB2	1.77	0.66
2:D9:168:LEU:HD22	2:D9:174:VAL:HG23	1.77	0.66
1:A9:155:PRO:HG2	1:B7:157:THR:CG2	2.25	0.66
1:B11:188:VAL:HG13	2:D11:141:ILE:HD11	1.75	0.66
2:D4:168:LEU:HD21	2:D4:174:VAL:HG23	1.73	0.66
1:A5:155:PRO:HG2	1:B3:157:THR:CG2	2.25	0.65
1:A6:155:PRO:HG2	1:B4:157:THR:CG2	2.25	0.65
2:D1:168:LEU:HD22	2:D1:174:VAL:HG23	1.77	0.65
1:A4:187:ARG:CD	1:B4:184:GLN:OE1	2.44	0.65
1:A10:187:ARG:CD	1:B10:184:GLN:OE1	2.44	0.65
2:D11:168:LEU:HD22	2:D11:174:VAL:HG23	1.77	0.65
2:D13:168:LEU:HD22	2:D13:174:VAL:HG23	1.77	0.65
2:C8:35:GLY:C	2:D8:27:PRO:HD3	2.15	0.65
2:D4:168:LEU:HD22	2:D4:174:VAL:HG23	1.77	0.65
1:A8:155:PRO:HG2	1:B6:157:THR:CG2	2.25	0.65
2:D3:168:LEU:HD21	2:D3:174:VAL:HG23	1.73	0.65
1:A1:187:ARG:CD	1:B1:184:GLN:OE1	2.44	0.65
1:A13:187:ARG:CD	1:B13:184:GLN:OE1	2.44	0.65
1:A7:155:PRO:HG2	1:B5:157:THR:CG2	2.25	0.65
1:A13:155:PRO:HG2	1:B11:157:THR:CG2	2.25	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D1:43:SER:N	2:D1:48:ASN:HD21	1.93	0.65
1:A1:155:PRO:HG2	1:B12:157:THR:CG2	2.25	0.65
1:A11:187:ARG:CD	1:B11:184:GLN:OE1	2.44	0.65
2:D2:168:LEU:HD22	2:D2:174:VAL:HG23	1.77	0.65
2:D5:168:LEU:HD22	2:D5:174:VAL:HG23	1.77	0.65
2:D6:168:LEU:HD22	2:D6:174:VAL:HG23	1.77	0.65
1:A3:187:ARG:CD	1:B3:184:GLN:OE1	2.44	0.65
1:A6:187:ARG:HG3	1:B6:184:GLN:OE1	1.97	0.65
1:A9:187:ARG:HG3	1:B9:184:GLN:OE1	1.97	0.65
1:A12:187:ARG:HG3	1:B12:184:GLN:OE1	1.97	0.65
2:D7:168:LEU:HD22	2:D7:174:VAL:HG23	1.77	0.65
1:A10:187:ARG:HG3	1:B10:184:GLN:OE1	1.97	0.64
1:B10:98:VAL:CG1	2:D11:208:TRP:CG	2.81	0.64
2:D5:43:SER:N	2:D5:48:ASN:HD21	1.93	0.64
2:D8:168:LEU:HD22	2:D8:174:VAL:HG23	1.77	0.64
1:B12:170:VAL:HG11	2:D12:144:ASN:HD22	1.63	0.64
2:C13:35:GLY:CA	2:D13:27:PRO:HD3	2.27	0.64
2:D2:168:LEU:HD21	2:D2:174:VAL:HG23	1.73	0.64
2:D3:168:LEU:HD22	2:D3:174:VAL:HG23	1.77	0.64
1:B6:98:VAL:CG1	2:D7:208:TRP:CG	2.81	0.64
1:B7:98:VAL:CG1	2:D8:208:TRP:CG	2.81	0.64
1:B9:98:VAL:CG1	2:D10:208:TRP:CG	2.81	0.64
1:B11:98:VAL:CG1	2:D12:208:TRP:CG	2.81	0.64
1:B13:170:VAL:HG11	2:D13:144:ASN:HD22	1.63	0.64
2:C8:35:GLY:CA	2:D8:27:PRO:HD3	2.27	0.64
2:C12:35:GLY:CA	2:D12:27:PRO:HD3	2.27	0.64
1:B11:170:VAL:HG11	2:D11:144:ASN:HD22	1.63	0.64
2:C1:42:ILE:HB	2:C1:104:ALA:HB1	1.80	0.64
2:D12:168:LEU:HD22	2:D12:174:VAL:HG23	1.77	0.64
1:A2:187:ARG:CD	1:B2:184:GLN:OE1	2.44	0.64
1:B8:98:VAL:CG1	2:D9:208:TRP:CG	2.81	0.64
1:B8:170:VAL:HG11	2:D8:144:ASN:HD22	1.63	0.64
1:B12:98:VAL:CG1	2:D13:208:TRP:CG	2.81	0.64
2:C3:42:ILE:HB	2:C3:104:ALA:HB1	1.80	0.64
2:C7:42:ILE:HB	2:C7:104:ALA:HB1	1.80	0.64
2:D3:37:GLN:NE2	2:D3:103:VAL:HG23	2.13	0.64
2:D5:37:GLN:NE2	2:D5:103:VAL:HG23	2.13	0.64
2:D10:43:SER:N	2:D10:48:ASN:HD21	1.93	0.64
1:A3:187:ARG:HG3	1:B3:184:GLN:OE1	1.97	0.64
1:A4:187:ARG:HG3	1:B4:184:GLN:OE1	1.97	0.64
1:A12:187:ARG:CD	1:B12:184:GLN:OE1	2.44	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B2:188:VAL:HG13	2:D2:141:ILE:HD11	1.75	0.64
1:B3:98:VAL:CG1	2:D4:208:TRP:CG	2.81	0.64
1:B10:170:VAL:HG11	2:D10:144:ASN:HD22	1.63	0.64
2:C4:35:GLY:CA	2:D4:27:PRO:HD3	2.27	0.64
2:C5:35:GLY:CA	2:D5:27:PRO:HD3	2.27	0.64
2:C5:42:ILE:HB	2:C5:104:ALA:HB1	1.80	0.64
2:C7:35:GLY:CA	2:D7:27:PRO:HD3	2.27	0.64
1:A5:187:ARG:HG3	1:B5:184:GLN:OE1	1.97	0.64
1:A7:187:ARG:HG3	1:B7:184:GLN:OE1	1.97	0.64
1:B4:98:VAL:CG1	2:D5:208:TRP:CG	2.81	0.64
2:C11:35:GLY:CA	2:D11:27:PRO:HD3	2.27	0.64
2:D2:37:GLN:NE2	2:D2:103:VAL:HG23	2.13	0.64
1:A1:187:ARG:HG3	1:B1:184:GLN:OE1	1.97	0.64
1:B1:170:VAL:HG11	2:D1:144:ASN:HD22	1.63	0.64
1:B2:98:VAL:CG1	2:D3:208:TRP:CG	2.81	0.64
1:B7:170:VAL:HG11	2:D7:144:ASN:HD22	1.63	0.64
1:B9:170:VAL:HG11	2:D9:144:ASN:HD22	1.63	0.64
1:B13:98:VAL:CG1	2:D1:208:TRP:CG	2.81	0.64
2:C1:35:GLY:CA	2:D1:27:PRO:HD3	2.27	0.64
2:C8:42:ILE:HB	2:C8:104:ALA:HB1	1.80	0.64
2:C8:202:LEU:CD1	2:C8:217:PHE:CZ	2.76	0.64
2:C9:35:GLY:CA	2:D9:27:PRO:HD3	2.27	0.64
2:C12:42:ILE:HB	2:C12:104:ALA:HB1	1.80	0.64
2:C13:42:ILE:HB	2:C13:104:ALA:HB1	1.80	0.64
1:B1:98:VAL:CG1	2:D2:208:TRP:CG	2.81	0.64
1:B6:170:VAL:HG11	2:D6:144:ASN:HD22	1.63	0.64
2:C6:42:ILE:HB	2:C6:104:ALA:HB1	1.80	0.64
2:C7:202:LEU:CD1	2:C7:217:PHE:CZ	2.76	0.64
2:C9:42:ILE:HB	2:C9:104:ALA:HB1	1.80	0.64
2:D13:37:GLN:NE2	2:D13:103:VAL:HG23	2.13	0.64
1:B5:98:VAL:CG1	2:D6:208:TRP:CG	2.81	0.64
2:C2:42:ILE:HB	2:C2:104:ALA:HB1	1.80	0.64
2:C4:42:ILE:HB	2:C4:104:ALA:HB1	1.80	0.64
2:C9:202:LEU:CD1	2:C9:217:PHE:CZ	2.76	0.64
2:D6:37:GLN:NE2	2:D6:103:VAL:HG23	2.13	0.64
2:C10:42:ILE:HB	2:C10:104:ALA:HB1	1.80	0.63
2:D8:168:LEU:HD21	2:D8:174:VAL:HG23	1.73	0.63
2:C11:42:ILE:HB	2:C11:104:ALA:HB1	1.80	0.63
1:B5:170:VAL:HG11	2:D5:144:ASN:HD22	1.63	0.63
2:C3:35:GLY:CA	2:D3:27:PRO:HD3	2.27	0.63
2:C3:194:ASN:OD1	2:C3:224:LEU:CD2	2.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A8:187:ARG:HG3	1:B8:184:GLN:OE1	1.97	0.63
1:A11:187:ARG:HG3	1:B11:184:GLN:OE1	1.97	0.63
2:C6:35:GLY:CA	2:D6:27:PRO:HD3	2.27	0.63
2:C6:202:LEU:CD1	2:C6:217:PHE:CZ	2.76	0.63
2:D12:43:SER:N	2:D12:48:ASN:HD21	1.93	0.63
1:A2:187:ARG:HG3	1:B2:184:GLN:OE1	1.97	0.63
1:B8:98:VAL:HG21	2:D9:208:TRP:CD1	2.12	0.63
2:C2:194:ASN:OD1	2:C2:224:LEU:CD2	2.47	0.63
2:D8:37:GLN:NE2	2:D8:103:VAL:HG23	2.13	0.63
2:D12:37:GLN:NE2	2:D12:103:VAL:HG23	2.13	0.63
1:A13:187:ARG:HG3	1:B13:184:GLN:OE1	1.97	0.63
2:C1:194:ASN:OD1	2:C1:224:LEU:CD2	2.47	0.63
2:C4:194:ASN:OD1	2:C4:224:LEU:CD2	2.47	0.63
2:D1:37:GLN:NE2	2:D1:103:VAL:HG23	2.13	0.63
2:D13:43:SER:N	2:D13:48:ASN:HD21	1.93	0.63
1:B2:170:VAL:HG11	2:D2:144:ASN:HD22	1.63	0.63
2:C2:35:GLY:CA	2:D2:27:PRO:HD3	2.27	0.63
2:C9:194:ASN:OD1	2:C9:224:LEU:CD2	2.47	0.63
2:C10:35:GLY:CA	2:D10:27:PRO:HD3	2.27	0.63
2:C10:194:ASN:OD1	2:C10:224:LEU:CD2	2.47	0.63
2:C10:202:LEU:CD1	2:C10:217:PHE:CZ	2.76	0.63
2:C13:194:ASN:OD1	2:C13:224:LEU:CD2	2.47	0.63
2:D4:37:GLN:NE2	2:D4:103:VAL:HG23	2.13	0.63
2:D9:37:GLN:NE2	2:D9:103:VAL:HG23	2.13	0.63
2:C11:194:ASN:OD1	2:C11:224:LEU:CD2	2.47	0.63
2:C12:194:ASN:OD1	2:C12:224:LEU:CD2	2.47	0.63
2:D4:43:SER:N	2:D4:48:ASN:HD21	1.93	0.63
2:D10:37:GLN:NE2	2:D10:103:VAL:HG23	2.13	0.63
2:C8:194:ASN:OD1	2:C8:224:LEU:CD2	2.47	0.62
2:D7:43:SER:N	2:D7:48:ASN:HD21	1.93	0.62
2:C5:194:ASN:OD1	2:C5:224:LEU:CD2	2.47	0.62
2:C5:202:LEU:CD1	2:C5:217:PHE:CZ	2.76	0.62
2:D7:37:GLN:NE2	2:D7:103:VAL:HG23	2.13	0.62
2:D12:168:LEU:HD21	2:D12:174:VAL:HG23	1.73	0.62
1:B3:170:VAL:HG11	2:D3:144:ASN:HD22	1.63	0.62
2:D5:224:LEU:HD11	2:D5:230:MET:HG3	1.82	0.62
2:D3:224:LEU:HD11	2:D3:230:MET:HG3	1.82	0.62
2:D10:224:LEU:HD11	2:D10:230:MET:HG3	1.82	0.62
2:D11:224:LEU:HD11	2:D11:230:MET:HG3	1.82	0.62
2:D12:224:LEU:HD11	2:D12:230:MET:HG3	1.82	0.62
1:B4:170:VAL:HG11	2:D4:144:ASN:HD22	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C6:194:ASN:OD1	2:C6:224:LEU:CD2	2.47	0.62
2:C7:194:ASN:OD1	2:C7:224:LEU:CD2	2.47	0.62
2:D1:224:LEU:HD11	2:D1:230:MET:HG3	1.82	0.62
2:D2:224:LEU:HD11	2:D2:230:MET:HG3	1.82	0.62
2:D9:224:LEU:HD11	2:D9:230:MET:HG3	1.82	0.62
2:D11:37:GLN:NE2	2:D11:103:VAL:HG23	2.13	0.62
2:D4:224:LEU:HD11	2:D4:230:MET:HG3	1.82	0.62
1:A10:167:ILE:CG2	1:B9:197:TRP:CH2	2.83	0.62
2:C4:202:LEU:CD1	2:C4:217:PHE:CZ	2.76	0.62
2:D7:224:LEU:HD11	2:D7:230:MET:HG3	1.82	0.62
1:A7:167:ILE:CG2	1:B6:197:TRP:CH2	2.83	0.62
1:A8:167:ILE:CG2	1:B7:197:TRP:CH2	2.83	0.62
1:A9:167:ILE:CG2	1:B8:197:TRP:CH2	2.83	0.62
2:D13:224:LEU:HD11	2:D13:230:MET:HG3	1.82	0.62
2:D6:224:LEU:HD11	2:D6:230:MET:HG3	1.82	0.61
2:D8:224:LEU:HD11	2:D8:230:MET:HG3	1.82	0.61
1:A11:167:ILE:CG2	1:B10:197:TRP:CH2	2.83	0.61
2:C11:202:LEU:CD1	2:C11:217:PHE:CZ	2.76	0.61
1:A9:192:VAL:HG11	2:C9:148:LEU:CD2	2.31	0.61
1:A10:192:VAL:HG11	2:C10:148:LEU:CD2	2.31	0.61
1:A11:167:ILE:HG22	1:B10:197:TRP:CH2	2.36	0.61
1:A11:192:VAL:HG11	2:C11:148:LEU:CD2	2.31	0.61
1:B7:98:VAL:HG21	2:D8:208:TRP:CD1	2.12	0.61
1:A4:158:VAL:HG21	1:A4:200:PRO:HB3	1.83	0.61
1:A4:192:VAL:HG11	2:C4:148:LEU:CD2	2.31	0.61
1:A9:167:ILE:HG22	1:B8:197:TRP:CH2	2.36	0.61
2:C3:202:LEU:CD1	2:C3:217:PHE:CZ	2.76	0.61
1:A1:192:VAL:CG1	2:C1:148:LEU:CD2	2.79	0.61
1:A5:158:VAL:HG21	1:A5:200:PRO:HB3	1.83	0.61
1:A5:192:VAL:HG11	2:C5:148:LEU:CD2	2.31	0.61
1:A6:167:ILE:HG22	1:B5:197:TRP:CH2	2.36	0.61
1:A12:167:ILE:CG2	1:B11:197:TRP:CH2	2.83	0.61
1:A12:192:VAL:HG11	2:C12:148:LEU:CD2	2.31	0.61
1:A13:192:VAL:HG11	2:C13:148:LEU:CD2	2.31	0.61
1:A2:167:ILE:HG21	1:B1:197:TRP:CZ3	2.36	0.61
1:A2:167:ILE:CG2	1:B1:197:TRP:CH2	2.83	0.61
1:A2:192:VAL:CG1	2:C2:148:LEU:CD2	2.79	0.61
1:A5:167:ILE:CG2	1:B4:197:TRP:CH2	2.83	0.61
1:A6:167:ILE:CG2	1:B5:197:TRP:CH2	2.83	0.61
1:A8:167:ILE:HG22	1:B7:197:TRP:CH2	2.36	0.61
1:A8:192:VAL:HG11	2:C8:148:LEU:CD2	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A1:192:VAL:HG11	2:C1:148:LEU:CD2	2.31	0.61
1:A3:158:VAL:HG21	1:A3:200:PRO:HB3	1.83	0.61
1:A4:167:ILE:HG21	1:B3:197:TRP:CZ3	2.36	0.61
1:A8:167:ILE:HG21	1:B7:197:TRP:CZ3	2.36	0.61
1:A12:167:ILE:HG22	1:B11:197:TRP:CH2	2.36	0.61
1:A12:167:ILE:HG21	1:B11:197:TRP:CZ3	2.36	0.61
1:A13:167:ILE:CG2	1:B12:197:TRP:CH2	2.83	0.61
1:A13:192:VAL:CG1	2:C13:148:LEU:CD2	2.79	0.61
2:D9:43:SER:N	2:D9:48:ASN:HD21	1.93	0.61
1:A1:158:VAL:HG21	1:A1:200:PRO:HB3	1.83	0.61
1:A2:158:VAL:HG21	1:A2:200:PRO:HB3	1.83	0.61
1:A3:192:VAL:CG1	2:C3:148:LEU:CD2	2.79	0.61
1:A3:192:VAL:HG11	2:C3:148:LEU:CD2	2.31	0.61
1:A11:167:ILE:HG21	1:B10:197:TRP:CZ3	2.36	0.61
1:A1:167:ILE:CG2	1:B13:197:TRP:CH2	2.83	0.61
1:A5:167:ILE:HG21	1:B4:197:TRP:CZ3	2.36	0.61
1:A6:158:VAL:HG21	1:A6:200:PRO:HB3	1.83	0.61
1:A9:167:ILE:HG21	1:B8:197:TRP:CZ3	2.36	0.61
1:A12:192:VAL:CG1	2:C12:148:LEU:CD2	2.79	0.61
2:D2:43:SER:N	2:D2:48:ASN:HD21	1.93	0.61
1:A1:167:ILE:HG22	1:B13:197:TRP:CH2	2.36	0.60
1:A3:167:ILE:CG2	1:B2:197:TRP:CH2	2.83	0.60
1:A4:167:ILE:CG2	1:B3:197:TRP:CH2	2.83	0.60
1:A5:167:ILE:HG22	1:B4:197:TRP:CH2	2.36	0.60
1:A6:192:VAL:HG11	2:C6:148:LEU:CD2	2.31	0.60
1:A11:192:VAL:CG1	2:C11:148:LEU:CD2	2.79	0.60
1:A9:192:VAL:CG1	2:C9:148:LEU:CD2	2.79	0.60
1:A10:192:VAL:CG1	2:C10:148:LEU:CD2	2.79	0.60
1:A1:167:ILE:HG21	1:B13:197:TRP:CZ3	2.36	0.60
1:A2:167:ILE:HG22	1:B1:197:TRP:CH2	2.36	0.60
1:A4:192:VAL:CG1	2:C4:148:LEU:CD2	2.79	0.60
1:A7:192:VAL:HG11	2:C7:148:LEU:CD2	2.31	0.60
1:A7:158:VAL:HG21	1:A7:200:PRO:HB3	1.83	0.60
1:A7:167:ILE:HG22	1:B6:197:TRP:CH2	2.36	0.60
1:A8:192:VAL:CG1	2:C8:148:LEU:CD2	2.79	0.60
1:B2:95:THR:HG21	1:B2:197:TRP:HB2	1.83	0.60
1:A7:167:ILE:HG21	1:B6:197:TRP:CZ3	2.36	0.60
2:D3:43:SER:N	2:D3:48:ASN:HD21	1.93	0.60
1:A2:192:VAL:HG11	2:C2:148:LEU:CD2	2.31	0.60
1:A5:192:VAL:CG1	2:C5:148:LEU:CD2	2.79	0.60
1:A7:192:VAL:CG1	2:C7:148:LEU:CD2	2.79	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B13:95:THR:HG21	1:B13:197:TRP:HB2	1.83	0.60
1:A6:167:ILE:HG21	1:B5:197:TRP:CZ3	2.36	0.60
2:D6:43:SER:N	2:D6:48:ASN:HD21	1.93	0.60
1:A3:167:ILE:HG22	1:B2:197:TRP:CH2	2.36	0.60
1:A3:167:ILE:HG21	1:B2:197:TRP:CZ3	2.36	0.60
1:A6:192:VAL:CG1	2:C6:148:LEU:CD2	2.79	0.60
1:A8:158:VAL:HG21	1:A8:200:PRO:HB3	1.83	0.60
1:A10:167:ILE:HG22	1:B9:197:TRP:CH2	2.36	0.60
1:A13:158:VAL:HG21	1:A13:200:PRO:HB3	1.83	0.60
1:A13:167:ILE:HG21	1:B12:197:TRP:CZ3	2.36	0.60
1:B12:95:THR:HG21	1:B12:197:TRP:HB2	1.83	0.60
1:A13:167:ILE:HG22	1:B12:197:TRP:CH2	2.36	0.60
1:B7:95:THR:HG21	1:B7:197:TRP:HB2	1.83	0.60
1:A12:158:VAL:HG21	1:A12:200:PRO:HB3	1.83	0.59
2:C12:202:LEU:CD1	2:C12:217:PHE:CZ	2.76	0.59
1:A9:158:VAL:HG21	1:A9:200:PRO:HB3	1.83	0.59
1:A10:158:VAL:HG21	1:A10:200:PRO:HB3	1.83	0.59
1:B8:95:THR:HG21	1:B8:197:TRP:HB2	1.83	0.59
2:D8:43:SER:N	2:D8:48:ASN:HD21	1.93	0.59
1:A4:167:ILE:HG22	1:B3:197:TRP:CH2	2.36	0.59
1:B3:95:THR:HG21	1:B3:197:TRP:HB2	1.83	0.59
1:B6:95:THR:HG21	1:B6:197:TRP:HB2	1.83	0.59
1:A10:167:ILE:HG21	1:B9:197:TRP:CZ3	2.36	0.59
1:B1:95:THR:HG21	1:B1:197:TRP:HB2	1.83	0.59
2:C6:136:TYR:HE1	2:C6:213:ARG:HD3	1.68	0.59
1:A9:185:PRO:HG2	1:A10:156:GLY:O	2.03	0.59
1:A11:158:VAL:HG21	1:A11:200:PRO:HB3	1.83	0.59
1:B9:95:THR:HG21	1:B9:197:TRP:HB2	1.83	0.59
1:A5:185:PRO:HG2	1:A6:156:GLY:O	2.03	0.59
1:A7:185:PRO:HG2	1:A8:156:GLY:O	2.03	0.59
1:A12:185:PRO:HG2	1:A13:156:GLY:O	2.03	0.59
1:B4:95:THR:HG21	1:B4:197:TRP:HB2	1.83	0.59
2:C10:136:TYR:HE1	2:C10:213:ARG:HD3	1.68	0.59
1:A1:156:GLY:O	1:A13:185:PRO:HG2	2.03	0.59
1:B5:95:THR:HG21	1:B5:197:TRP:HB2	1.83	0.59
1:B10:95:THR:HG21	1:B10:197:TRP:HB2	1.83	0.59
2:C7:136:TYR:HE1	2:C7:213:ARG:HD3	1.68	0.59
2:C9:136:TYR:HE1	2:C9:213:ARG:HD3	1.68	0.59
1:A3:185:PRO:HG2	1:A4:156:GLY:O	2.03	0.58
1:A6:185:PRO:HG2	1:A7:156:GLY:O	2.03	0.58
1:A6:192:VAL:HG11	2:C6:148:LEU:HD23	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A11:185:PRO:HG2	1:A12:156:GLY:O	2.03	0.58
2:C1:136:TYR:HE1	2:C1:213:ARG:HD3	1.68	0.58
2:C3:136:TYR:HE1	2:C3:213:ARG:HD3	1.68	0.58
2:C5:136:TYR:HE1	2:C5:213:ARG:HD3	1.68	0.58
2:C13:136:TYR:HE1	2:C13:213:ARG:HD3	1.68	0.58
1:A2:192:VAL:HG11	2:C2:148:LEU:HD23	1.86	0.58
1:A4:185:PRO:HG2	1:A5:156:GLY:O	2.03	0.58
2:C11:136:TYR:HE1	2:C11:213:ARG:HD3	1.68	0.58
1:A1:185:PRO:HG2	1:A2:156:GLY:O	2.03	0.58
1:A10:155:PRO:HG2	1:B8:157:THR:HG22	1.86	0.58
2:C7:169:PRO:HD2	2:C7:172:PHE:CD2	2.39	0.58
1:A1:192:VAL:HG11	2:C1:148:LEU:HD23	1.85	0.58
2:C5:202:LEU:O	2:C5:202:LEU:HD12	2.04	0.58
2:C13:202:LEU:HD12	2:C13:202:LEU:O	2.04	0.58
1:A1:155:PRO:HG2	1:B12:157:THR:HG22	1.86	0.58
1:A8:185:PRO:HG2	1:A9:156:GLY:O	2.03	0.58
2:C1:169:PRO:HD2	2:C1:172:PHE:CD2	2.39	0.58
2:C5:169:PRO:HD2	2:C5:172:PHE:CD2	2.39	0.58
2:C9:202:LEU:HD12	2:C9:202:LEU:O	2.04	0.58
2:C11:169:PRO:HD2	2:C11:172:PHE:CD2	2.39	0.58
2:C12:136:TYR:HE1	2:C12:213:ARG:HD3	1.68	0.58
1:A4:155:PRO:HG2	1:B2:157:THR:HG22	1.86	0.58
1:A7:155:PRO:HG2	1:B5:157:THR:HG22	1.86	0.58
2:C2:202:LEU:HD12	2:C2:202:LEU:O	2.04	0.58
2:C4:169:PRO:HD2	2:C4:172:PHE:CD2	2.39	0.58
2:C6:202:LEU:HD12	2:C6:202:LEU:O	2.04	0.58
2:C8:169:PRO:HD2	2:C8:172:PHE:CD2	2.39	0.58
2:C11:202:LEU:HD12	2:C11:202:LEU:O	2.04	0.58
2:C12:169:PRO:HD2	2:C12:172:PHE:CD2	2.39	0.58
2:C13:169:PRO:HD2	2:C13:172:PHE:CD2	2.39	0.58
1:A12:155:PRO:HG2	1:B10:157:THR:HG22	1.86	0.58
1:B11:95:THR:HG21	1:B11:197:TRP:HB2	1.83	0.58
2:C2:136:TYR:HE1	2:C2:213:ARG:HD3	1.68	0.58
2:C13:224:LEU:HD11	2:C13:228:GLY:HA3	1.86	0.58
1:A2:155:PRO:HG2	1:B13:157:THR:HG22	1.86	0.58
1:A5:192:VAL:HG11	2:C5:148:LEU:HD23	1.86	0.58
1:A10:185:PRO:HG2	1:A11:156:GLY:O	2.03	0.58
2:C12:224:LEU:HD11	2:C12:228:GLY:HA3	1.85	0.58
1:A9:172:ILE:HD12	2:C9:140:LEU:CD1	2.30	0.58
2:C6:169:PRO:HD2	2:C6:172:PHE:CD2	2.39	0.58
1:A2:185:PRO:HG2	1:A3:156:GLY:O	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:155:PRO:HG2	1:B3:157:THR:HG22	1.86	0.57
1:A11:155:PRO:HG2	1:B9:157:THR:HG22	1.86	0.57
1:A13:155:PRO:HG2	1:B11:157:THR:HG22	1.86	0.57
2:C1:224:LEU:HD11	2:C1:228:GLY:HA3	1.86	0.57
2:C6:224:LEU:HD11	2:C6:228:GLY:HA3	1.85	0.57
2:C10:202:LEU:HD12	2:C10:202:LEU:O	2.04	0.57
1:B8:98:VAL:HG13	2:D9:208:TRP:CG	2.40	0.57
2:C2:72:LEU:HD22	3:E2:185:PHE:HB3	1.86	0.57
2:C4:202:LEU:HD12	2:C4:202:LEU:O	2.04	0.57
2:C11:224:LEU:HD11	2:C11:228:GLY:HA3	1.85	0.57
2:C12:202:LEU:HD12	2:C12:202:LEU:O	2.04	0.57
1:A2:172:ILE:HD12	2:C2:140:LEU:CD1	2.30	0.57
1:A9:155:PRO:HG2	1:B7:157:THR:HG22	1.86	0.57
1:B4:98:VAL:HG11	2:D5:208:TRP:CG	2.40	0.57
2:C2:169:PRO:HD2	2:C2:172:PHE:CD2	2.39	0.57
2:C3:169:PRO:HD2	2:C3:172:PHE:CD2	2.39	0.57
2:C5:224:LEU:HD11	2:C5:228:GLY:HA3	1.85	0.57
2:C7:224:LEU:HD11	2:C7:228:GLY:HA3	1.86	0.57
2:C8:202:LEU:O	2:C8:202:LEU:HD12	2.04	0.57
2:C10:169:PRO:HD2	2:C10:172:PHE:CD2	2.39	0.57
1:A1:172:ILE:HD12	2:C1:140:LEU:CD1	2.30	0.57
1:B5:98:VAL:HG11	2:D6:208:TRP:CG	2.40	0.57
1:B8:98:VAL:HG11	2:D9:208:TRP:CG	2.40	0.57
2:C2:224:LEU:HD11	2:C2:228:GLY:HA3	1.86	0.57
2:C3:72:LEU:HD22	3:E3:185:PHE:HB3	1.86	0.57
1:A3:172:ILE:HD12	2:C3:140:LEU:CD1	2.30	0.57
1:B1:98:VAL:HG11	2:D2:208:TRP:CG	2.40	0.57
1:B9:98:VAL:HG11	2:D10:208:TRP:CG	2.40	0.57
2:C1:202:LEU:HD12	2:C1:202:LEU:O	2.04	0.57
2:C4:224:LEU:HD11	2:C4:228:GLY:HA3	1.85	0.57
2:C7:72:LEU:HD22	3:E7:185:PHE:HB3	1.86	0.57
2:C8:72:LEU:HD22	3:E8:185:PHE:HB3	1.86	0.57
2:C9:72:LEU:HD22	3:E9:185:PHE:HB3	1.86	0.57
2:C10:72:LEU:HD22	3:E10:185:PHE:HB3	1.86	0.57
1:A8:155:PRO:HG2	1:B6:157:THR:HG22	1.86	0.57
1:B10:98:VAL:HG13	2:D11:208:TRP:CG	2.40	0.57
1:B11:98:VAL:HG13	2:D12:208:TRP:CG	2.40	0.57
2:C4:136:TYR:HE1	2:C4:213:ARG:HD3	1.68	0.57
2:C8:136:TYR:HE1	2:C8:213:ARG:HD3	1.68	0.57
2:C8:224:LEU:HD11	2:C8:228:GLY:HA3	1.85	0.57
2:C9:169:PRO:HD2	2:C9:172:PHE:CD2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C10:224:LEU:HD11	2:C10:228:GLY:HA3	1.86	0.57
1:A9:192:VAL:HG11	2:C9:148:LEU:HD23	1.85	0.57
1:B11:98:VAL:HG11	2:D12:208:TRP:CG	2.40	0.57
2:C3:202:LEU:HD12	2:C3:202:LEU:O	2.04	0.57
2:C7:202:LEU:HD12	2:C7:202:LEU:O	2.04	0.57
2:C9:64:GLY:HA3	3:E9:179:MET:O	2.05	0.57
1:B5:98:VAL:HG13	2:D6:208:TRP:CG	2.40	0.57
1:B12:98:VAL:HG11	2:D13:208:TRP:CG	2.40	0.57
1:B13:98:VAL:HG11	2:D1:208:TRP:CG	2.40	0.57
2:C11:72:LEU:HD22	3:E11:185:PHE:HB3	1.86	0.57
2:D11:43:SER:N	2:D11:48:ASN:HD21	1.93	0.57
1:B3:98:VAL:HG11	2:D4:208:TRP:CG	2.40	0.57
1:B7:98:VAL:HG13	2:D8:208:TRP:CG	2.40	0.57
2:C7:64:GLY:HA3	3:E7:179:MET:O	2.05	0.57
1:B2:98:VAL:HG11	2:D3:208:TRP:CG	2.40	0.57
1:B7:98:VAL:HG11	2:D8:208:TRP:CG	2.40	0.57
1:B9:98:VAL:HG13	2:D10:208:TRP:CG	2.40	0.57
2:C8:64:GLY:HA3	3:E8:179:MET:O	2.05	0.57
1:A4:172:ILE:HD12	2:C4:140:LEU:CD1	2.30	0.56
2:C1:64:GLY:HA3	3:E1:179:MET:O	2.05	0.56
2:C1:72:LEU:HD22	3:E1:185:PHE:HB3	1.86	0.56
2:C11:64:GLY:HA3	3:E11:179:MET:O	2.05	0.56
2:C12:64:GLY:HA3	3:E12:179:MET:O	2.05	0.56
2:C13:64:GLY:HA3	3:E13:179:MET:O	2.05	0.56
2:D12:159:VAL:CG1	2:D12:160:LYS:N	2.44	0.56
1:A6:155:PRO:HG2	1:B4:157:THR:HG22	1.86	0.56
1:A13:172:ILE:HD12	2:C13:140:LEU:CD1	2.30	0.56
2:C3:224:LEU:HD11	2:C3:228:GLY:HA3	1.86	0.56
2:C9:224:LEU:HD11	2:C9:228:GLY:HA3	1.85	0.56
1:A3:155:PRO:HG2	1:B1:157:THR:HG22	1.86	0.56
1:B1:98:VAL:HG13	2:D2:208:TRP:CG	2.40	0.56
1:B10:98:VAL:HG11	2:D11:208:TRP:CG	2.40	0.56
2:C5:72:LEU:HD22	3:E5:185:PHE:HB3	1.86	0.56
2:C6:72:LEU:HD22	3:E6:185:PHE:HB3	1.86	0.56
2:C12:72:LEU:HD22	3:E12:185:PHE:HB3	1.86	0.56
1:B4:98:VAL:HG13	2:D5:208:TRP:CG	2.40	0.56
1:B13:98:VAL:HG13	2:D1:208:TRP:CG	2.40	0.56
2:C5:64:GLY:HA3	3:E5:179:MET:O	2.05	0.56
1:B6:98:VAL:HG11	2:D7:208:TRP:CG	2.40	0.56
1:A2:167:ILE:O	2:C2:220:ASN:ND2	2.38	0.56
1:A5:172:ILE:HD12	2:C5:140:LEU:CD1	2.30	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A8:155:PRO:CD	1:B6:157:THR:CG2	2.84	0.56
1:A9:155:PRO:CD	1:B7:157:THR:CG2	2.84	0.56
2:C4:72:LEU:HD22	3:E4:185:PHE:HB3	1.86	0.56
2:C13:72:LEU:HD22	3:E13:185:PHE:HB3	1.86	0.56
1:A10:156:GLY:N	2:C9:205:GLN:OE1	2.39	0.56
2:C3:64:GLY:HA3	3:E3:179:MET:O	2.05	0.56
2:C6:64:GLY:HA3	3:E6:179:MET:O	2.05	0.56
2:C10:64:GLY:HA3	3:E10:179:MET:O	2.05	0.56
2:D1:30:ILE:HG13	2:D1:116:LEU:HD23	1.88	0.56
2:D12:30:ILE:HG13	2:D12:116:LEU:HD23	1.88	0.56
1:A12:156:GLY:N	2:C11:205:GLN:OE1	2.39	0.56
1:A13:167:ILE:O	2:C13:220:ASN:ND2	2.38	0.56
1:B3:98:VAL:HG13	2:D4:208:TRP:CG	2.40	0.56
2:D3:30:ILE:HG13	2:D3:116:LEU:HD23	1.88	0.56
1:A5:155:PRO:CD	1:B3:157:THR:CG2	2.84	0.56
1:A8:156:GLY:N	2:C7:205:GLN:OE1	2.39	0.56
1:A10:167:ILE:O	2:C10:220:ASN:ND2	2.38	0.56
2:D2:30:ILE:HG13	2:D2:116:LEU:HD23	1.88	0.56
2:D13:30:ILE:HG13	2:D13:116:LEU:HD23	1.88	0.56
1:A3:156:GLY:N	2:C2:205:GLN:OE1	2.39	0.55
2:C2:64:GLY:HA3	3:E2:179:MET:O	2.05	0.55
1:A4:155:PRO:CD	1:B2:157:THR:CG2	2.84	0.55
1:A4:156:GLY:N	2:C3:205:GLN:OE1	2.39	0.55
1:A7:155:PRO:CD	1:B5:157:THR:CG2	2.84	0.55
1:B6:98:VAL:HG13	2:D7:208:TRP:CG	2.40	0.55
1:A10:155:PRO:CD	1:B8:157:THR:CG2	2.84	0.55
1:A12:172:ILE:HD12	2:C12:140:LEU:CD1	2.30	0.55
2:D4:30:ILE:HG13	2:D4:116:LEU:HD23	1.88	0.55
1:A6:155:PRO:CD	1:B4:157:THR:CG2	2.84	0.55
1:A6:156:GLY:N	2:C5:205:GLN:OE1	2.39	0.55
1:A7:156:GLY:N	2:C6:205:GLN:OE1	2.39	0.55
1:B12:98:VAL:HG13	2:D13:208:TRP:CG	2.40	0.55
2:C1:202:LEU:CD1	2:C1:217:PHE:CZ	2.76	0.55
1:A1:156:GLY:N	2:C13:205:GLN:OE1	2.39	0.55
1:A10:172:ILE:HD12	2:C10:140:LEU:CD1	2.30	0.55
2:C4:64:GLY:HA3	3:E4:179:MET:O	2.05	0.55
2:D9:56:LYS:HA	2:D9:76:GLY:HA3	1.89	0.55
1:A2:155:PRO:CD	1:B13:157:THR:CG2	2.84	0.55
1:A6:172:ILE:HD12	2:C6:140:LEU:CD1	2.30	0.55
2:D10:30:ILE:HG13	2:D10:116:LEU:HD23	1.88	0.55
2:D11:30:ILE:HG13	2:D11:116:LEU:HD23	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A3:155:PRO:CD	1:B1:157:THR:CG2	2.84	0.55
1:B1:91:THR:CG2	2:D2:213:ARG:HH12	2.20	0.55
1:B8:91:THR:CG2	2:D9:213:ARG:HH12	2.20	0.55
1:B11:91:THR:CG2	2:D12:213:ARG:HH12	2.20	0.55
1:B12:91:THR:CG2	2:D13:213:ARG:HH12	2.20	0.55
1:B13:91:THR:CG2	2:D1:213:ARG:HH12	2.20	0.55
2:D5:30:ILE:HG13	2:D5:116:LEU:HD23	1.88	0.55
2:D7:56:LYS:HA	2:D7:76:GLY:HA3	1.89	0.55
2:D8:56:LYS:HA	2:D8:76:GLY:HA3	1.89	0.55
2:D9:168:LEU:HD21	2:D9:174:VAL:HG23	1.73	0.55
2:D10:56:LYS:HA	2:D10:76:GLY:HA3	1.89	0.55
1:A1:155:PRO:CD	1:B12:157:THR:CG2	2.84	0.55
1:A2:155:PRO:HD2	1:B13:157:THR:HG21	1.89	0.55
1:A9:156:GLY:N	2:C8:205:GLN:OE1	2.39	0.55
1:B7:91:THR:CG2	2:D8:213:ARG:HH12	2.20	0.55
1:A1:155:PRO:HD2	1:B12:157:THR:HG21	1.89	0.55
1:A13:156:GLY:N	2:C12:205:GLN:OE1	2.39	0.55
1:B10:91:THR:CG2	2:D11:213:ARG:HH12	2.20	0.55
2:D1:159:VAL:CG1	2:D1:160:LYS:N	2.44	0.55
2:D11:56:LYS:HA	2:D11:76:GLY:HA3	1.89	0.55
1:A9:167:ILE:HD12	1:B8:160:PRO:O	2.07	0.55
1:A11:192:VAL:HG11	2:C11:148:LEU:HD23	1.85	0.55
1:B2:91:THR:CG2	2:D3:213:ARG:HH12	2.20	0.55
1:A3:155:PRO:HD2	1:B1:157:THR:HG21	1.89	0.54
1:A5:156:GLY:N	2:C4:205:GLN:OE1	2.39	0.54
1:A7:172:ILE:HD12	2:C7:140:LEU:CD1	2.30	0.54
1:A12:167:ILE:HD12	1:B11:160:PRO:O	2.08	0.54
1:B2:98:VAL:HG13	2:D3:208:TRP:CG	2.40	0.54
1:B3:91:THR:CG2	2:D4:213:ARG:HH12	2.20	0.54
1:B9:91:THR:CG2	2:D10:213:ARG:HH12	2.20	0.54
2:D6:30:ILE:HG13	2:D6:116:LEU:HD23	1.88	0.54
1:A2:156:GLY:N	2:C1:205:GLN:OE1	2.39	0.54
1:A11:155:PRO:HD2	1:B9:157:THR:HG21	1.89	0.54
1:A12:155:PRO:CD	1:B10:157:THR:CG2	2.84	0.54
1:A12:155:PRO:HD2	1:B10:157:THR:HG21	1.89	0.54
2:D9:30:ILE:HG13	2:D9:116:LEU:HD23	1.88	0.54
2:D10:159:VAL:CG1	2:D10:160:LYS:N	2.44	0.54
1:A1:167:ILE:HD12	1:B13:160:PRO:O	2.07	0.54
1:A5:167:ILE:HD12	1:B4:160:PRO:O	2.07	0.54
1:A11:155:PRO:CD	1:B9:157:THR:CG2	2.84	0.54
1:A11:156:GLY:N	2:C10:205:GLN:OE1	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A12:167:ILE:O	2:C12:220:ASN:ND2	2.38	0.54
1:A13:155:PRO:CD	1:B11:157:THR:CG2	2.84	0.54
1:A13:155:PRO:HD2	1:B11:157:THR:HG21	1.89	0.54
1:B6:91:THR:CG2	2:D7:213:ARG:HH12	2.20	0.54
2:D6:56:LYS:HA	2:D6:76:GLY:HA3	1.89	0.54
1:A11:167:ILE:HD12	1:B10:160:PRO:O	2.07	0.54
2:D8:30:ILE:HG13	2:D8:116:LEU:HD23	1.88	0.54
1:A2:167:ILE:HD12	1:B1:160:PRO:O	2.08	0.54
1:A3:167:ILE:CG2	1:B2:197:TRP:HH2	2.21	0.54
1:A8:172:ILE:HD12	2:C8:140:LEU:CD1	2.30	0.54
1:A4:155:PRO:HD2	1:B2:157:THR:HG21	1.89	0.54
1:A10:155:PRO:HD2	1:B8:157:THR:HG21	1.89	0.54
2:D12:56:LYS:HA	2:D12:76:GLY:HA3	1.89	0.54
1:A2:167:ILE:CG2	1:B1:197:TRP:HH2	2.21	0.54
1:A5:155:PRO:HD2	1:B3:157:THR:HG21	1.89	0.54
1:A6:167:ILE:HD12	1:B5:160:PRO:O	2.08	0.54
2:D7:30:ILE:HG13	2:D7:116:LEU:HD23	1.88	0.54
1:A4:167:ILE:CG2	1:B3:197:TRP:HH2	2.21	0.54
1:B4:91:THR:CG2	2:D5:213:ARG:HH12	2.20	0.54
1:A3:167:ILE:HD12	1:B2:160:PRO:O	2.08	0.54
1:A6:155:PRO:HD2	1:B4:157:THR:HG21	1.89	0.54
1:A8:167:ILE:HD12	1:B7:160:PRO:O	2.08	0.54
1:B13:171:TRP:HB3	2:D13:204:GLU:OE1	2.08	0.54
2:D2:56:LYS:HA	2:D2:76:GLY:HA3	1.89	0.54
1:A10:167:ILE:HD12	1:B9:160:PRO:O	2.08	0.54
1:A11:172:ILE:HD12	2:C11:140:LEU:CD1	2.30	0.54
1:B5:91:THR:CG2	2:D6:213:ARG:HH12	2.20	0.54
1:B11:171:TRP:HB3	2:D11:204:GLU:OE1	2.08	0.54
2:D7:60:ILE:HG22	3:F7:185:PHE:CE2	2.43	0.54
1:A9:155:PRO:HD2	1:B7:157:THR:HG21	1.89	0.53
1:B10:171:TRP:HB3	2:D10:204:GLU:OE1	2.08	0.53
2:C8:74:ARG:HH11	2:D7:58:THR:HG21	1.73	0.53
2:D1:56:LYS:HA	2:D1:76:GLY:HA3	1.89	0.53
2:D5:56:LYS:HA	2:D5:76:GLY:HA3	1.89	0.53
1:A1:167:ILE:O	2:C1:220:ASN:ND2	2.38	0.53
1:A7:155:PRO:HD2	1:B5:157:THR:HG21	1.89	0.53
1:A8:155:PRO:HD2	1:B6:157:THR:HG21	1.89	0.53
1:A12:167:ILE:CG2	1:B11:197:TRP:HH2	2.21	0.53
1:A12:192:VAL:HG11	2:C12:148:LEU:HD23	1.86	0.53
2:C2:202:LEU:CD1	2:C2:217:PHE:CZ	2.76	0.53
2:D13:56:LYS:HA	2:D13:76:GLY:HA3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D3:56:LYS:HA	2:D3:76:GLY:HA3	1.89	0.53
2:D4:60:ILE:HG22	3:F4:185:PHE:CE2	2.43	0.53
2:D6:60:ILE:HG22	3:F6:185:PHE:CE2	2.43	0.53
1:A3:167:ILE:O	2:C3:220:ASN:ND2	2.38	0.53
1:A4:167:ILE:HD12	1:B3:160:PRO:O	2.07	0.53
1:A5:167:ILE:CG2	1:B4:197:TRP:HH2	2.21	0.53
1:B2:171:TRP:HB3	2:D2:204:GLU:OE1	2.08	0.53
2:D5:60:ILE:HG22	3:F5:185:PHE:CE2	2.43	0.53
1:A5:167:ILE:O	2:C5:220:ASN:ND2	2.38	0.53
1:A7:167:ILE:HD12	1:B6:160:PRO:O	2.07	0.53
1:B8:171:TRP:HB3	2:D8:204:GLU:OE1	2.08	0.53
1:A7:167:ILE:O	2:C7:220:ASN:ND2	2.38	0.53
1:B12:171:TRP:HB3	2:D12:204:GLU:OE1	2.08	0.53
1:A13:167:ILE:HD12	1:B12:160:PRO:O	2.08	0.53
1:B9:171:TRP:HB3	2:D9:204:GLU:OE1	2.08	0.53
2:D4:56:LYS:HA	2:D4:76:GLY:HA3	1.89	0.53
1:B1:170:VAL:CG1	2:D1:144:ASN:ND2	2.72	0.53
1:B2:170:VAL:CG1	2:D2:144:ASN:ND2	2.72	0.53
2:C6:32:LEU:HB3	2:C6:36:GLY:HA3	1.91	0.53
1:A9:167:ILE:O	2:C9:220:ASN:ND2	2.38	0.53
1:B1:171:TRP:HB3	2:D1:204:GLU:OE1	2.08	0.53
2:C3:64:GLY:N	3:E3:180:MET:HA	2.24	0.53
1:A8:192:VAL:HG11	2:C8:148:LEU:HD23	1.86	0.52
1:A13:167:ILE:CG2	1:B12:197:TRP:HH2	2.21	0.52
1:B4:170:VAL:CG1	2:D4:144:ASN:ND2	2.72	0.52
1:B12:170:VAL:CG1	2:D12:144:ASN:ND2	2.72	0.52
2:C5:32:LEU:HB3	2:C5:36:GLY:HA3	1.91	0.52
2:C13:64:GLY:N	3:E13:180:MET:HA	2.25	0.52
2:D5:30:ILE:HG13	2:D5:30:ILE:O	2.10	0.52
1:A5:201:ALA:O	2:C4:208:TRP:HZ3	1.92	0.52
1:A6:167:ILE:CG2	1:B5:197:TRP:HH2	2.21	0.52
1:B11:170:VAL:CG1	2:D11:144:ASN:ND2	2.72	0.52
2:D6:30:ILE:HG13	2:D6:30:ILE:O	2.10	0.52
1:A4:201:ALA:O	2:C3:208:TRP:HZ3	1.92	0.52
1:A7:192:VAL:HG11	2:C7:148:LEU:HD23	1.86	0.52
2:C1:32:LEU:HB3	2:C1:36:GLY:HA3	1.91	0.52
2:C2:32:LEU:HB3	2:C2:36:GLY:HA3	1.91	0.52
2:C7:32:LEU:HB3	2:C7:36:GLY:HA3	1.91	0.52
2:C7:74:ARG:HH11	2:D6:58:THR:HG21	1.73	0.52
2:D4:30:ILE:HG13	2:D4:30:ILE:O	2.10	0.52
1:A2:174:PRO:HG3	1:A2:185:PRO:HD3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A4:174:PRO:HG3	1:A4:185:PRO:HD3	1.92	0.52
1:A7:175:TRP:CE2	2:C7:136:TYR:CE2	2.98	0.52
1:B5:170:VAL:CG1	2:D5:144:ASN:ND2	2.72	0.52
1:B6:171:TRP:HB3	2:D6:204:GLU:OE1	2.08	0.52
2:C5:64:GLY:N	3:E5:180:MET:HA	2.25	0.52
2:C6:64:GLY:N	3:E6:180:MET:HA	2.25	0.52
2:C11:74:ARG:HH11	2:D10:58:THR:HG21	1.73	0.52
2:C12:74:ARG:HH11	2:D11:58:THR:HG21	1.73	0.52
2:D7:168:LEU:HD21	2:D7:174:VAL:HG23	1.73	0.52
1:A2:175:TRP:CE2	2:C2:136:TYR:CE2	2.98	0.52
1:A3:175:TRP:CE2	2:C3:136:TYR:CE2	2.98	0.52
1:A6:201:ALA:O	2:C5:208:TRP:HZ3	1.93	0.52
1:A8:175:TRP:CE2	2:C8:136:TYR:CE2	2.98	0.52
1:A11:201:ALA:O	2:C10:208:TRP:HZ3	1.93	0.52
2:C2:64:GLY:N	3:E2:180:MET:HA	2.25	0.52
1:A1:201:ALA:O	2:C13:208:TRP:HZ3	1.93	0.52
1:A3:201:ALA:O	2:C2:208:TRP:HZ3	1.92	0.52
2:C1:64:GLY:N	3:E1:180:MET:HA	2.25	0.52
2:D7:30:ILE:HG13	2:D7:30:ILE:O	2.10	0.52
1:B7:171:TRP:HB3	2:D7:204:GLU:OE1	2.08	0.52
2:C10:64:GLY:N	3:E10:180:MET:HA	2.25	0.52
2:C12:64:GLY:N	3:E12:180:MET:HA	2.24	0.52
1:A1:175:TRP:CE2	2:C1:136:TYR:CE2	2.98	0.52
1:A6:174:PRO:HG3	1:A6:185:PRO:HD3	1.92	0.52
1:A6:175:TRP:CE2	2:C6:136:TYR:CE2	2.98	0.52
1:A7:201:ALA:O	2:C6:208:TRP:HZ3	1.92	0.52
1:A12:201:ALA:O	2:C11:208:TRP:HZ3	1.93	0.52
1:A13:201:ALA:O	2:C12:208:TRP:HZ3	1.92	0.52
1:B4:171:TRP:HB3	2:D4:204:GLU:OE1	2.08	0.52
1:B9:170:VAL:CG1	2:D9:144:ASN:ND2	2.72	0.52
1:B13:170:VAL:CG1	2:D13:144:ASN:ND2	2.72	0.52
2:C3:32:LEU:HB3	2:C3:36:GLY:HA3	1.91	0.52
2:C13:32:LEU:HB3	2:C13:36:GLY:HA3	1.91	0.52
1:A9:175:TRP:CE2	2:C9:136:TYR:CE2	2.98	0.52
1:A13:174:PRO:HG3	1:A13:185:PRO:HD3	1.92	0.52
2:C4:32:LEU:HB3	2:C4:36:GLY:HA3	1.91	0.52
2:C9:64:GLY:N	3:E9:180:MET:HA	2.25	0.52
1:A4:175:TRP:CE2	2:C4:136:TYR:CE2	2.98	0.51
1:A9:201:ALA:O	2:C8:208:TRP:HZ3	1.92	0.51
1:B7:170:VAL:CG1	2:D7:144:ASN:ND2	2.72	0.51
2:C8:32:LEU:HB3	2:C8:36:GLY:HA3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C11:32:LEU:HB3	2:C11:36:GLY:HA3	1.91	0.51
2:C11:64:GLY:N	3:E11:180:MET:HA	2.25	0.51
1:B3:170:VAL:CG1	2:D3:144:ASN:ND2	2.72	0.51
1:B3:171:TRP:HB3	2:D3:204:GLU:OE1	2.08	0.51
1:B5:171:TRP:HB3	2:D5:204:GLU:OE1	2.08	0.51
2:C4:64:GLY:N	3:E4:180:MET:HA	2.25	0.51
2:C5:74:ARG:HH11	2:D4:58:THR:HG21	1.73	0.51
2:D2:60:ILE:HG22	3:F2:185:PHE:CE2	2.43	0.51
2:D3:30:ILE:HG13	2:D3:30:ILE:O	2.10	0.51
1:A2:201:ALA:O	2:C1:208:TRP:HZ3	1.93	0.51
2:C7:64:GLY:N	3:E7:180:MET:HA	2.24	0.51
1:A4:155:PRO:CD	1:B2:157:THR:HG21	2.41	0.51
1:A4:167:ILE:HG21	1:B3:197:TRP:CH2	2.46	0.51
1:A5:155:PRO:CD	1:B3:157:THR:HG21	2.41	0.51
1:A5:167:ILE:HG21	1:B4:197:TRP:CH2	2.46	0.51
1:A8:167:ILE:HG21	1:B7:197:TRP:CH2	2.46	0.51
1:A11:167:ILE:HG21	1:B10:197:TRP:CH2	2.46	0.51
1:A11:167:ILE:O	2:C11:220:ASN:ND2	2.38	0.51
1:A13:175:TRP:CE2	2:C13:136:TYR:CE2	2.98	0.51
1:B6:170:VAL:CG1	2:D6:144:ASN:ND2	2.72	0.51
1:B10:170:VAL:CG1	2:D10:144:ASN:ND2	2.72	0.51
2:C8:64:GLY:N	3:E8:180:MET:HA	2.25	0.51
2:C10:32:LEU:HB3	2:C10:36:GLY:HA3	1.91	0.51
2:D8:30:ILE:HG13	2:D8:30:ILE:O	2.10	0.51
2:D12:30:ILE:HG13	2:D12:30:ILE:O	2.10	0.51
1:A1:167:ILE:CG2	1:B13:197:TRP:HH2	2.21	0.51
1:A3:167:ILE:HG21	1:B2:197:TRP:CH2	2.46	0.51
1:A4:155:PRO:CG	1:B2:157:THR:CG2	2.88	0.51
1:A5:155:PRO:CG	1:B3:157:THR:CG2	2.88	0.51
1:A7:167:ILE:HG21	1:B6:197:TRP:CH2	2.46	0.51
1:A10:175:TRP:CE2	2:C10:136:TYR:CE2	2.98	0.51
2:C9:32:LEU:HB3	2:C9:36:GLY:HA3	1.91	0.51
2:C12:32:LEU:HB3	2:C12:36:GLY:HA3	1.91	0.51
1:A3:155:PRO:CD	1:B1:157:THR:HG21	2.41	0.51
1:A11:155:PRO:CG	1:B9:157:THR:CG2	2.88	0.51
1:A12:155:PRO:CG	1:B10:157:THR:CG2	2.88	0.51
2:C2:61:THR:HG21	3:E2:180:MET:SD	2.51	0.51
2:C6:61:THR:HG21	3:E6:180:MET:SD	2.51	0.51
2:D1:30:ILE:HG13	2:D1:30:ILE:O	2.10	0.51
1:A5:175:TRP:CE2	2:C5:136:TYR:CE2	2.98	0.51
1:A6:155:PRO:CG	1:B4:157:THR:CG2	2.88	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A6:167:ILE:HG21	1:B5:197:TRP:CH2	2.46	0.51
1:A8:174:PRO:HG3	1:A8:185:PRO:HD3	1.92	0.51
1:A8:201:ALA:O	2:C7:208:TRP:HZ3	1.93	0.51
1:A11:174:PRO:HG3	1:A11:185:PRO:HD3	1.92	0.51
1:A11:175:TRP:CE2	2:C11:136:TYR:CE2	2.98	0.51
1:A12:175:TRP:CE2	2:C12:136:TYR:CE2	2.98	0.51
1:A13:155:PRO:CG	1:B11:157:THR:CG2	2.88	0.51
2:C13:61:THR:HG21	3:E13:180:MET:SD	2.51	0.51
2:D11:30:ILE:HG13	2:D11:30:ILE:O	2.10	0.51
1:A2:155:PRO:CD	1:B13:157:THR:HG21	2.41	0.51
1:A6:155:PRO:CD	1:B4:157:THR:HG21	2.41	0.51
1:A9:167:ILE:HG21	1:B8:197:TRP:CH2	2.46	0.51
1:A10:155:PRO:CG	1:B8:157:THR:CG2	2.88	0.51
2:D2:30:ILE:HG13	2:D2:30:ILE:O	2.10	0.51
2:D3:215:VAL:HG13	2:D3:232:VAL:HG21	1.93	0.51
2:D5:215:VAL:HG13	2:D5:232:VAL:HG21	1.93	0.51
2:D10:30:ILE:HG13	2:D10:30:ILE:O	2.10	0.51
1:A1:155:PRO:CD	1:B12:157:THR:HG21	2.41	0.51
1:A1:174:PRO:HG3	1:A1:185:PRO:HD3	1.92	0.51
1:A2:167:ILE:HG21	1:B1:197:TRP:CH2	2.46	0.51
1:A7:155:PRO:CG	1:B5:157:THR:CG2	2.88	0.51
1:A10:201:ALA:O	2:C9:208:TRP:HZ3	1.93	0.51
1:A12:167:ILE:HG21	1:B11:197:TRP:CH2	2.46	0.51
2:C3:61:THR:HG21	3:E3:180:MET:SD	2.51	0.51
2:C7:61:THR:HG21	3:E7:180:MET:SD	2.51	0.51
2:C8:61:THR:HG21	3:E8:180:MET:SD	2.51	0.51
2:C12:61:THR:HG21	3:E12:180:MET:SD	2.51	0.51
2:D7:215:VAL:HG13	2:D7:232:VAL:HG21	1.93	0.51
2:D13:30:ILE:HG13	2:D13:30:ILE:O	2.10	0.51
1:A3:155:PRO:CG	1:B1:157:THR:CG2	2.88	0.51
1:A7:155:PRO:CD	1:B5:157:THR:HG21	2.41	0.51
1:A8:155:PRO:CG	1:B6:157:THR:CG2	2.88	0.51
1:A9:155:PRO:CG	1:B7:157:THR:CG2	2.88	0.51
2:C9:61:THR:HG21	3:E9:180:MET:SD	2.51	0.51
2:D3:60:ILE:HG22	3:F3:185:PHE:CE2	2.43	0.51
2:D8:159:VAL:CG1	2:D8:160:LYS:N	2.44	0.51
1:A1:155:PRO:CG	1:B12:157:THR:CG2	2.88	0.50
1:A3:174:PRO:HG3	1:A3:185:PRO:HD3	1.92	0.50
1:A9:155:PRO:CD	1:B7:157:THR:HG21	2.41	0.50
1:A10:155:PRO:CD	1:B8:157:THR:HG21	2.41	0.50
1:A13:155:PRO:CD	1:B11:157:THR:HG21	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C10:74:ARG:HH11	2:D9:58:THR:HG21	1.73	0.50
2:D4:215:VAL:HG13	2:D4:232:VAL:HG21	1.93	0.50
2:D6:215:VAL:HG13	2:D6:232:VAL:HG21	1.93	0.50
2:D7:44:ASN:OD1	2:D7:44:ASN:N	2.44	0.50
1:A10:167:ILE:HG21	1:B9:197:TRP:CH2	2.46	0.50
1:B8:170:VAL:CG1	2:D8:144:ASN:ND2	2.72	0.50
2:C1:61:THR:HG21	3:E1:180:MET:SD	2.51	0.50
2:C5:61:THR:HG21	3:E5:180:MET:SD	2.51	0.50
2:D2:215:VAL:HG13	2:D2:232:VAL:HG21	1.93	0.50
2:D9:30:ILE:HG13	2:D9:30:ILE:O	2.10	0.50
1:A1:167:ILE:HG21	1:B13:197:TRP:CH2	2.46	0.50
2:D1:215:VAL:HG13	2:D1:232:VAL:HG21	1.93	0.50
1:A5:174:PRO:HG3	1:A5:185:PRO:HD3	1.92	0.50
1:A6:167:ILE:O	2:C6:220:ASN:ND2	2.38	0.50
1:A7:188:VAL:HG11	2:C7:141:ILE:HD11	1.93	0.50
1:A8:167:ILE:O	2:C8:220:ASN:ND2	2.38	0.50
1:A8:188:VAL:HG11	2:C8:141:ILE:HD11	1.93	0.50
2:C11:61:THR:HG21	3:E11:180:MET:SD	2.51	0.50
2:D13:168:LEU:HD21	2:D13:174:VAL:HG23	1.73	0.50
1:A2:155:PRO:CG	1:B13:157:THR:CG2	2.88	0.50
1:A6:188:VAL:HG11	2:C6:141:ILE:HD11	1.93	0.50
1:A9:174:PRO:HG3	1:A9:185:PRO:HD3	1.92	0.50
1:A9:188:VAL:HG11	2:C9:141:ILE:HD11	1.93	0.50
1:A10:188:VAL:HG11	2:C10:141:ILE:HD11	1.93	0.50
2:C10:61:THR:HG21	3:E10:180:MET:SD	2.51	0.50
1:A11:155:PRO:CD	1:B9:157:THR:HG21	2.41	0.50
1:A13:167:ILE:HG21	1:B12:197:TRP:CH2	2.46	0.50
2:C4:74:ARG:HH11	2:D3:58:THR:HG21	1.73	0.50
2:D8:215:VAL:HG13	2:D8:232:VAL:HG21	1.93	0.50
1:A12:155:PRO:CD	1:B10:157:THR:HG21	2.41	0.50
2:C4:61:THR:HG21	3:E4:180:MET:SD	2.51	0.50
2:C13:74:ARG:HH11	2:D12:58:THR:HG21	1.73	0.50
2:C2:74:ARG:HH11	2:D1:58:THR:HG21	1.73	0.50
2:D9:215:VAL:HG13	2:D9:232:VAL:HG21	1.93	0.50
2:D13:215:VAL:HG13	2:D13:232:VAL:HG21	1.93	0.50
1:A8:155:PRO:CD	1:B6:157:THR:HG21	2.41	0.50
1:A10:174:PRO:HG3	1:A10:185:PRO:HD3	1.92	0.49
2:C9:89:THR:HG22	2:C9:103:VAL:HG22	1.94	0.49
2:C10:89:THR:HG22	2:C10:103:VAL:HG22	1.94	0.49
1:A7:174:PRO:HG3	1:A7:185:PRO:HD3	1.92	0.49
2:C1:74:ARG:HH11	2:D13:58:THR:HG21	1.73	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C8:89:THR:HG22	2:C8:103:VAL:HG22	1.94	0.49
1:B1:98:VAL:CB	2:D2:208:TRP:CD1	2.95	0.49
2:C8:110:GLU:H	2:C8:110:GLU:CD	2.16	0.49
1:A1:188:VAL:HG11	2:C1:141:ILE:HD11	1.93	0.49
1:A3:192:VAL:HG11	2:C3:148:LEU:HD23	1.86	0.49
1:A12:174:PRO:HG3	1:A12:185:PRO:HD3	1.92	0.49
2:D10:215:VAL:HG13	2:D10:232:VAL:HG21	1.93	0.49
1:A4:167:ILE:O	2:C4:220:ASN:ND2	2.38	0.49
1:A13:188:VAL:HG11	2:C13:141:ILE:HD11	1.93	0.49
2:C5:110:GLU:H	2:C5:110:GLU:CD	2.16	0.49
2:C9:110:GLU:H	2:C9:110:GLU:CD	2.16	0.49
2:C12:110:GLU:H	2:C12:110:GLU:CD	2.16	0.49
2:D11:215:VAL:HG13	2:D11:232:VAL:HG21	1.93	0.49
2:C6:74:ARG:HH11	2:D5:58:THR:HG21	1.73	0.49
2:C7:89:THR:HG22	2:C7:103:VAL:HG22	1.94	0.49
2:C11:89:THR:HG22	2:C11:103:VAL:HG22	1.94	0.49
2:D3:159:VAL:CG1	2:D3:160:LYS:N	2.44	0.49
2:D8:60:ILE:HG22	3:F8:185:PHE:CE2	2.43	0.49
2:D12:215:VAL:HG13	2:D12:232:VAL:HG21	1.93	0.49
2:C4:110:GLU:H	2:C4:110:GLU:CD	2.16	0.49
2:C7:110:GLU:H	2:C7:110:GLU:CD	2.16	0.49
2:C11:110:GLU:H	2:C11:110:GLU:CD	2.16	0.49
2:C2:110:GLU:H	2:C2:110:GLU:CD	2.16	0.49
2:D11:60:ILE:HG22	3:F11:185:PHE:CE2	2.43	0.48
1:A2:188:VAL:HG11	2:C2:141:ILE:HD11	1.93	0.48
1:A5:167:ILE:CD1	1:B4:161:GLN:HA	2.44	0.48
2:C1:110:GLU:CD	2:C1:110:GLU:H	2.16	0.48
2:D12:60:ILE:HG22	3:F12:185:PHE:CE2	2.43	0.48
1:A10:167:ILE:CD1	1:B9:161:GLN:HA	2.44	0.48
2:C6:89:THR:HG22	2:C6:103:VAL:HG22	1.94	0.48
1:A2:167:ILE:CD1	1:B1:161:GLN:HA	2.44	0.48
1:A4:167:ILE:CD1	1:B3:161:GLN:HA	2.44	0.48
1:A11:167:ILE:CD1	1:B10:161:GLN:HA	2.44	0.48
1:A13:167:ILE:CD1	1:B12:161:GLN:HA	2.44	0.48
2:C2:50:ILE:HG12	2:C2:114:TYR:HB2	1.96	0.48
2:C3:89:THR:HG22	2:C3:103:VAL:HG22	1.94	0.48
2:C13:110:GLU:H	2:C13:110:GLU:CD	2.16	0.48
2:D6:44:ASN:OD1	2:D6:44:ASN:N	2.44	0.48
2:D9:60:ILE:HG22	3:F9:185:PHE:CE2	2.43	0.48
2:D10:60:ILE:HG22	3:F10:185:PHE:CE2	2.43	0.48
1:A6:167:ILE:CD1	1:B5:161:GLN:HA	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A12:188:VAL:HG11	2:C12:141:ILE:HD11	1.93	0.48
2:C1:50:ILE:HG12	2:C1:114:TYR:HB2	1.96	0.48
2:C4:89:THR:HG22	2:C4:103:VAL:HG22	1.94	0.48
2:C6:110:GLU:H	2:C6:110:GLU:CD	2.16	0.48
2:C10:110:GLU:H	2:C10:110:GLU:CD	2.16	0.48
2:C12:89:THR:HG22	2:C12:103:VAL:HG22	1.94	0.48
2:D8:168:LEU:CD2	2:D8:174:VAL:HG21	2.40	0.48
2:D8:200:VAL:HG12	2:D8:224:LEU:O	2.14	0.48
2:D13:159:VAL:CG1	2:D13:160:LYS:N	2.44	0.48
1:A11:152:CYS:SG	1:B9:150:VAL:HA	2.54	0.48
2:C2:89:THR:HG22	2:C2:103:VAL:HG22	1.94	0.48
2:C3:50:ILE:HG12	2:C3:114:TYR:HB2	1.96	0.48
2:C7:93:GLU:OE2	2:D7:71:ARG:NH2	2.47	0.48
2:C8:93:GLU:OE2	2:D8:71:ARG:NH2	2.47	0.48
2:C10:93:GLU:OE2	2:D10:71:ARG:NH2	2.47	0.48
2:D3:215:VAL:HG13	2:D3:232:VAL:CG2	2.44	0.48
1:A9:167:ILE:CD1	1:B8:161:GLN:HA	2.44	0.48
1:A12:167:ILE:CD1	1:B11:161:GLN:HA	2.44	0.48
2:C11:93:GLU:OE2	2:D11:71:ARG:NH2	2.47	0.48
2:C13:93:GLU:OE2	2:D13:71:ARG:NH2	2.47	0.48
2:D1:200:VAL:HG12	2:D1:224:LEU:O	2.14	0.48
2:D8:44:ASN:OD1	2:D8:44:ASN:N	2.44	0.48
2:D9:200:VAL:HG12	2:D9:224:LEU:O	2.14	0.48
2:D9:215:VAL:HG13	2:D9:232:VAL:CG2	2.44	0.48
1:A3:167:ILE:CD1	1:B2:161:GLN:HA	2.44	0.48
1:A12:152:CYS:SG	1:B10:150:VAL:HA	2.54	0.48
1:B7:98:VAL:CB	2:D8:208:TRP:CD1	2.95	0.48
2:D7:200:VAL:HG12	2:D7:224:LEU:O	2.14	0.48
2:D8:215:VAL:HG13	2:D8:232:VAL:CG2	2.44	0.48
2:D11:159:VAL:CG1	2:D11:160:LYS:N	2.44	0.48
2:D11:200:VAL:HG12	2:D11:224:LEU:O	2.14	0.48
2:D13:200:VAL:HG12	2:D13:224:LEU:O	2.14	0.48
1:A4:188:VAL:HG11	2:C4:141:ILE:HD11	1.93	0.48
2:C1:89:THR:HG22	2:C1:103:VAL:HG22	1.94	0.48
2:C9:74:ARG:HH11	2:D8:58:THR:HG21	1.73	0.48
2:D5:215:VAL:HG13	2:D5:232:VAL:CG2	2.44	0.48
2:D6:215:VAL:HG13	2:D6:232:VAL:CG2	2.44	0.48
2:D12:215:VAL:HG13	2:D12:232:VAL:CG2	2.44	0.48
2:D13:60:ILE:HG22	3:F13:185:PHE:CE2	2.43	0.48
2:D13:215:VAL:HG13	2:D13:232:VAL:CG2	2.44	0.48
1:A3:188:VAL:HG11	2:C3:141:ILE:HD11	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C5:89:THR:HG22	2:C5:103:VAL:HG22	1.94	0.48
2:C5:93:GLU:OE2	2:D5:71:ARG:NH2	2.47	0.48
2:C13:50:ILE:HG12	2:C13:114:TYR:HB2	1.96	0.48
2:D2:200:VAL:HG12	2:D2:224:LEU:O	2.14	0.48
2:D5:200:VAL:HG12	2:D5:224:LEU:O	2.14	0.48
2:C9:50:ILE:HG12	2:C9:114:TYR:HB2	1.96	0.47
2:C10:50:ILE:HG12	2:C10:114:TYR:HB2	1.96	0.47
2:D9:168:LEU:CD2	2:D9:174:VAL:HG21	2.40	0.47
2:D12:32:LEU:HD22	2:D12:38:PHE:HB2	1.96	0.47
1:A1:152:CYS:SG	1:B12:150:VAL:HA	2.54	0.47
1:A4:152:CYS:SG	1:B2:150:VAL:HA	2.54	0.47
1:A7:167:ILE:CD1	1:B6:161:GLN:HA	2.44	0.47
1:A10:152:CYS:SG	1:B8:150:VAL:HA	2.54	0.47
1:A13:152:CYS:SG	1:B11:150:VAL:HA	2.54	0.47
2:C3:110:GLU:H	2:C3:110:GLU:CD	2.16	0.47
2:C8:50:ILE:HG12	2:C8:114:TYR:HB2	1.96	0.47
2:D1:32:LEU:HD22	2:D1:38:PHE:HB2	1.96	0.47
2:D1:60:ILE:HG22	3:F1:185:PHE:CE2	2.43	0.47
2:D2:32:LEU:HD22	2:D2:38:PHE:HB2	1.96	0.47
2:D2:215:VAL:HG13	2:D2:232:VAL:CG2	2.44	0.47
2:D10:200:VAL:HG12	2:D10:224:LEU:O	2.14	0.47
2:D12:200:VAL:HG12	2:D12:224:LEU:O	2.14	0.47
1:B13:98:VAL:CB	2:D1:208:TRP:CD1	2.95	0.47
2:C7:50:ILE:HG12	2:C7:114:TYR:HB2	1.96	0.47
2:D3:200:VAL:HG12	2:D3:224:LEU:O	2.14	0.47
1:A1:167:ILE:CD1	1:B13:161:GLN:HA	2.44	0.47
1:A8:152:CYS:SG	1:B6:150:VAL:HA	2.54	0.47
2:C1:93:GLU:OE2	2:D1:71:ARG:NH2	2.47	0.47
2:C3:93:GLU:OE2	2:D3:71:ARG:NH2	2.47	0.47
2:C13:89:THR:HG22	2:C13:103:VAL:HG22	1.94	0.47
2:D1:215:VAL:HG13	2:D1:232:VAL:CG2	2.44	0.47
2:D6:200:VAL:HG12	2:D6:224:LEU:O	2.14	0.47
1:B6:98:VAL:CB	2:D7:208:TRP:CD1	2.95	0.47
2:C2:93:GLU:OE2	2:D2:71:ARG:NH2	2.47	0.47
2:C4:50:ILE:HG12	2:C4:114:TYR:HB2	1.96	0.47
2:C6:50:ILE:HG12	2:C6:114:TYR:HB2	1.96	0.47
2:C11:50:ILE:HG12	2:C11:114:TYR:HB2	1.96	0.47
2:C12:93:GLU:OE2	2:D12:71:ARG:NH2	2.47	0.47
2:D7:215:VAL:HG13	2:D7:232:VAL:CG2	2.44	0.47
2:D10:215:VAL:HG13	2:D10:232:VAL:CG2	2.44	0.47
2:D11:168:LEU:CD2	2:D11:174:VAL:HG21	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A6:152:CYS:SG	1:B4:150:VAL:HA	2.54	0.47
1:A9:152:CYS:SG	1:B7:150:VAL:HA	2.54	0.47
1:B8:98:VAL:CB	2:D9:208:TRP:CD1	2.95	0.47
2:C9:93:GLU:OE2	2:D9:71:ARG:NH2	2.47	0.47
2:D11:215:VAL:HG13	2:D11:232:VAL:CG2	2.44	0.47
1:A5:152:CYS:SG	1:B3:150:VAL:HA	2.54	0.47
1:A5:188:VAL:HG11	2:C5:141:ILE:HD11	1.93	0.47
1:A8:167:ILE:CD1	1:B7:161:GLN:HA	2.44	0.47
1:B2:98:VAL:CB	2:D3:208:TRP:CD1	2.95	0.47
2:C6:93:GLU:OE2	2:D6:71:ARG:NH2	2.47	0.47
2:D4:32:LEU:HD22	2:D4:38:PHE:HB2	1.96	0.47
2:D4:215:VAL:HG13	2:D4:232:VAL:CG2	2.44	0.47
1:A3:152:CYS:SG	1:B1:150:VAL:HA	2.54	0.47
1:A7:152:CYS:SG	1:B5:150:VAL:HA	2.54	0.47
2:C1:140:LEU:HD22	2:C1:235:ILE:HD11	1.97	0.47
2:C4:93:GLU:OE2	2:D4:71:ARG:NH2	2.47	0.47
2:C5:50:ILE:HG12	2:C5:114:TYR:HB2	1.96	0.47
2:C12:50:ILE:HG12	2:C12:114:TYR:HB2	1.96	0.47
2:D4:200:VAL:HG12	2:D4:224:LEU:O	2.14	0.47
1:A9:167:ILE:CG2	1:B8:197:TRP:HH2	2.21	0.47
1:A11:188:VAL:HG11	2:C11:141:ILE:HD11	1.93	0.47
2:C3:74:ARG:HH11	2:D2:58:THR:HG21	1.73	0.47
2:D13:32:LEU:HD22	2:D13:38:PHE:HB2	1.96	0.47
1:A2:152:CYS:SG	1:B13:150:VAL:HA	2.54	0.47
2:C2:140:LEU:HD22	2:C2:235:ILE:HD11	1.97	0.47
2:C4:140:LEU:HD22	2:C4:235:ILE:HD11	1.97	0.47
2:C13:140:LEU:HD22	2:C13:235:ILE:HD11	1.97	0.47
2:D8:32:LEU:HD22	2:D8:38:PHE:HB2	1.96	0.47
2:D11:32:LEU:HD22	2:D11:38:PHE:HB2	1.96	0.47
2:C5:140:LEU:HD22	2:C5:235:ILE:HD11	1.97	0.46
2:D7:32:LEU:HD22	2:D7:38:PHE:HB2	1.96	0.46
1:A6:188:VAL:HB	2:C6:141:ILE:HD11	1.97	0.46
1:A7:188:VAL:HB	2:C7:141:ILE:HD11	1.97	0.46
1:B9:98:VAL:CB	2:D10:208:TRP:CD1	2.95	0.46
2:C3:140:LEU:HD22	2:C3:235:ILE:HD11	1.97	0.46
2:C11:140:LEU:HD22	2:C11:235:ILE:HD11	1.97	0.46
2:C12:140:LEU:HD22	2:C12:235:ILE:HD11	1.97	0.46
2:D12:168:LEU:CD2	2:D12:174:VAL:HG21	2.40	0.46
2:C6:140:LEU:HD22	2:C6:235:ILE:HD11	1.97	0.46
2:C10:140:LEU:HD22	2:C10:235:ILE:HD11	1.97	0.46
2:D1:48:ASN:OD1	2:D1:111:GLY:HA2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D5:32:LEU:HD22	2:D5:38:PHE:HB2	1.96	0.46
2:D6:32:LEU:HD22	2:D6:38:PHE:HB2	1.96	0.46
2:D9:32:LEU:HD22	2:D9:38:PHE:HB2	1.96	0.46
1:A4:188:VAL:HB	2:C4:141:ILE:HD11	1.97	0.46
1:A12:188:VAL:HB	2:C12:141:ILE:HD11	1.97	0.46
1:B5:98:VAL:CB	2:D6:208:TRP:CD1	2.95	0.46
1:B10:98:VAL:CB	2:D11:208:TRP:CD1	2.95	0.46
2:C9:140:LEU:HD22	2:C9:235:ILE:HD11	1.97	0.46
2:D10:32:LEU:HD22	2:D10:38:PHE:HB2	1.96	0.46
1:A5:188:VAL:HB	2:C5:141:ILE:HD11	1.97	0.46
2:D2:48:ASN:OD1	2:D2:111:GLY:HA2	2.16	0.46
2:D3:32:LEU:HD22	2:D3:38:PHE:HB2	1.96	0.46
2:D13:48:ASN:OD1	2:D13:111:GLY:HA2	2.16	0.46
2:C1:60:ILE:CG2	3:E1:185:PHE:HE2	2.25	0.46
2:C3:136:TYR:CE1	2:C3:213:ARG:HD3	2.50	0.46
2:C7:140:LEU:HD22	2:C7:235:ILE:HD11	1.97	0.46
2:C8:140:LEU:HD22	2:C8:235:ILE:HD11	1.97	0.46
1:A4:175:TRP:CE2	2:C4:136:TYR:HE2	2.34	0.46
1:A5:175:TRP:CE2	2:C5:136:TYR:HE2	2.34	0.46
1:A8:188:VAL:HB	2:C8:141:ILE:HD11	1.97	0.46
1:A9:172:ILE:CD1	2:C9:140:LEU:HD12	2.35	0.46
1:A11:188:VAL:HB	2:C11:141:ILE:HD11	1.97	0.46
1:B4:98:VAL:CB	2:D5:208:TRP:CD1	2.95	0.46
2:C2:70:LYS:HE2	3:E2:183:GLN:HB2	1.98	0.46
2:C7:110:GLU:OE1	2:C7:110:GLU:N	2.44	0.46
2:C13:136:TYR:CE1	2:C13:213:ARG:HD3	2.50	0.46
1:A3:188:VAL:HB	2:C3:141:ILE:HD11	1.97	0.46
1:A13:188:VAL:HB	2:C13:141:ILE:HD11	1.97	0.46
1:B13:91:THR:HG1	2:D1:213:ARG:HH22	1.62	0.46
2:C3:70:LYS:HE2	3:E3:183:GLN:HB2	1.98	0.46
2:D1:71:ARG:CD	3:E1:182:SER:OG	2.64	0.46
2:D2:52:ILE:HD12	2:D2:57:VAL:HG22	1.98	0.46
2:D3:48:ASN:OD1	2:D3:111:GLY:HA2	2.16	0.46
2:D3:52:ILE:HD12	2:D3:57:VAL:HG22	1.98	0.46
2:D10:52:ILE:HD12	2:D10:57:VAL:HG22	1.98	0.46
1:A3:175:TRP:CE2	2:C3:136:TYR:HE2	2.34	0.46
1:A7:175:TRP:CE2	2:C7:136:TYR:HE2	2.34	0.46
1:A11:167:ILE:CG2	1:B10:197:TRP:HH2	2.21	0.46
2:C1:136:TYR:CE1	2:C1:213:ARG:HD3	2.50	0.46
2:C1:159:VAL:O	2:C1:179:ALA:HB3	2.16	0.46
2:C2:159:VAL:O	2:C2:179:ALA:HB3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C3:159:VAL:O	2:C3:179:ALA:HB3	2.16	0.46
2:C5:110:GLU:OE1	2:C5:110:GLU:N	2.44	0.46
2:C8:45:THR:HB	2:D7:86:ARG:HH22	1.81	0.46
2:C11:45:THR:HB	2:D10:86:ARG:HH22	1.81	0.46
2:C12:159:VAL:O	2:C12:179:ALA:HB3	2.16	0.46
2:C13:159:VAL:O	2:C13:179:ALA:HB3	2.16	0.46
2:D2:71:ARG:CD	3:E2:182:SER:OG	2.64	0.46
2:D4:88:PHE:CE2	2:D4:90:ILE:CG2	2.99	0.46
2:D9:52:ILE:HD12	2:D9:57:VAL:HG22	1.98	0.46
2:D9:71:ARG:CD	3:E9:182:SER:OG	2.64	0.46
2:D11:52:ILE:HD12	2:D11:57:VAL:HG22	1.98	0.46
2:D12:48:ASN:OD1	2:D12:111:GLY:HA2	2.16	0.46
1:B11:170:VAL:HG21	2:D11:144:ASN:HD22	1.82	0.45
1:B12:170:VAL:HG21	2:D12:144:ASN:HD22	1.82	0.45
2:C1:70:LYS:HE2	3:E1:183:GLN:HB2	1.98	0.45
2:C4:159:VAL:O	2:C4:179:ALA:HB3	2.16	0.45
2:C5:45:THR:HB	2:D4:86:ARG:HH22	1.81	0.45
2:C6:174:VAL:CG2	2:C6:190:TYR:HB3	2.46	0.45
2:C11:159:VAL:O	2:C11:179:ALA:HB3	2.16	0.45
2:C12:136:TYR:CE1	2:C12:213:ARG:HD3	2.50	0.45
2:D1:52:ILE:HD12	2:D1:57:VAL:HG22	1.98	0.45
2:D3:88:PHE:CE2	2:D3:90:ILE:CG2	2.99	0.45
2:D4:52:ILE:HD12	2:D4:57:VAL:HG22	1.98	0.45
2:D11:71:ARG:CD	3:E11:182:SER:OG	2.64	0.45
2:D13:52:ILE:HD12	2:D13:57:VAL:HG22	1.98	0.45
2:D13:71:ARG:CD	3:E13:182:SER:OG	2.64	0.45
1:A13:175:TRP:CE2	2:C13:136:TYR:HE2	2.34	0.45
2:C1:45:THR:HB	2:D13:86:ARG:HH22	1.81	0.45
2:C3:45:THR:HB	2:D2:86:ARG:HH22	1.81	0.45
2:C6:194:ASN:CG	2:C6:224:LEU:HD23	2.37	0.45
2:C7:174:VAL:CG2	2:C7:190:TYR:HB3	2.47	0.45
2:C12:70:LYS:HE2	3:E12:183:GLN:HB2	1.98	0.45
2:C13:70:LYS:HE2	3:E13:183:GLN:HB2	1.98	0.45
2:D6:152:ILE:HD13	2:D6:152:ILE:HA	1.82	0.45
2:D7:71:ARG:CD	3:E7:182:SER:OG	2.64	0.45
2:D9:48:ASN:OD1	2:D9:111:GLY:HA2	2.16	0.45
2:D12:52:ILE:HD12	2:D12:57:VAL:HG22	1.98	0.45
2:D13:88:PHE:CE2	2:D13:90:ILE:CG2	2.99	0.45
1:A6:175:TRP:CE2	2:C6:136:TYR:HE2	2.34	0.45
1:A7:182:PHE:HB3	1:B7:189:SER:OG	2.17	0.45
2:C1:174:VAL:CG2	2:C1:190:TYR:HB3	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:174:VAL:CG2	2:C2:190:TYR:HB3	2.46	0.45
2:C4:70:LYS:HE2	3:E4:183:GLN:HB2	1.98	0.45
2:C5:174:VAL:CG2	2:C5:190:TYR:HB3	2.46	0.45
2:C7:194:ASN:CG	2:C7:224:LEU:HD23	2.37	0.45
2:C8:174:VAL:CG2	2:C8:190:TYR:HB3	2.46	0.45
2:D3:71:ARG:CD	3:E3:182:SER:OG	2.64	0.45
2:D4:48:ASN:OD1	2:D4:111:GLY:HA2	2.16	0.45
2:D5:161:PRO:HB2	2:D5:176:PRO:HB3	1.99	0.45
2:D6:48:ASN:OD1	2:D6:111:GLY:HA2	2.16	0.45
2:D7:48:ASN:OD1	2:D7:111:GLY:HA2	2.16	0.45
2:D7:161:PRO:HB2	2:D7:176:PRO:HB3	1.99	0.45
2:D8:52:ILE:HD12	2:D8:57:VAL:HG22	1.98	0.45
2:D12:71:ARG:CD	3:E12:182:SER:OG	2.64	0.45
1:A2:188:VAL:HB	2:C2:141:ILE:HD11	1.97	0.45
1:A10:175:TRP:CE2	2:C10:136:TYR:HE2	2.34	0.45
2:C5:159:VAL:O	2:C5:179:ALA:HB3	2.16	0.45
2:C5:194:ASN:CG	2:C5:224:LEU:HD23	2.37	0.45
2:C6:45:THR:HB	2:D5:86:ARG:HH22	1.81	0.45
2:C13:45:THR:HB	2:D12:86:ARG:HH22	1.81	0.45
2:D1:88:PHE:CE2	2:D1:90:ILE:CG2	2.99	0.45
2:D8:48:ASN:OD1	2:D8:111:GLY:HA2	2.16	0.45
1:A2:182:PHE:HB3	1:B2:189:SER:OG	2.17	0.45
1:A3:182:PHE:HB3	1:B3:189:SER:OG	2.17	0.45
1:A6:182:PHE:HB3	1:B6:189:SER:OG	2.17	0.45
1:A9:188:VAL:HB	2:C9:141:ILE:HD11	1.97	0.45
1:A10:182:PHE:HB3	1:B10:189:SER:OG	2.17	0.45
1:A13:172:ILE:CD1	2:C13:140:LEU:HD12	2.35	0.45
2:C3:174:VAL:CG2	2:C3:190:TYR:HB3	2.46	0.45
2:C4:174:VAL:CG2	2:C4:190:TYR:HB3	2.46	0.45
2:C11:174:VAL:CG2	2:C11:190:TYR:HB3	2.46	0.45
2:C12:174:VAL:CG2	2:C12:190:TYR:HB3	2.46	0.45
2:C13:174:VAL:CG2	2:C13:190:TYR:HB3	2.46	0.45
2:D4:71:ARG:CD	3:E4:182:SER:OG	2.64	0.45
2:D5:52:ILE:HD12	2:D5:57:VAL:HG22	1.98	0.45
2:D5:71:ARG:CD	3:E5:182:SER:OG	2.64	0.45
2:D6:71:ARG:CD	3:E6:182:SER:OG	2.64	0.45
2:D6:161:PRO:HB2	2:D6:176:PRO:HB3	1.99	0.45
1:A8:182:PHE:HB3	1:B8:189:SER:OG	2.17	0.45
1:B13:170:VAL:HG21	2:D13:144:ASN:HD22	1.82	0.45
2:C3:60:ILE:CG2	3:E3:185:PHE:HE2	2.25	0.45
2:D4:161:PRO:HB2	2:D4:176:PRO:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D10:71:ARG:CD	3:E10:182:SER:OG	2.64	0.45
1:A12:182:PHE:HB3	1:B12:189:SER:OG	2.17	0.45
1:B10:170:VAL:HG21	2:D10:144:ASN:HD22	1.81	0.45
1:B11:98:VAL:CB	2:D12:208:TRP:CD1	2.95	0.45
2:C7:159:VAL:O	2:C7:179:ALA:HB3	2.16	0.45
2:C10:159:VAL:O	2:C10:179:ALA:HB3	2.17	0.45
2:C11:70:LYS:HE2	3:E11:183:GLN:HB2	1.98	0.45
2:C11:136:TYR:CE1	2:C11:213:ARG:HD3	2.50	0.45
2:D2:88:PHE:CE2	2:D2:90:ILE:CG2	2.99	0.45
2:D4:168:LEU:CD2	2:D4:174:VAL:HG21	2.40	0.45
2:D5:48:ASN:OD1	2:D5:111:GLY:HA2	2.16	0.45
2:D5:88:PHE:CE2	2:D5:90:ILE:CG2	2.99	0.45
2:D5:168:LEU:CD2	2:D5:174:VAL:HG21	2.40	0.45
2:D7:52:ILE:HD12	2:D7:57:VAL:HG22	1.98	0.45
2:D8:161:PRO:HB2	2:D8:176:PRO:HB3	1.99	0.45
1:A13:182:PHE:HB3	1:B13:189:SER:OG	2.17	0.45
1:B10:188:VAL:HG13	2:D10:141:ILE:CD1	2.47	0.45
2:C2:136:TYR:CE1	2:C2:213:ARG:HD3	2.50	0.45
2:C5:70:LYS:HE2	3:E5:183:GLN:HB2	1.98	0.45
2:D6:52:ILE:HD12	2:D6:57:VAL:HG22	1.98	0.45
2:D6:88:PHE:CE2	2:D6:90:ILE:CG2	2.99	0.45
2:D7:172:PHE:HB3	2:D7:192:LEU:HD12	1.99	0.45
2:D8:58:THR:O	3:F8:185:PHE:HD2	2.00	0.45
2:D9:88:PHE:CE2	2:D9:90:ILE:CG2	2.99	0.45
2:D9:159:VAL:CG1	2:D9:160:LYS:N	2.44	0.45
2:D9:161:PRO:HB2	2:D9:176:PRO:HB3	1.99	0.45
2:D10:88:PHE:CE2	2:D10:90:ILE:CG2	2.99	0.45
2:D10:172:PHE:HB3	2:D10:192:LEU:HD12	1.99	0.45
1:A2:175:TRP:CE2	2:C2:136:TYR:HE2	2.34	0.45
2:C7:45:THR:HB	2:D6:86:ARG:HH22	1.81	0.45
2:C8:159:VAL:O	2:C8:179:ALA:HB3	2.16	0.45
2:C9:45:THR:HB	2:D8:86:ARG:HH22	1.81	0.45
2:C10:174:VAL:CG2	2:C10:190:TYR:HB3	2.46	0.45
2:C10:202:LEU:HD11	2:C10:217:PHE:CE2	2.51	0.45
2:D8:71:ARG:CD	3:E8:182:SER:OG	2.64	0.45
2:D9:58:THR:O	3:F9:185:PHE:HD2	2.00	0.45
2:D9:172:PHE:HB3	2:D9:192:LEU:HD12	1.99	0.45
2:D11:48:ASN:OD1	2:D11:111:GLY:HA2	2.16	0.45
2:D13:168:LEU:CD2	2:D13:174:VAL:HG21	2.40	0.45
1:A9:182:PHE:HB3	1:B9:189:SER:OG	2.17	0.45
1:A11:182:PHE:HB3	1:B11:189:SER:OG	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:188:VAL:HG13	2:D5:141:ILE:CD1	2.46	0.45
2:C6:159:VAL:O	2:C6:179:ALA:HB3	2.16	0.45
2:C8:70:LYS:HE2	3:E8:183:GLN:HB2	1.98	0.45
2:C10:45:THR:HB	2:D9:86:ARG:HH22	1.82	0.45
2:D3:161:PRO:HB2	2:D3:176:PRO:HB3	1.99	0.45
2:D6:172:PHE:HB3	2:D6:192:LEU:HD12	1.99	0.45
2:D7:88:PHE:CE2	2:D7:90:ILE:CG2	2.99	0.45
2:D8:88:PHE:CE2	2:D8:90:ILE:CG2	2.99	0.45
2:D11:37:GLN:HE21	2:D11:37:GLN:HB3	1.59	0.45
2:D11:172:PHE:HB3	2:D11:192:LEU:HD12	1.99	0.45
1:A1:188:VAL:HB	2:C1:141:ILE:HD11	1.97	0.44
1:A10:188:VAL:HB	2:C10:141:ILE:HD11	1.97	0.44
1:B7:170:VAL:HG21	2:D7:144:ASN:HD22	1.82	0.44
2:C1:194:ASN:CG	2:C1:224:LEU:HD23	2.37	0.44
2:C4:45:THR:HB	2:D3:86:ARG:HH22	1.81	0.44
2:C6:70:LYS:HE2	3:E6:183:GLN:HB2	1.98	0.44
2:C9:174:VAL:CG2	2:C9:190:TYR:HB3	2.46	0.44
2:C12:45:THR:HB	2:D11:86:ARG:HH22	1.81	0.44
2:D3:168:LEU:CD2	2:D3:174:VAL:HG21	2.40	0.44
2:D7:58:THR:O	3:F7:185:PHE:HD2	2.00	0.44
2:D8:172:PHE:HB3	2:D8:192:LEU:HD12	1.99	0.44
2:D9:37:GLN:HE22	2:D9:103:VAL:CG2	2.28	0.44
2:D11:88:PHE:CE2	2:D11:90:ILE:CG2	2.99	0.44
1:A4:182:PHE:HB3	1:B4:189:SER:OG	2.17	0.44
1:A8:175:TRP:CE2	2:C8:136:TYR:HE2	2.34	0.44
1:A11:175:TRP:CE2	2:C11:136:TYR:HE2	2.34	0.44
2:C2:194:ASN:CG	2:C2:224:LEU:HD23	2.37	0.44
2:D5:172:PHE:HB3	2:D5:192:LEU:HD12	1.99	0.44
2:D10:161:PRO:HB2	2:D10:176:PRO:HB3	1.99	0.44
2:D12:88:PHE:CE2	2:D12:90:ILE:CG2	2.99	0.44
1:A13:155:PRO:HG2	1:B11:157:THR:HG21	2.00	0.44
1:B3:170:VAL:HG21	2:D3:144:ASN:HD22	1.82	0.44
1:B4:170:VAL:HG21	2:D4:144:ASN:HD22	1.82	0.44
1:B5:170:VAL:HG21	2:D5:144:ASN:HD22	1.82	0.44
1:B6:170:VAL:HG21	2:D6:144:ASN:HD22	1.82	0.44
2:C5:136:TYR:CE1	2:C5:213:ARG:HD3	2.50	0.44
2:C9:159:VAL:O	2:C9:179:ALA:HB3	2.16	0.44
2:D2:161:PRO:HB2	2:D2:176:PRO:HB3	1.99	0.44
2:D8:37:GLN:HE22	2:D8:103:VAL:CG2	2.28	0.44
2:D10:37:GLN:HE22	2:D10:103:VAL:CG2	2.28	0.44
2:D10:48:ASN:OD1	2:D10:111:GLY:HA2	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D10:58:THR:O	3:F10:185:PHE:HD2	2.00	0.44
2:D12:172:PHE:HB3	2:D12:192:LEU:HD12	1.99	0.44
1:A1:182:PHE:HB3	1:B1:189:SER:OG	2.17	0.44
2:C3:110:GLU:OE1	2:C3:110:GLU:N	2.44	0.44
2:C10:70:LYS:HE2	3:E10:183:GLN:HB2	1.98	0.44
2:C13:194:ASN:CG	2:C13:224:LEU:HD23	2.37	0.44
2:D2:159:VAL:CG1	2:D2:160:LYS:N	2.44	0.44
2:D6:58:THR:O	3:F6:185:PHE:HD2	2.00	0.44
2:D12:58:THR:O	3:F12:185:PHE:HD2	2.00	0.44
1:B8:170:VAL:HG21	2:D8:144:ASN:HD22	1.82	0.44
2:C2:45:THR:HB	2:D1:86:ARG:HH22	1.81	0.44
2:C7:70:LYS:HE2	3:E7:183:GLN:HB2	1.98	0.44
2:D10:71:ARG:HH21	2:D10:79:LEU:HD22	1.83	0.44
1:A10:172:ILE:CD1	2:C10:140:LEU:HD12	2.35	0.44
1:A12:175:TRP:CE2	2:C12:136:TYR:HE2	2.34	0.44
1:B1:170:VAL:HG21	2:D1:144:ASN:HD22	1.82	0.44
1:B11:188:VAL:HG13	2:D11:141:ILE:CD1	2.47	0.44
2:C3:194:ASN:CG	2:C3:224:LEU:HD23	2.37	0.44
2:C6:202:LEU:HD11	2:C6:217:PHE:CE2	2.51	0.44
2:C9:70:LYS:HE2	3:E9:183:GLN:HB2	1.98	0.44
2:D2:71:ARG:HH21	2:D2:79:LEU:HD22	1.83	0.44
2:D2:168:LEU:CD2	2:D2:174:VAL:HG21	2.40	0.44
2:D4:71:ARG:HH21	2:D4:79:LEU:HD22	1.83	0.44
2:D5:44:ASN:OD1	2:D5:44:ASN:N	2.44	0.44
1:A1:175:TRP:CE2	2:C1:136:TYR:HE2	2.34	0.44
1:A4:202:ARG:HA	1:A4:202:ARG:HD2	1.87	0.44
1:A5:182:PHE:HB3	1:B5:189:SER:OG	2.17	0.44
1:B2:170:VAL:HG21	2:D2:144:ASN:HD22	1.82	0.44
2:D4:172:PHE:HB3	2:D4:192:LEU:HD12	1.99	0.44
2:D11:161:PRO:HB2	2:D11:176:PRO:HB3	1.99	0.44
2:D7:71:ARG:HH21	2:D7:79:LEU:HD22	1.83	0.44
2:D11:37:GLN:HE22	2:D11:103:VAL:CG2	2.28	0.44
2:D13:172:PHE:HB3	2:D13:192:LEU:HD12	1.99	0.44
2:C11:60:ILE:CG2	3:E11:185:PHE:HE2	2.25	0.44
2:D4:159:VAL:CG1	2:D4:160:LYS:N	2.44	0.44
2:D5:71:ARG:HH21	2:D5:79:LEU:HD22	1.83	0.44
2:D5:159:VAL:CG1	2:D5:160:LYS:N	2.44	0.44
2:D7:37:GLN:HE22	2:D7:103:VAL:CG2	2.28	0.44
2:D13:58:THR:O	3:F13:185:PHE:HD2	2.00	0.44
1:B9:170:VAL:HG21	2:D9:144:ASN:HD22	1.82	0.43
2:C2:202:LEU:HD11	2:C2:217:PHE:CE2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D1:71:ARG:HH21	2:D1:79:LEU:HD22	1.83	0.43
2:D1:161:PRO:HB2	2:D1:176:PRO:HB3	1.99	0.43
2:D2:32:LEU:HD11	2:D2:100:PHE:HB3	2.01	0.43
2:D8:71:ARG:HH21	2:D8:79:LEU:HD22	1.83	0.43
2:D12:71:ARG:HH21	2:D12:79:LEU:HD22	1.83	0.43
1:A9:175:TRP:CE2	2:C9:136:TYR:HE2	2.34	0.43
1:B6:188:VAL:HG13	2:D6:141:ILE:CD1	2.47	0.43
1:B12:98:VAL:CB	2:D13:208:TRP:CD1	2.95	0.43
2:C12:194:ASN:CG	2:C12:224:LEU:HD23	2.37	0.43
2:D1:172:PHE:HB3	2:D1:192:LEU:HD12	1.99	0.43
2:D2:172:PHE:HB3	2:D2:192:LEU:HD12	1.99	0.43
2:D3:172:PHE:HB3	2:D3:192:LEU:HD12	1.99	0.43
2:D7:152:ILE:HD13	2:D7:152:ILE:HA	1.82	0.43
2:D10:32:LEU:HD11	2:D10:100:PHE:HB3	2.00	0.43
2:D13:161:PRO:HB2	2:D13:176:PRO:HB3	1.99	0.43
2:C10:194:ASN:CG	2:C10:224:LEU:HD23	2.37	0.43
2:C11:194:ASN:CG	2:C11:224:LEU:HD23	2.37	0.43
2:D1:32:LEU:HD11	2:D1:100:PHE:HB3	2.00	0.43
2:D1:200:VAL:HG22	2:D1:201:ALA:N	2.34	0.43
2:D3:58:THR:O	3:F3:185:PHE:HD2	2.00	0.43
2:D9:200:VAL:HG22	2:D9:201:ALA:N	2.34	0.43
2:D11:58:THR:O	3:F11:185:PHE:HD2	2.00	0.43
2:D11:200:VAL:HG22	2:D11:201:ALA:N	2.34	0.43
2:D13:71:ARG:HH21	2:D13:79:LEU:HD22	1.83	0.43
1:A7:167:ILE:CG2	1:B6:197:TRP:HH2	2.21	0.43
2:D1:37:GLN:HE21	2:D1:37:GLN:HB3	1.58	0.43
2:D3:32:LEU:HD11	2:D3:100:PHE:HB3	2.01	0.43
2:D4:58:THR:O	3:F4:185:PHE:HD2	2.00	0.43
2:D4:200:VAL:HG22	2:D4:201:ALA:N	2.34	0.43
2:D12:161:PRO:HB2	2:D12:176:PRO:HB3	1.99	0.43
2:C4:194:ASN:CG	2:C4:224:LEU:HD23	2.37	0.43
2:C11:89:THR:HG21	2:D11:111:GLY:H	1.84	0.43
2:D3:71:ARG:HH21	2:D3:79:LEU:HD22	1.83	0.43
2:D6:200:VAL:HG22	2:D6:201:ALA:N	2.34	0.43
2:D7:200:VAL:HG22	2:D7:201:ALA:N	2.34	0.43
2:D9:32:LEU:HD11	2:D9:100:PHE:HB3	2.01	0.43
1:A1:172:ILE:CD1	2:C1:140:LEU:HD12	2.35	0.43
2:D10:200:VAL:HG22	2:D10:201:ALA:N	2.34	0.43
2:D11:32:LEU:HD11	2:D11:100:PHE:HB3	2.00	0.43
2:D12:37:GLN:HE22	2:D12:103:VAL:CG2	2.28	0.43
2:D13:200:VAL:HG22	2:D13:201:ALA:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A3:155:PRO:HG2	1:B1:157:THR:HG21	2.00	0.43
1:B4:188:VAL:CG1	2:D4:141:ILE:CD1	2.79	0.43
1:B12:188:VAL:HG13	2:D12:141:ILE:CD1	2.46	0.43
2:C8:60:ILE:CG2	3:E8:185:PHE:HE2	2.25	0.43
2:C12:89:THR:HG21	2:D12:111:GLY:H	1.84	0.43
2:D3:200:VAL:HG22	2:D3:201:ALA:N	2.34	0.43
2:D8:32:LEU:HD11	2:D8:100:PHE:HB3	2.00	0.43
1:B7:188:VAL:CG1	2:D7:141:ILE:CD1	2.79	0.43
2:C7:89:THR:HG21	2:D7:111:GLY:H	1.84	0.43
2:C9:194:ASN:CG	2:C9:224:LEU:HD23	2.37	0.43
2:D2:58:THR:O	3:F2:185:PHE:HD2	2.00	0.43
2:D2:200:VAL:HG22	2:D2:201:ALA:N	2.34	0.43
2:D9:71:ARG:HH21	2:D9:79:LEU:HD22	1.83	0.43
2:D11:71:ARG:HH21	2:D11:79:LEU:HD22	1.83	0.43
1:A1:155:PRO:HG2	1:B12:157:THR:HG21	2.00	0.43
1:A6:202:ARG:HD2	1:A6:202:ARG:HA	1.87	0.43
1:B3:188:VAL:CG1	2:D3:141:ILE:CD1	2.79	0.43
2:C4:89:THR:HG21	2:D4:111:GLY:H	1.84	0.43
2:C6:89:THR:HG21	2:D6:111:GLY:H	1.84	0.43
2:C8:89:THR:HG21	2:D8:111:GLY:H	1.84	0.43
2:C11:202:LEU:HD11	2:C11:217:PHE:CE2	2.51	0.43
2:D1:58:THR:O	3:F1:185:PHE:HD2	2.00	0.43
2:D1:168:LEU:CD2	2:D1:174:VAL:HG21	2.40	0.43
2:D3:69:ASP:OD1	2:D3:70:LYS:N	2.52	0.43
2:D5:58:THR:O	3:F5:185:PHE:HD2	2.00	0.43
2:D5:69:ASP:OD1	2:D5:70:LYS:N	2.52	0.43
2:D8:200:VAL:HG22	2:D8:201:ALA:N	2.34	0.43
2:D13:32:LEU:HD11	2:D13:100:PHE:HB3	2.00	0.43
1:A5:202:ARG:HD2	1:A5:202:ARG:HA	1.87	0.43
1:A8:167:ILE:CG2	1:B7:197:TRP:HH2	2.21	0.43
2:C2:89:THR:HG21	2:D2:111:GLY:H	1.84	0.43
2:C3:89:THR:HG21	2:D3:111:GLY:H	1.84	0.43
2:C5:89:THR:HG21	2:D5:111:GLY:H	1.84	0.43
2:C9:89:THR:HG21	2:D9:111:GLY:H	1.84	0.43
2:D4:32:LEU:HD11	2:D4:100:PHE:HB3	2.01	0.43
2:D6:37:GLN:HE22	2:D6:103:VAL:CG2	2.28	0.43
2:D7:69:ASP:OD1	2:D7:70:LYS:N	2.52	0.43
1:A9:202:ARG:HA	1:A9:202:ARG:HD2	1.87	0.42
1:A10:167:ILE:CG2	1:B9:197:TRP:HH2	2.21	0.42
1:B9:91:THR:HG21	2:D10:213:ARG:HH12	1.83	0.42
2:C5:60:ILE:CG2	3:E5:185:PHE:HE2	2.25	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C10:89:THR:HG21	2:D10:111:GLY:H	1.84	0.42
2:D1:69:ASP:OD1	2:D1:70:LYS:N	2.52	0.42
2:D4:69:ASP:OD1	2:D4:70:LYS:N	2.52	0.42
1:A7:188:VAL:CB	2:C7:141:ILE:HD11	2.50	0.42
1:B1:91:THR:HG23	2:D2:213:ARG:HH12	1.85	0.42
1:B4:91:THR:HG21	2:D5:213:ARG:HH12	1.83	0.42
1:B5:91:THR:HG21	2:D6:213:ARG:HH12	1.83	0.42
1:B5:188:VAL:CG1	2:D5:141:ILE:CD1	2.79	0.42
2:C1:89:THR:HG21	2:D1:111:GLY:H	1.84	0.42
2:C7:202:LEU:HD11	2:C7:217:PHE:CE2	2.51	0.42
2:C12:208:TRP:CD1	2:C12:212:VAL:HG22	2.54	0.42
2:D6:71:ARG:HH21	2:D6:79:LEU:HD22	1.83	0.42
2:D9:44:ASN:OD1	2:D9:44:ASN:N	2.44	0.42
2:D12:200:VAL:HG22	2:D12:201:ALA:N	2.34	0.42
1:A2:175:TRP:CD2	2:C2:136:TYR:CE2	3.08	0.42
1:A3:188:VAL:CB	2:C3:141:ILE:HD11	2.50	0.42
1:A7:175:TRP:CD2	2:C7:136:TYR:CE2	3.08	0.42
1:A8:188:VAL:CB	2:C8:141:ILE:HD11	2.50	0.42
1:A11:202:ARG:HD2	1:A11:202:ARG:HA	1.88	0.42
2:C1:110:GLU:OE1	2:C1:110:GLU:N	2.44	0.42
2:C7:136:TYR:CE1	2:C7:213:ARG:HD3	2.50	0.42
2:C8:194:ASN:CG	2:C8:224:LEU:HD23	2.37	0.42
2:C10:136:TYR:CE1	2:C10:213:ARG:HD3	2.50	0.42
2:D7:32:LEU:HD11	2:D7:100:PHE:HB3	2.00	0.42
1:A1:175:TRP:CD2	2:C1:136:TYR:CE2	3.08	0.42
1:A4:188:VAL:CB	2:C4:141:ILE:HD11	2.50	0.42
1:A6:175:TRP:CD2	2:C6:136:TYR:CE2	3.08	0.42
1:B10:91:THR:HG21	2:D11:213:ARG:HH12	1.83	0.42
2:C5:208:TRP:CD1	2:C5:212:VAL:HG22	2.54	0.42
2:C10:208:TRP:CD1	2:C10:212:VAL:HG22	2.54	0.42
2:C12:37:GLN:HA	2:C12:101:SER:O	2.20	0.42
2:D7:159:VAL:CG1	2:D7:160:LYS:N	2.44	0.42
2:D9:69:ASP:OD1	2:D9:70:LYS:N	2.52	0.42
1:A4:175:TRP:CD2	2:C4:136:TYR:CE2	3.08	0.42
1:A5:175:TRP:CD2	2:C5:136:TYR:CE2	3.08	0.42
1:B2:91:THR:HG23	2:D3:213:ARG:HH12	1.85	0.42
1:B2:188:VAL:CG1	2:D2:141:ILE:CD1	2.79	0.42
1:B3:91:THR:HG21	2:D4:213:ARG:HH12	1.83	0.42
1:B7:91:THR:HG21	2:D8:213:ARG:HH12	1.83	0.42
1:B7:188:VAL:HG13	2:D7:141:ILE:CD1	2.47	0.42
1:B8:91:THR:HG21	2:D9:213:ARG:HH12	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C6:60:ILE:CG2	3:E6:185:PHE:HE2	2.25	0.42
2:C6:208:TRP:CD1	2:C6:212:VAL:HG22	2.54	0.42
2:C7:208:TRP:CD1	2:C7:212:VAL:HG22	2.54	0.42
2:C8:55:ASP:OD2	2:C8:94:THR:OG1	2.33	0.42
2:C9:138:LYS:HB3	2:C9:138:LYS:HE2	1.75	0.42
2:C11:110:GLU:OE1	2:C11:110:GLU:N	2.44	0.42
2:C11:208:TRP:CD1	2:C11:212:VAL:HG22	2.54	0.42
2:C13:89:THR:HG21	2:D13:111:GLY:H	1.84	0.42
2:C13:208:TRP:CD1	2:C13:212:VAL:HG22	2.54	0.42
2:D3:37:GLN:HE21	2:D3:37:GLN:HB3	1.58	0.42
2:D5:200:VAL:HG22	2:D5:201:ALA:N	2.34	0.42
2:D10:37:GLN:HE21	2:D10:37:GLN:HB3	1.58	0.42
2:D12:32:LEU:HD11	2:D12:100:PHE:HB3	2.01	0.42
1:A3:175:TRP:CD2	2:C3:136:TYR:CE2	3.08	0.42
1:A8:175:TRP:CD2	2:C8:136:TYR:CE2	3.08	0.42
1:A11:193:SER:HA	1:A11:194:PRO:HD3	1.93	0.42
1:A12:155:PRO:HG2	1:B10:157:THR:HG21	2.00	0.42
1:A13:175:TRP:CD2	2:C13:136:TYR:CE2	3.08	0.42
1:B6:91:THR:HG21	2:D7:213:ARG:HH12	1.83	0.42
1:B13:91:THR:HG23	2:D1:213:ARG:HH12	1.85	0.42
2:C3:52:ILE:HD13	2:C3:116:LEU:HB3	2.02	0.42
2:C4:208:TRP:CD1	2:C4:212:VAL:HG22	2.54	0.42
2:C7:60:ILE:CG2	3:E7:185:PHE:HE2	2.25	0.42
2:C10:37:GLN:HA	2:C10:101:SER:O	2.20	0.42
1:A9:175:TRP:CD2	2:C9:136:TYR:CE2	3.08	0.42
2:C2:37:GLN:HA	2:C2:101:SER:O	2.20	0.42
2:C10:172:PHE:HB3	2:C10:192:LEU:HD12	2.02	0.42
2:C11:37:GLN:HA	2:C11:101:SER:O	2.20	0.42
2:C13:37:GLN:HA	2:C13:101:SER:O	2.20	0.42
2:C13:110:GLU:OE1	2:C13:110:GLU:N	2.44	0.42
2:D5:37:GLN:HE21	2:D5:37:GLN:HB3	1.58	0.42
2:D8:69:ASP:OD1	2:D8:70:LYS:N	2.52	0.42
2:D8:152:ILE:HD13	2:D8:152:ILE:HA	1.82	0.42
2:D11:69:ASP:OD1	2:D11:70:LYS:N	2.52	0.42
2:D13:37:GLN:HE22	2:D13:103:VAL:CG2	2.28	0.42
1:A3:202:ARG:HD2	1:A3:202:ARG:HA	1.87	0.42
1:A4:201:ALA:O	2:C3:208:TRP:CZ3	2.73	0.42
1:A6:188:VAL:CB	2:C6:141:ILE:HD11	2.50	0.42
1:A9:201:ALA:O	2:C8:208:TRP:CZ3	2.73	0.42
1:A11:175:TRP:CD2	2:C11:136:TYR:CE2	3.08	0.42
1:A12:175:TRP:CD2	2:C12:136:TYR:CE2	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A13:193:SER:HA	1:A13:194:PRO:HD3	1.93	0.42
1:B7:91:THR:HG23	2:D8:213:ARG:HH12	1.85	0.42
1:B8:91:THR:HG23	2:D9:213:ARG:HH12	1.85	0.42
1:B13:91:THR:HG21	2:D1:213:ARG:HH12	1.83	0.42
2:C1:208:TRP:CD1	2:C1:212:VAL:HG22	2.54	0.42
2:C2:52:ILE:HD13	2:C2:116:LEU:HB3	2.02	0.42
2:C3:208:TRP:CD1	2:C3:212:VAL:HG22	2.54	0.42
2:C4:52:ILE:HD13	2:C4:116:LEU:HB3	2.02	0.42
2:D5:32:LEU:HD11	2:D5:100:PHE:HB3	2.00	0.42
2:D12:69:ASP:OD1	2:D12:70:LYS:N	2.52	0.42
1:A10:155:PRO:HG2	1:B8:157:THR:HG21	2.00	0.42
1:A10:175:TRP:CD2	2:C10:136:TYR:CE2	3.08	0.42
1:A13:202:ARG:HA	1:A13:202:ARG:HD2	1.87	0.42
1:B12:91:THR:HG21	2:D13:213:ARG:HH12	1.83	0.42
1:B13:188:VAL:HG13	2:D13:141:ILE:CD1	2.47	0.42
2:C3:37:GLN:HA	2:C3:101:SER:O	2.20	0.42
2:C3:172:PHE:HB3	2:C3:192:LEU:HD12	2.02	0.42
2:C3:230:MET:HE2	2:C3:230:MET:HB3	1.92	0.42
2:C4:172:PHE:HB3	2:C4:192:LEU:HD12	2.02	0.42
2:C5:138:LYS:HB3	2:C5:138:LYS:HE2	1.75	0.42
2:C8:37:GLN:HA	2:C8:101:SER:O	2.20	0.42
2:C9:172:PHE:HB3	2:C9:192:LEU:HD12	2.02	0.42
2:C11:52:ILE:HD13	2:C11:116:LEU:HB3	2.02	0.42
2:D6:69:ASP:OD1	2:D6:70:LYS:N	2.52	0.42
1:A6:155:PRO:HG2	1:B4:157:THR:HG21	2.00	0.42
1:A10:188:VAL:CB	2:C10:141:ILE:HD11	2.49	0.42
1:A11:188:VAL:CB	2:C11:141:ILE:HD11	2.50	0.42
1:B9:91:THR:HG23	2:D10:213:ARG:HH12	1.85	0.42
1:B11:91:THR:HG21	2:D12:213:ARG:HH12	1.83	0.42
1:B12:91:THR:HG23	2:D13:213:ARG:HH12	1.85	0.42
2:C10:52:ILE:HD13	2:C10:116:LEU:HB3	2.02	0.42
2:C11:172:PHE:HB3	2:C11:192:LEU:HD12	2.02	0.42
2:D5:70:LYS:HE3	2:D5:70:LYS:HB2	1.86	0.42
2:D6:32:LEU:HD11	2:D6:100:PHE:HB3	2.01	0.42
1:A13:188:VAL:CB	2:C13:141:ILE:HD11	2.50	0.41
1:B11:91:THR:HG23	2:D12:213:ARG:HH12	1.85	0.41
2:C2:208:TRP:CD1	2:C2:212:VAL:HG22	2.54	0.41
2:C5:172:PHE:HB3	2:C5:192:LEU:HD12	2.02	0.41
2:C6:67:LEU:HD23	2:C6:67:LEU:HA	1.91	0.41
2:C12:52:ILE:HD13	2:C12:116:LEU:HB3	2.02	0.41
2:D2:69:ASP:OD1	2:D2:70:LYS:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D5:37:GLN:HE22	2:D5:103:VAL:CG2	2.28	0.41
2:D10:69:ASP:OD1	2:D10:70:LYS:N	2.52	0.41
1:A1:188:VAL:CB	2:C1:141:ILE:HD11	2.50	0.41
1:A2:188:VAL:CB	2:C2:141:ILE:HD11	2.50	0.41
1:A5:188:VAL:CB	2:C5:141:ILE:HD11	2.50	0.41
1:A7:155:PRO:HG2	1:B5:157:THR:HG21	2.00	0.41
1:A9:155:PRO:HG2	1:B7:157:THR:HG21	2.00	0.41
1:A11:172:ILE:CD1	2:C11:140:LEU:HD12	2.35	0.41
1:B3:91:THR:HG23	2:D4:213:ARG:HH12	1.85	0.41
2:C7:37:GLN:HA	2:C7:101:SER:O	2.20	0.41
1:A6:201:ALA:O	2:C5:208:TRP:CZ3	2.73	0.41
1:A9:188:VAL:CB	2:C9:141:ILE:HD11	2.49	0.41
2:C3:202:LEU:HD11	2:C3:217:PHE:CE2	2.51	0.41
2:C5:37:GLN:HA	2:C5:101:SER:O	2.20	0.41
2:C6:63:PRO:HG3	2:D6:47:PRO:HD3	2.03	0.41
2:C9:37:GLN:HA	2:C9:101:SER:O	2.20	0.41
2:C9:208:TRP:CD1	2:C9:212:VAL:HG22	2.54	0.41
2:C13:63:PRO:HG3	2:D13:47:PRO:HD3	2.03	0.41
2:D13:69:ASP:OD1	2:D13:70:LYS:N	2.52	0.41
1:A2:172:ILE:CD1	2:C2:140:LEU:HD12	2.35	0.41
1:A12:201:ALA:O	2:C11:208:TRP:CZ3	2.73	0.41
1:B1:188:VAL:CG1	2:D1:141:ILE:CD1	2.79	0.41
1:B6:91:THR:HG23	2:D7:213:ARG:HH12	1.85	0.41
1:B6:188:VAL:CG1	2:D6:141:ILE:CD1	2.79	0.41
2:C1:52:ILE:HD13	2:C1:116:LEU:HB3	2.02	0.41
2:C2:172:PHE:HB3	2:C2:192:LEU:HD12	2.02	0.41
2:C3:63:PRO:HG3	2:D3:47:PRO:HD3	2.03	0.41
2:C4:37:GLN:HA	2:C4:101:SER:O	2.20	0.41
2:C8:172:PHE:HB3	2:C8:192:LEU:HD12	2.02	0.41
2:C8:208:TRP:CD1	2:C8:212:VAL:HG22	2.54	0.41
2:C13:60:ILE:CG2	3:E13:185:PHE:HE2	2.25	0.41
2:D1:192:LEU:HD13	2:D1:192:LEU:HA	1.93	0.41
1:A5:155:PRO:HG2	1:B3:157:THR:HG21	2.00	0.41
1:A8:155:PRO:HG2	1:B6:157:THR:HG21	2.00	0.41
1:B2:91:THR:HG21	2:D3:213:ARG:HH12	1.83	0.41
2:C1:63:PRO:HG3	2:D1:47:PRO:HD3	2.03	0.41
2:C5:52:ILE:HD13	2:C5:116:LEU:HB3	2.02	0.41
2:C9:52:ILE:HD13	2:C9:116:LEU:HB3	2.02	0.41
2:D1:37:GLN:HE22	2:D1:103:VAL:CG2	2.28	0.41
1:A1:201:ALA:O	2:C13:208:TRP:CZ3	2.73	0.41
1:B10:91:THR:HG23	2:D11:213:ARG:HH12	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C4:72:LEU:HD22	3:E4:185:PHE:CB	2.50	0.41
2:C4:136:TYR:CE1	2:C4:213:ARG:HD3	2.50	0.41
2:C12:172:PHE:HB3	2:C12:192:LEU:HD12	2.02	0.41
2:D7:37:GLN:HE21	2:D7:37:GLN:HB3	1.59	0.41
2:D11:70:LYS:HE3	2:D11:70:LYS:HB2	1.86	0.41
2:C6:136:TYR:CE1	2:C6:213:ARG:HD3	2.51	0.41
2:C9:63:PRO:HG3	2:D9:47:PRO:HD3	2.03	0.41
2:C9:110:GLU:OE1	2:C9:110:GLU:N	2.44	0.41
2:C12:110:GLU:OE1	2:C12:110:GLU:N	2.44	0.41
2:C13:52:ILE:HD13	2:C13:116:LEU:HB3	2.02	0.41
2:D7:152:ILE:HA	2:D7:153:PRO:HD3	1.97	0.41
2:D8:70:LYS:HB2	2:D8:70:LYS:HE3	1.86	0.41
2:D9:152:ILE:HD13	2:D9:152:ILE:HA	1.82	0.41
2:C4:63:PRO:HG3	2:D4:47:PRO:HD3	2.03	0.41
2:C8:136:TYR:CE1	2:C8:213:ARG:HD3	2.50	0.41
2:C10:63:PRO:HG3	2:D10:47:PRO:HD3	2.03	0.41
2:D7:192:LEU:HD13	2:D7:192:LEU:HA	1.93	0.41
1:A2:202:ARG:HD2	1:A2:202:ARG:HA	1.87	0.41
1:A3:201:ALA:O	2:C2:208:TRP:CZ3	2.73	0.41
1:A9:193:SER:HA	1:A9:194:PRO:HD3	1.93	0.41
1:A10:158:VAL:HG21	1:A10:200:PRO:CB	2.51	0.41
1:A11:201:ALA:O	2:C10:208:TRP:CZ3	2.73	0.41
1:B1:188:VAL:HG13	2:D1:141:ILE:CD1	2.46	0.41
1:B3:155:PRO:CD	2:D4:205:GLN:HG3	2.51	0.41
1:B4:155:PRO:CD	2:D5:205:GLN:HG3	2.51	0.41
1:B5:155:PRO:CD	2:D6:205:GLN:HG3	2.51	0.41
2:C1:37:GLN:HA	2:C1:101:SER:O	2.20	0.41
2:C2:67:LEU:HD23	2:C2:67:LEU:HA	1.91	0.41
2:C2:203:ARG:H	2:C2:203:ARG:HG2	1.77	0.41
2:C4:60:ILE:CG2	3:E4:185:PHE:HE2	2.25	0.41
2:C6:37:GLN:HA	2:C6:101:SER:O	2.20	0.41
2:C6:172:PHE:HB3	2:C6:192:LEU:HD12	2.02	0.41
2:C7:63:PRO:HG3	2:D7:47:PRO:HD3	2.03	0.41
2:C11:138:LYS:HE2	2:C11:138:LYS:HB3	1.75	0.41
2:D1:70:LYS:HE3	2:D1:70:LYS:HB2	1.86	0.41
1:A8:201:ALA:O	2:C7:208:TRP:CZ3	2.73	0.41
1:A12:164:ARG:HB3	1:B11:164:ARG:HH11	1.86	0.41
1:A12:188:VAL:CB	2:C12:141:ILE:HD11	2.50	0.41
1:B8:188:VAL:HG13	2:D8:141:ILE:CD1	2.46	0.41
1:B11:155:PRO:CD	2:D12:205:GLN:HG3	2.51	0.41
2:C5:63:PRO:HG3	2:D5:47:PRO:HD3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C7:52:ILE:HD13	2:C7:116:LEU:HB3	2.02	0.41
2:D7:209:LYS:HE3	2:D7:209:LYS:HB2	1.95	0.41
2:D10:152:ILE:HD13	2:D10:152:ILE:HA	1.82	0.41
2:D12:209:LYS:HE3	2:D12:209:LYS:HB2	1.95	0.41
2:D13:209:LYS:HE3	2:D13:209:LYS:HB2	1.95	0.41
1:A6:158:VAL:HG21	1:A6:200:PRO:CB	2.51	0.40
1:B5:91:THR:HG23	2:D6:213:ARG:HH12	1.85	0.40
1:B10:155:PRO:CD	2:D11:205:GLN:HG3	2.51	0.40
2:C1:172:PHE:HB3	2:C1:192:LEU:HD12	2.02	0.40
2:C2:46:ASP:HA	2:C2:47:PRO:HD3	1.98	0.40
2:C3:72:LEU:HD22	3:E3:185:PHE:CB	2.51	0.40
2:C6:52:ILE:HD13	2:C6:116:LEU:HB3	2.02	0.40
2:C8:63:PRO:HG3	2:D8:47:PRO:HD3	2.03	0.40
2:C13:172:PHE:HB3	2:C13:192:LEU:HD12	2.02	0.40
2:C13:185:LEU:HD23	2:C13:185:LEU:HA	1.89	0.40
1:A1:193:SER:HA	1:A1:194:PRO:HD3	1.93	0.40
1:A8:164:ARG:HB3	1:B7:164:ARG:HH11	1.87	0.40
1:B6:155:PRO:CD	2:D7:205:GLN:HG3	2.51	0.40
2:C2:90:ILE:HD13	2:C2:90:ILE:HG21	1.81	0.40
2:C2:110:GLU:OE1	2:C2:110:GLU:N	2.44	0.40
2:C8:52:ILE:HD13	2:C8:116:LEU:HB3	2.02	0.40
2:C9:60:ILE:CG2	3:E9:185:PHE:HE2	2.25	0.40
2:C11:72:LEU:HD22	3:E11:185:PHE:CB	2.50	0.40
2:C12:63:PRO:HG3	2:D12:47:PRO:HD3	2.03	0.40
2:C12:72:LEU:HD22	3:E12:185:PHE:CB	2.51	0.40
1:A4:155:PRO:HG2	1:B2:157:THR:HG21	2.00	0.40
1:B2:155:PRO:CD	2:D3:205:GLN:HG3	2.51	0.40
1:B4:91:THR:HG23	2:D5:213:ARG:HH12	1.85	0.40
1:B10:170:VAL:CG1	2:D10:144:ASN:HD22	2.33	0.40
2:C2:138:LYS:HE2	2:C2:138:LYS:HB3	1.75	0.40
2:C7:202:LEU:HD12	2:C7:202:LEU:C	2.42	0.40
2:C9:136:TYR:CE1	2:C9:213:ARG:HD3	2.50	0.40
2:C12:46:ASP:HA	2:C12:47:PRO:HD3	1.98	0.40
2:D4:37:GLN:HE22	2:D4:103:VAL:CG2	2.28	0.40
2:D11:144:ASN:OD1	2:D11:235:ILE:HD13	2.22	0.40
2:D11:152:ILE:HD13	2:D11:152:ILE:HA	1.82	0.40
1:A7:164:ARG:HB3	1:B6:164:ARG:HH11	1.87	0.40
1:A11:155:PRO:HG2	1:B9:157:THR:HG21	2.00	0.40
1:A11:164:ARG:HB3	1:B10:164:ARG:HH11	1.87	0.40
1:B8:98:VAL:HG13	2:D9:208:TRP:NE1	2.37	0.40
1:B9:155:PRO:CD	2:D10:205:GLN:HG3	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B12:155:PRO:CD	2:D13:205:GLN:HG3	2.51	0.40
1:B13:188:VAL:CG1	2:D13:141:ILE:CD1	2.79	0.40
2:C4:202:LEU:HD12	2:C4:202:LEU:C	2.42	0.40
2:C5:90:ILE:HD13	2:C5:90:ILE:HG21	1.81	0.40
2:C7:172:PHE:HB3	2:C7:192:LEU:HD12	2.02	0.40
2:C8:202:LEU:HD11	2:C8:217:PHE:CE2	2.51	0.40
2:C13:72:LEU:HD22	3:E13:185:PHE:CB	2.51	0.40
2:D10:144:ASN:OD1	2:D10:235:ILE:HD13	2.22	0.40
2:D12:70:LYS:HE3	2:D12:70:LYS:HB2	1.86	0.40
2:D12:152:ILE:HD13	2:D12:152:ILE:HA	1.82	0.40
1:B1:91:THR:HG21	2:D2:213:ARG:HH12	1.83	0.40
1:B3:98:VAL:HG13	2:D4:208:TRP:NE1	2.37	0.40
1:B5:98:VAL:HG13	2:D6:208:TRP:NE1	2.37	0.40
2:C2:63:PRO:HG3	2:D2:47:PRO:HD3	2.03	0.40
2:C6:72:LEU:HD22	3:E6:185:PHE:CB	2.51	0.40
2:C9:148:LEU:HD12	2:C9:148:LEU:HA	1.96	0.40
2:C9:202:LEU:HD12	2:C9:202:LEU:C	2.42	0.40
2:C11:63:PRO:HG3	2:D11:47:PRO:HD3	2.03	0.40
2:C13:49:MET:HB2	2:C13:79:LEU:HD23	2.04	0.40
2:D2:37:GLN:HE22	2:D2:103:VAL:CG2	2.28	0.40
2:D13:144:ASN:OD1	2:D13:235:ILE:HD13	2.22	0.40
2:D13:192:LEU:HD13	2:D13:192:LEU:HA	1.93	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 PDB entries followed by that with respect to all EM entries.

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	A1	53/204 (26%)	47 (89%)	6 (11%)	0	100	100
1	A10	53/204 (26%)	47 (89%)	6 (11%)	0	100	100
1	A11	53/204 (26%)	47 (89%)	6 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A12	53/204 (26%)	47 (89%)	6 (11%)	0	100	100
1	A13	53/204 (26%)	47 (89%)	6 (11%)	0	100	100
1	A2	53/204 (26%)	47 (89%)	6 (11%)	0	100	100
1	A3	53/204 (26%)	47 (89%)	6 (11%)	0	100	100
1	A4	53/204 (26%)	47 (89%)	6 (11%)	0	100	100
1	A5	53/204 (26%)	47 (89%)	6 (11%)	0	100	100
1	A6	53/204 (26%)	47 (89%)	6 (11%)	0	100	100
1	A7	53/204 (26%)	47 (89%)	6 (11%)	0	100	100
1	A8	53/204 (26%)	47 (89%)	6 (11%)	0	100	100
1	A9	53/204 (26%)	47 (89%)	6 (11%)	0	100	100
1	B1	61/204 (30%)	56 (92%)	4 (7%)	1 (2%)	9	37
1	B10	61/204 (30%)	56 (92%)	4 (7%)	1 (2%)	9	37
1	B11	61/204 (30%)	56 (92%)	4 (7%)	1 (2%)	9	37
1	B12	61/204 (30%)	56 (92%)	4 (7%)	1 (2%)	9	37
1	B13	61/204 (30%)	56 (92%)	4 (7%)	1 (2%)	9	37
1	B2	61/204 (30%)	56 (92%)	4 (7%)	1 (2%)	9	37
1	B3	61/204 (30%)	56 (92%)	4 (7%)	1 (2%)	9	37
1	B4	61/204 (30%)	56 (92%)	4 (7%)	1 (2%)	9	37
1	B5	61/204 (30%)	56 (92%)	4 (7%)	1 (2%)	9	37
1	B6	61/204 (30%)	56 (92%)	4 (7%)	1 (2%)	9	37
1	B7	61/204 (30%)	56 (92%)	4 (7%)	1 (2%)	9	37
1	B8	61/204 (30%)	56 (92%)	4 (7%)	1 (2%)	9	37
1	B9	61/204 (30%)	56 (92%)	4 (7%)	1 (2%)	9	37
2	C1	215/246 (87%)	208 (97%)	6 (3%)	1 (0%)	29	61
2	C10	215/246 (87%)	208 (97%)	6 (3%)	1 (0%)	29	61
2	C11	215/246 (87%)	208 (97%)	6 (3%)	1 (0%)	29	61
2	C12	215/246 (87%)	208 (97%)	6 (3%)	1 (0%)	29	61
2	C13	215/246 (87%)	208 (97%)	6 (3%)	1 (0%)	29	61
2	C2	215/246 (87%)	208 (97%)	6 (3%)	1 (0%)	29	61
2	C3	215/246 (87%)	208 (97%)	6 (3%)	1 (0%)	29	61
2	C4	215/246 (87%)	208 (97%)	6 (3%)	1 (0%)	29	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C5	215/246 (87%)	208 (97%)	6 (3%)	1 (0%)	29	61
2	C6	215/246 (87%)	208 (97%)	6 (3%)	1 (0%)	29	61
2	C7	215/246 (87%)	208 (97%)	6 (3%)	1 (0%)	29	61
2	C8	215/246 (87%)	208 (97%)	6 (3%)	1 (0%)	29	61
2	C9	215/246 (87%)	208 (97%)	6 (3%)	1 (0%)	29	61
2	D1	215/246 (87%)	205 (95%)	9 (4%)	1 (0%)	29	61
2	D10	215/246 (87%)	205 (95%)	9 (4%)	1 (0%)	29	61
2	D11	215/246 (87%)	205 (95%)	9 (4%)	1 (0%)	29	61
2	D12	215/246 (87%)	205 (95%)	9 (4%)	1 (0%)	29	61
2	D13	215/246 (87%)	205 (95%)	9 (4%)	1 (0%)	29	61
2	D2	215/246 (87%)	205 (95%)	9 (4%)	1 (0%)	29	61
2	D3	215/246 (87%)	205 (95%)	9 (4%)	1 (0%)	29	61
2	D4	215/246 (87%)	205 (95%)	9 (4%)	1 (0%)	29	61
2	D5	215/246 (87%)	205 (95%)	9 (4%)	1 (0%)	29	61
2	D6	215/246 (87%)	205 (95%)	9 (4%)	1 (0%)	29	61
2	D7	215/246 (87%)	205 (95%)	9 (4%)	1 (0%)	29	61
2	D8	215/246 (87%)	205 (95%)	9 (4%)	1 (0%)	29	61
2	D9	215/246 (87%)	205 (95%)	9 (4%)	1 (0%)	29	61
3	E1	9/453 (2%)	9 (100%)	0	0	100	100
3	E10	9/453 (2%)	9 (100%)	0	0	100	100
3	E11	9/453 (2%)	9 (100%)	0	0	100	100
3	E12	9/453 (2%)	9 (100%)	0	0	100	100
3	E13	9/453 (2%)	9 (100%)	0	0	100	100
3	E2	9/453 (2%)	9 (100%)	0	0	100	100
3	E3	9/453 (2%)	9 (100%)	0	0	100	100
3	E4	9/453 (2%)	9 (100%)	0	0	100	100
3	E5	9/453 (2%)	9 (100%)	0	0	100	100
3	E6	9/453 (2%)	9 (100%)	0	0	100	100
3	E7	9/453 (2%)	9 (100%)	0	0	100	100
3	E8	9/453 (2%)	9 (100%)	0	0	100	100
3	E9	9/453 (2%)	9 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F1	9/453 (2%)	9 (100%)	0	0	100	100
3	F10	9/453 (2%)	9 (100%)	0	0	100	100
3	F11	9/453 (2%)	9 (100%)	0	0	100	100
3	F12	9/453 (2%)	9 (100%)	0	0	100	100
3	F13	9/453 (2%)	9 (100%)	0	0	100	100
3	F2	9/453 (2%)	9 (100%)	0	0	100	100
3	F3	9/453 (2%)	9 (100%)	0	0	100	100
3	F4	9/453 (2%)	9 (100%)	0	0	100	100
3	F5	9/453 (2%)	9 (100%)	0	0	100	100
3	F6	9/453 (2%)	9 (100%)	0	0	100	100
3	F7	9/453 (2%)	9 (100%)	0	0	100	100
3	F8	9/453 (2%)	9 (100%)	0	0	100	100
3	F9	9/453 (2%)	9 (100%)	0	0	100	100
All	All	7306/23478 (31%)	6942 (95%)	325 (4%)	39 (0%)	32	61

All (39) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C1	169	PRO
2	C2	169	PRO
2	C3	169	PRO
2	C4	169	PRO
2	C5	169	PRO
2	C6	169	PRO
2	C7	169	PRO
2	C8	169	PRO
2	C9	169	PRO
2	C10	169	PRO
2	C11	169	PRO
2	C12	169	PRO
2	C13	169	PRO
1	B1	96	PRO
1	B2	96	PRO
1	B3	96	PRO
1	B6	96	PRO
1	B7	96	PRO
1	B8	96	PRO

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Mol	Chain	Res	Type
1	B9	96	PRO
1	B10	96	PRO
1	B12	96	PRO
1	B13	96	PRO
1	B4	96	PRO
1	B5	96	PRO
1	B11	96	PRO
2	D1	210	PRO
2	D2	210	PRO
2	D3	210	PRO
2	D4	210	PRO
2	D5	210	PRO
2	D6	210	PRO
2	D7	210	PRO
2	D8	210	PRO
2	D9	210	PRO
2	D10	210	PRO
2	D11	210	PRO
2	D12	210	PRO
2	D13	210	PRO

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	A1	48/168 (29%)	47 (98%)	1 (2%)	53 76
1	A10	48/168 (29%)	47 (98%)	1 (2%)	53 76
1	A11	48/168 (29%)	47 (98%)	1 (2%)	53 76
1	A12	48/168 (29%)	47 (98%)	1 (2%)	53 76
1	A13	48/168 (29%)	47 (98%)	1 (2%)	53 76
1	A2	48/168 (29%)	47 (98%)	1 (2%)	53 76
1	A3	48/168 (29%)	47 (98%)	1 (2%)	53 76
1	A4	48/168 (29%)	47 (98%)	1 (2%)	53 76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A5	48/168 (29%)	47 (98%)	1 (2%)	53	76
1	A6	48/168 (29%)	47 (98%)	1 (2%)	53	76
1	A7	48/168 (29%)	47 (98%)	1 (2%)	53	76
1	A8	48/168 (29%)	47 (98%)	1 (2%)	53	76
1	A9	48/168 (29%)	47 (98%)	1 (2%)	53	76
1	B1	56/168 (33%)	55 (98%)	1 (2%)	59	79
1	B10	56/168 (33%)	55 (98%)	1 (2%)	59	79
1	B11	56/168 (33%)	55 (98%)	1 (2%)	59	79
1	B12	56/168 (33%)	55 (98%)	1 (2%)	59	79
1	B13	56/168 (33%)	55 (98%)	1 (2%)	59	79
1	B2	56/168 (33%)	55 (98%)	1 (2%)	59	79
1	B3	56/168 (33%)	55 (98%)	1 (2%)	59	79
1	B4	56/168 (33%)	55 (98%)	1 (2%)	59	79
1	B5	56/168 (33%)	55 (98%)	1 (2%)	59	79
1	B6	56/168 (33%)	55 (98%)	1 (2%)	59	79
1	B7	56/168 (33%)	55 (98%)	1 (2%)	59	79
1	B8	56/168 (33%)	55 (98%)	1 (2%)	59	79
1	B9	56/168 (33%)	55 (98%)	1 (2%)	59	79
2	C1	173/195 (89%)	171 (99%)	2 (1%)	71	84
2	C10	173/195 (89%)	171 (99%)	2 (1%)	71	84
2	C11	173/195 (89%)	171 (99%)	2 (1%)	71	84
2	C12	173/195 (89%)	171 (99%)	2 (1%)	71	84
2	C13	173/195 (89%)	170 (98%)	3 (2%)	60	79
2	C2	173/195 (89%)	171 (99%)	2 (1%)	71	84
2	C3	173/195 (89%)	171 (99%)	2 (1%)	71	84
2	C4	173/195 (89%)	171 (99%)	2 (1%)	71	84
2	C5	173/195 (89%)	170 (98%)	3 (2%)	60	79
2	C6	173/195 (89%)	171 (99%)	2 (1%)	71	84
2	C7	173/195 (89%)	170 (98%)	3 (2%)	60	79
2	C8	173/195 (89%)	171 (99%)	2 (1%)	71	84
2	C9	173/195 (89%)	171 (99%)	2 (1%)	71	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D1	173/195 (89%)	168 (97%)	5 (3%)	42	70
2	D10	173/195 (89%)	168 (97%)	5 (3%)	42	70
2	D11	173/195 (89%)	168 (97%)	5 (3%)	42	70
2	D12	173/195 (89%)	168 (97%)	5 (3%)	42	70
2	D13	173/195 (89%)	168 (97%)	5 (3%)	42	70
2	D2	173/195 (89%)	168 (97%)	5 (3%)	42	70
2	D3	173/195 (89%)	168 (97%)	5 (3%)	42	70
2	D4	173/195 (89%)	168 (97%)	5 (3%)	42	70
2	D5	173/195 (89%)	168 (97%)	5 (3%)	42	70
2	D6	173/195 (89%)	168 (97%)	5 (3%)	42	70
2	D7	173/195 (89%)	168 (97%)	5 (3%)	42	70
2	D8	173/195 (89%)	168 (97%)	5 (3%)	42	70
2	D9	173/195 (89%)	168 (97%)	5 (3%)	42	70
3	E1	10/353 (3%)	10 (100%)	0	100	100
3	E10	10/353 (3%)	10 (100%)	0	100	100
3	E11	10/353 (3%)	10 (100%)	0	100	100
3	E12	10/353 (3%)	10 (100%)	0	100	100
3	E13	10/353 (3%)	10 (100%)	0	100	100
3	E2	10/353 (3%)	10 (100%)	0	100	100
3	E3	10/353 (3%)	10 (100%)	0	100	100
3	E4	10/353 (3%)	10 (100%)	0	100	100
3	E5	10/353 (3%)	10 (100%)	0	100	100
3	E6	10/353 (3%)	10 (100%)	0	100	100
3	E7	10/353 (3%)	10 (100%)	0	100	100
3	E8	10/353 (3%)	10 (100%)	0	100	100
3	E9	10/353 (3%)	10 (100%)	0	100	100
3	F1	10/353 (3%)	10 (100%)	0	100	100
3	F10	10/353 (3%)	10 (100%)	0	100	100
3	F11	10/353 (3%)	10 (100%)	0	100	100
3	F12	10/353 (3%)	10 (100%)	0	100	100
3	F13	10/353 (3%)	10 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F2	10/353 (3%)	10 (100%)	0	100	100
3	F3	10/353 (3%)	10 (100%)	0	100	100
3	F4	10/353 (3%)	10 (100%)	0	100	100
3	F5	10/353 (3%)	10 (100%)	0	100	100
3	F6	10/353 (3%)	10 (100%)	0	100	100
3	F7	10/353 (3%)	10 (100%)	0	100	100
3	F8	10/353 (3%)	10 (100%)	0	100	100
3	F9	10/353 (3%)	10 (100%)	0	100	100
All	All	6110/18616 (33%)	5990 (98%)	120 (2%)	57	77

All (120) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A1	159	HIS
1	A2	159	HIS
1	A3	159	HIS
1	A4	159	HIS
1	A5	159	HIS
1	A6	159	HIS
1	A7	159	HIS
1	A8	159	HIS
1	A9	159	HIS
1	A10	159	HIS
1	A11	159	HIS
1	A12	159	HIS
1	A13	159	HIS
1	B1	191	VAL
1	B2	191	VAL
1	B3	191	VAL
1	B4	191	VAL
1	B5	191	VAL
1	B6	191	VAL
1	B7	191	VAL
1	B8	191	VAL
1	B9	191	VAL
1	B10	191	VAL
1	B11	191	VAL
1	B12	191	VAL
1	B13	191	VAL

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Mol	Chain	Res	Type
2	C1	225	MET
2	C1	229	ARG
2	C2	225	MET
2	C2	229	ARG
2	C3	225	MET
2	C3	229	ARG
2	C4	225	MET
2	C4	229	ARG
2	C5	151	ASP
2	C5	225	MET
2	C5	229	ARG
2	C6	225	MET
2	C6	229	ARG
2	C7	151	ASP
2	C7	225	MET
2	C7	229	ARG
2	C8	225	MET
2	C8	229	ARG
2	C9	225	MET
2	C9	229	ARG
2	C10	225	MET
2	C10	229	ARG
2	C11	225	MET
2	C11	229	ARG
2	C12	225	MET
2	C12	229	ARG
2	C13	40	LEU
2	C13	225	MET
2	C13	229	ARG
2	D1	73	THR
2	D1	186	ARG
2	D1	225	MET
2	D1	230	MET
2	D1	240	GLU
2	D2	73	THR
2	D2	186	ARG
2	D2	225	MET
2	D2	230	MET
2	D2	240	GLU
2	D3	73	THR
2	D3	186	ARG
2	D3	225	MET

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Mol	Chain	Res	Type
2	D3	230	MET
2	D3	240	GLU
2	D4	73	THR
2	D4	186	ARG
2	D4	225	MET
2	D4	230	MET
2	D4	240	GLU
2	D5	73	THR
2	D5	186	ARG
2	D5	225	MET
2	D5	230	MET
2	D5	240	GLU
2	D6	73	THR
2	D6	186	ARG
2	D6	225	MET
2	D6	230	MET
2	D6	240	GLU
2	D7	73	THR
2	D7	186	ARG
2	D7	225	MET
2	D7	230	MET
2	D7	240	GLU
2	D8	73	THR
2	D8	186	ARG
2	D8	225	MET
2	D8	230	MET
2	D8	240	GLU
2	D9	73	THR
2	D9	186	ARG
2	D9	225	MET
2	D9	230	MET
2	D9	240	GLU
2	D10	73	THR
2	D10	186	ARG
2	D10	225	MET
2	D10	230	MET
2	D10	240	GLU
2	D11	73	THR
2	D11	186	ARG
2	D11	225	MET
2	D11	230	MET
2	D11	240	GLU

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Mol	Chain	Res	Type
2	D12	73	THR
2	D12	186	ARG
2	D12	225	MET
2	D12	230	MET
2	D12	240	GLU
2	D13	73	THR
2	D13	186	ARG
2	D13	225	MET
2	D13	230	MET
2	D13	240	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (65) such sidechains are listed below:

Mol	Chain	Res	Type
1	B1	159	HIS
1	B1	161	GLN
1	B2	159	HIS
1	B2	161	GLN
1	B3	159	HIS
1	B3	161	GLN
1	B4	159	HIS
1	B4	161	GLN
1	B5	159	HIS
1	B5	161	GLN
1	B6	159	HIS
1	B6	161	GLN
1	B7	159	HIS
1	B7	161	GLN
1	B8	159	HIS
1	B8	161	GLN
1	B9	159	HIS
1	B9	161	GLN
2	C1	37	GLN
2	C1	222	GLN
2	C2	37	GLN
2	C2	222	GLN
2	C3	37	GLN
2	C3	222	GLN
2	C4	37	GLN
2	C4	222	GLN
2	C5	37	GLN
2	C5	222	GLN

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Mol	Chain	Res	Type
2	C6	37	GLN
2	C6	222	GLN
2	C7	37	GLN
2	C7	222	GLN
2	C8	37	GLN
2	C8	222	GLN
2	C9	37	GLN
2	C9	222	GLN
2	D1	37	GLN
2	D1	98	GLN
2	D1	144	ASN
2	D2	37	GLN
2	D2	98	GLN
2	D2	144	ASN
2	D3	37	GLN
2	D3	98	GLN
2	D3	144	ASN
2	D4	37	GLN
2	D4	48	ASN
2	D4	98	GLN
2	D4	144	ASN
2	D5	37	GLN
2	D5	48	ASN
2	D5	98	GLN
2	D5	144	ASN
2	D6	37	GLN
2	D6	98	GLN
2	D6	144	ASN
2	D7	37	GLN
2	D7	98	GLN
2	D7	144	ASN
2	D8	37	GLN
2	D8	98	GLN
2	D8	144	ASN
2	D9	37	GLN
2	D9	98	GLN
2	D9	144	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

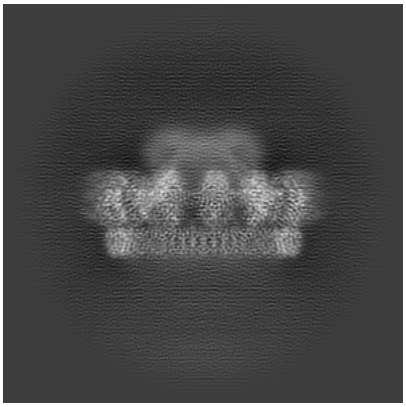
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-24769. These allow visual inspection of the internal detail of the map and identification of artifacts.

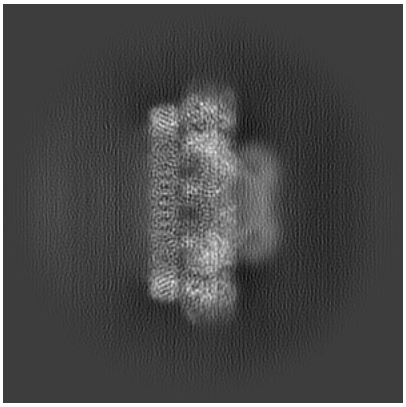
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

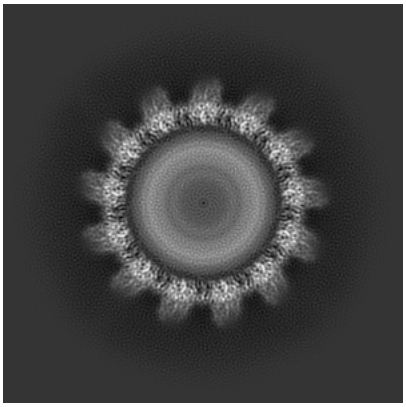
6.1.1 Primary map



X



Y

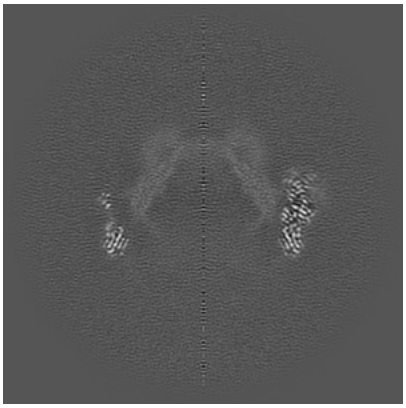


Z

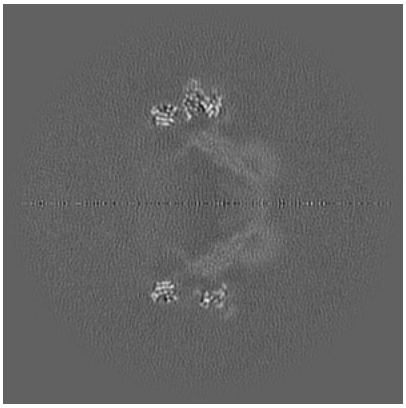
The images above show the map projected in three orthogonal directions.

6.2 Central slices

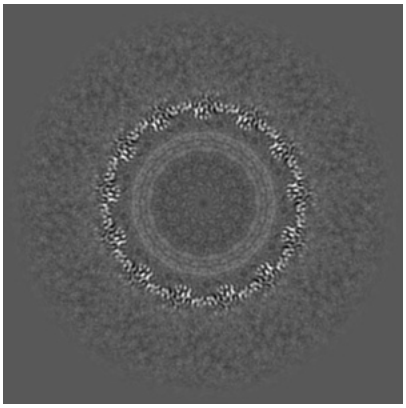
6.2.1 Primary map



X Index: 200



Y Index: 200

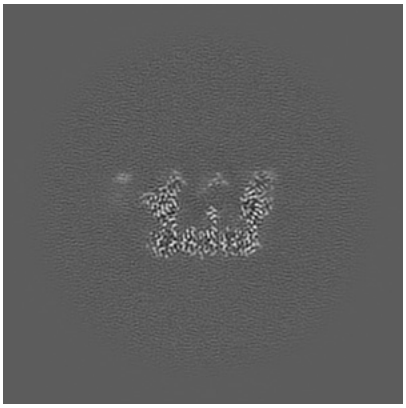


Z Index: 200

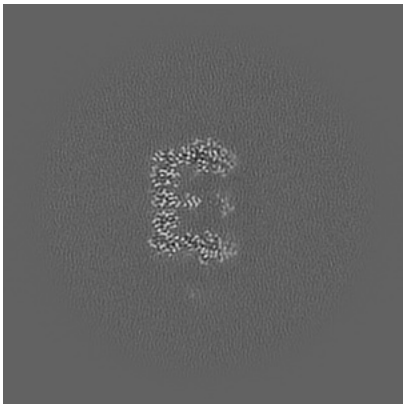
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

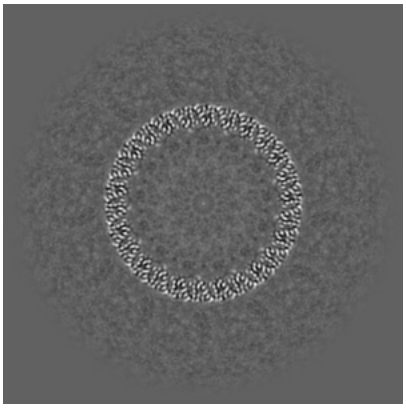
6.3.1 Primary map



X Index: 282



Y Index: 283

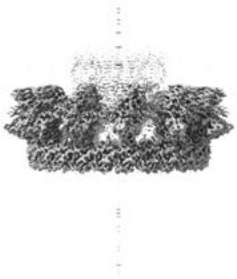


Z Index: 167

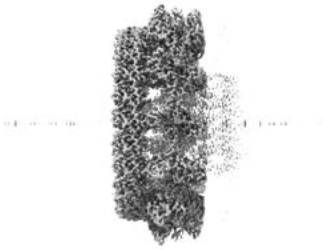
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

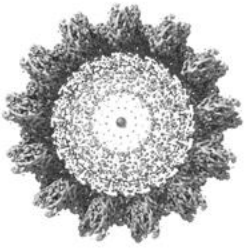
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

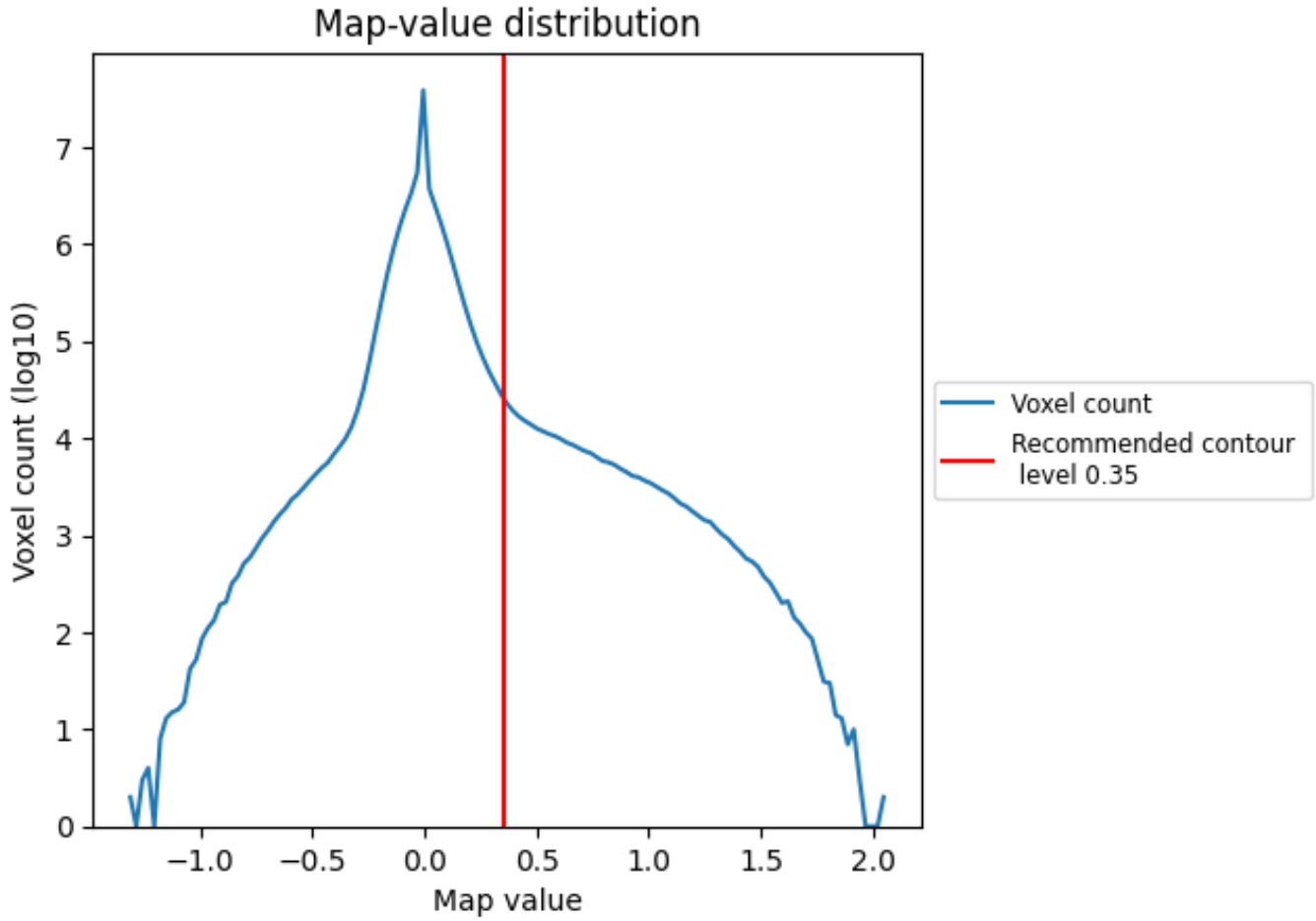
6.5 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

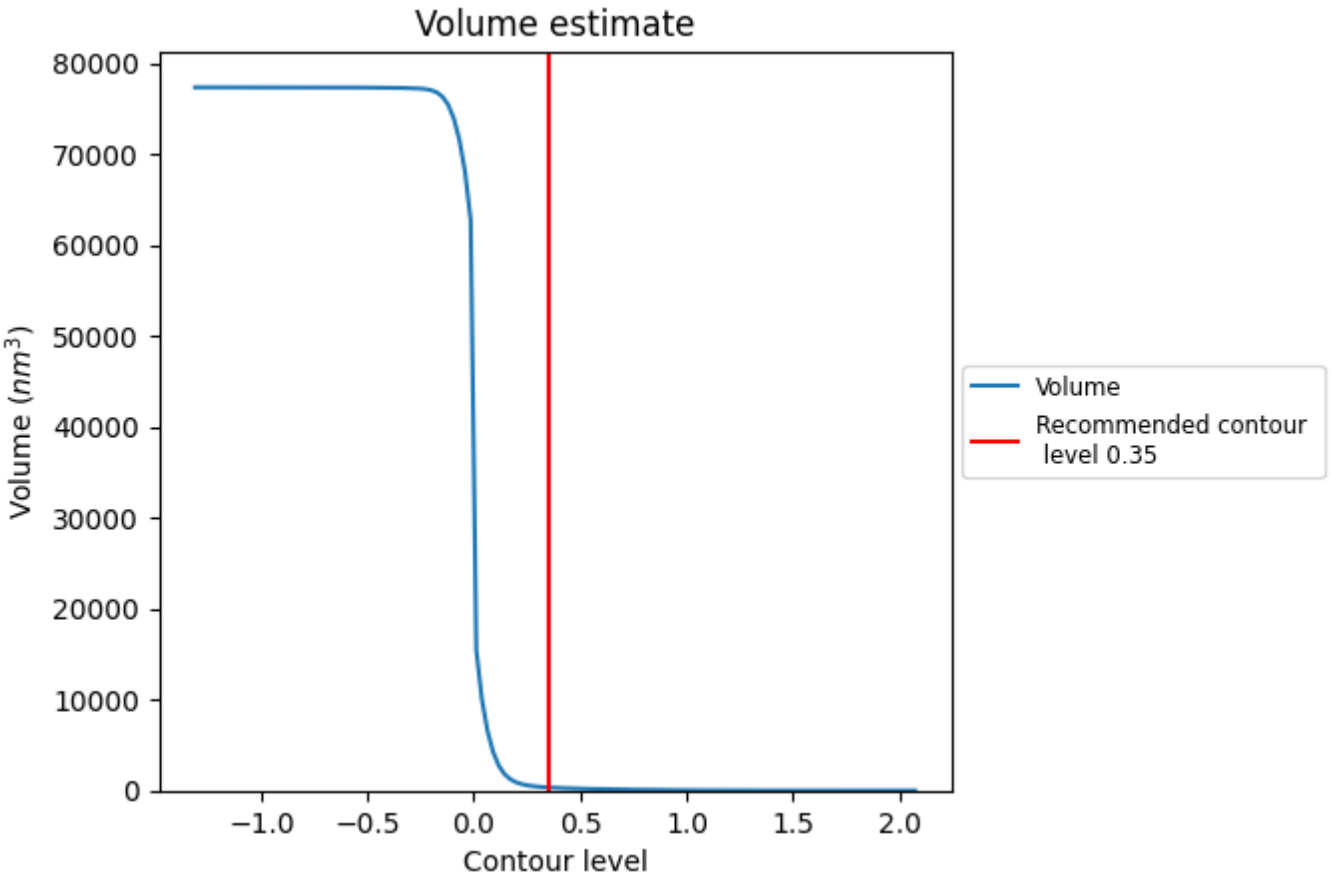
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

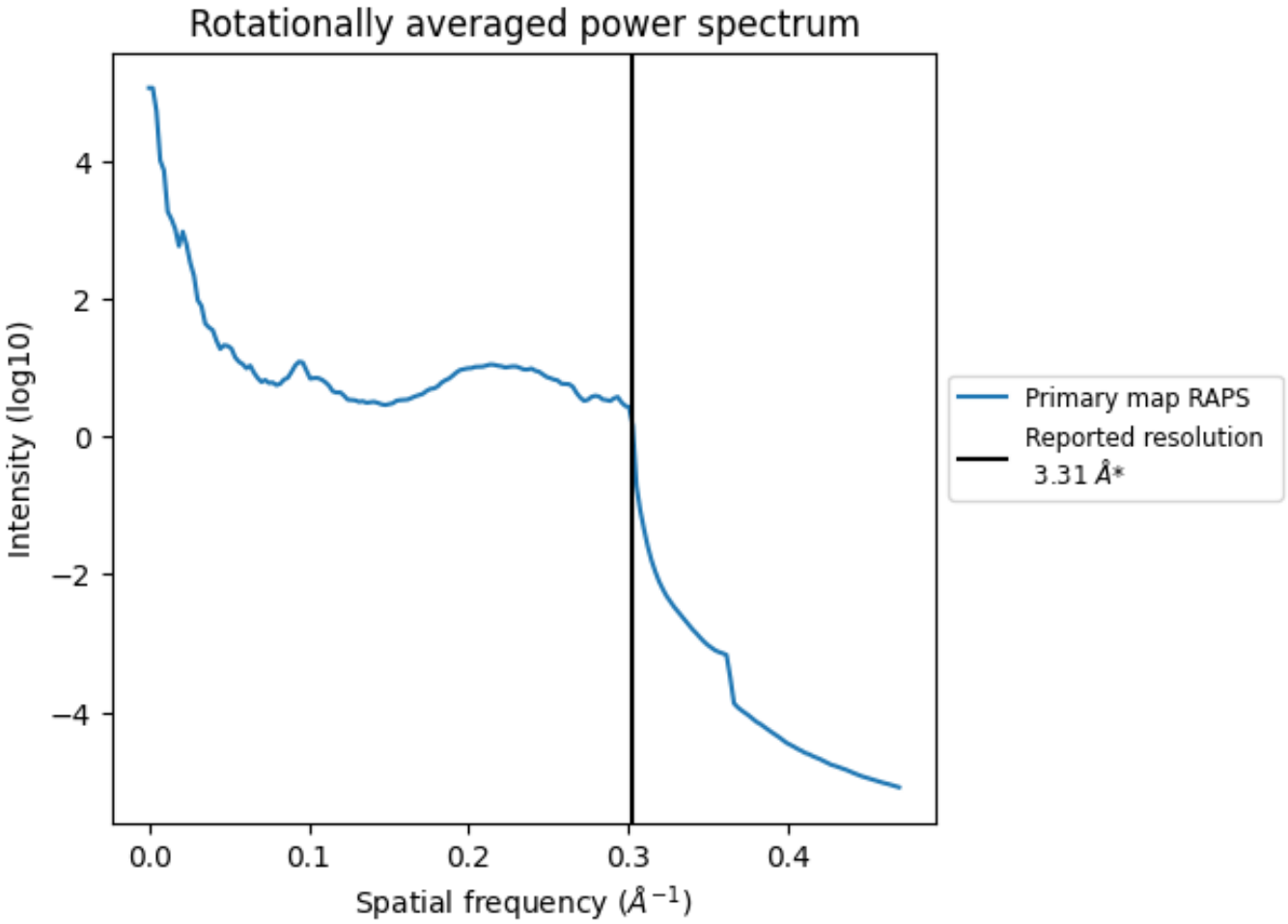
7.2 Volume estimate



The volume at the recommended contour level is 339 nm^3; this corresponds to an approximate mass of 306 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.302 Å^{-1}

8 Fourier-Shell correlation (i)

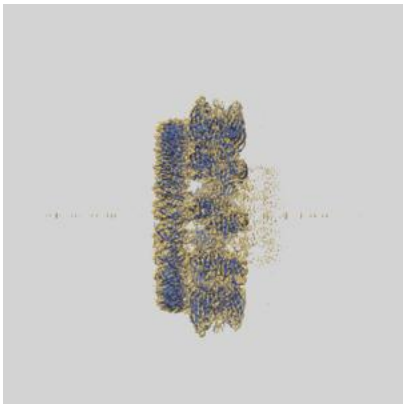
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

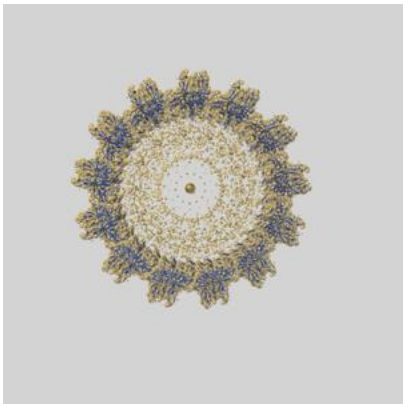
This section contains information regarding the fit between EMDB map EMD-24769 and PDB model 7SPB. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay

X



Y



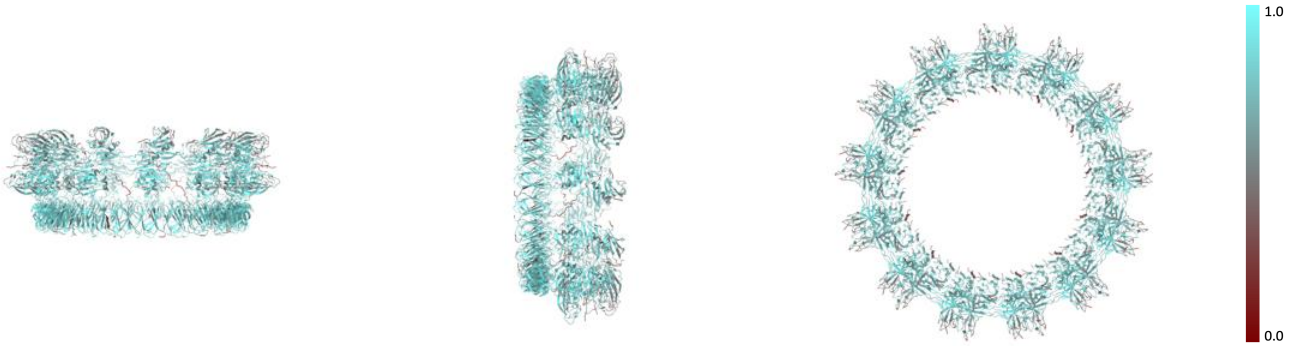
Z

The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model

This section was not generated.

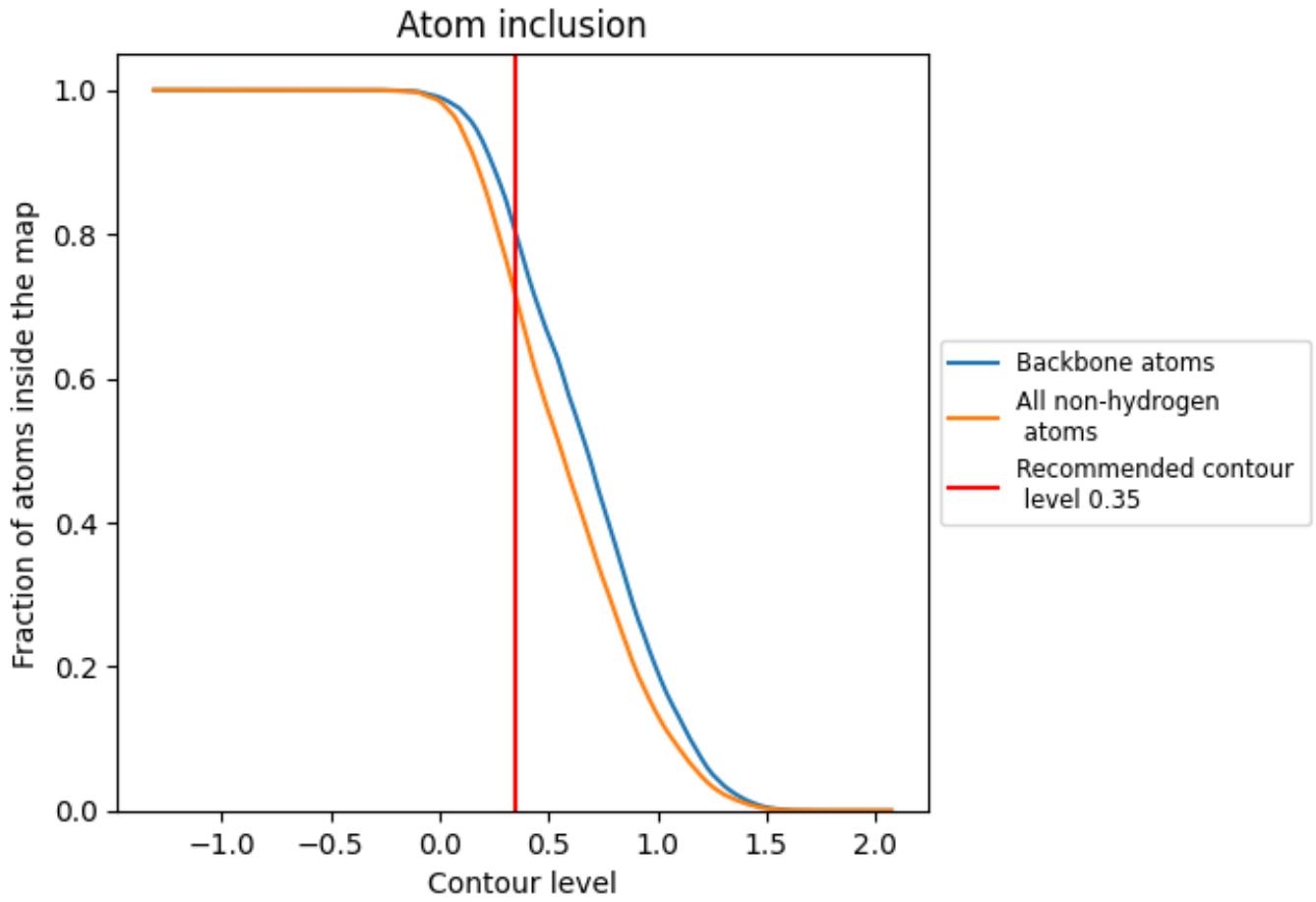
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.35).

9.4 Atom inclusion (i)



At the recommended contour level, 80% of all backbone atoms, 71% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	0.7126
A1	0.7045
A10	0.7021
A11	0.7069
A12	0.7116
A13	0.7069
A2	0.7069
A3	0.7069
A4	0.7069
A5	0.7021
A6	0.6998
A7	0.7116
A8	0.7092
A9	0.7116
B1	0.7010
B10	0.7093
B11	0.7134
B12	0.7093
B13	0.7155
B2	0.7113
B3	0.7093
B4	0.7072
B5	0.7052
B6	0.7113
B7	0.7113
B8	0.7093
B9	0.7031
C1	0.7795
C10	0.7807
C11	0.7814
C12	0.7801
C13	0.7776
C2	0.7795
C3	0.7776
C4	0.7795

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Chain	Atom inclusion
C5	0.7826
C6	0.7795
C7	0.7789
C8	0.7764
C9	0.7783
D1	0.6733
D10	0.6752
D11	0.6795
D12	0.6702
D13	0.6770
D2	0.6814
D3	0.6795
D4	0.6770
D5	0.6764
D6	0.6832
D7	0.6807
D8	0.6776
D9	0.6776
E1	0.2235
E10	0.2353
E11	0.2118
E12	0.2118
E13	0.2471
E2	0.2353
E3	0.2235
E4	0.2353
E5	0.2235
E6	0.2235
E7	0.2353
E8	0.2353
E9	0.2235
F1	0.6353
F10	0.6471
F11	0.6471
F12	0.6353
F13	0.6471
F2	0.6471
F3	0.6471
F4	0.6471
F5	0.6588
F6	0.6471
F7	0.6353

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Chain	Atom inclusion
F8	0.6353
F9	0.6471