



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 09:52 AM UTC

PDB ID : 7SPI / pdb_00007spi
EMDB ID : EMD-24771
Title : Models for C13 reconstruction of Outer Membrane Core Complex (OMCC) of Type IV Secretion System (T4SS) encoded by a plasmid overproducing TraV, TraK and TraB of pED208
Authors : Liu, X.; Khara, P.; Baker, M.L.; Christie, P.J.; Hu, B.
Deposited on : 2021-11-02
Resolution : 2.97 Å(reported)

This is a wwPDB EM Validation Summary 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:

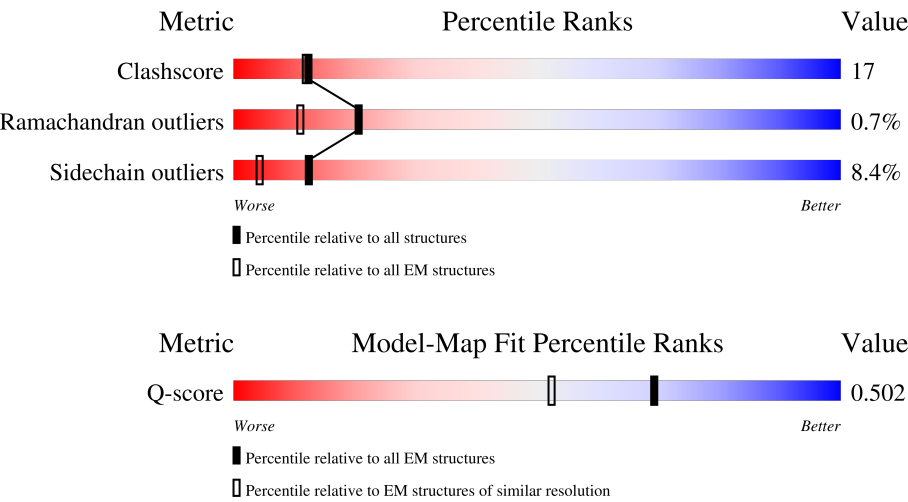
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.97 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.



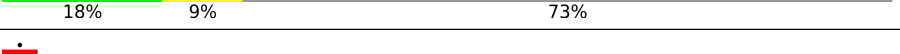
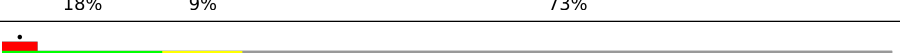
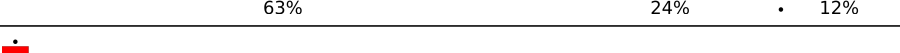
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13205 (2.47 - 3.47)

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 $\leq 5\%$. 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	
1	A10	204	
1	A11	204	
1	A12	204	

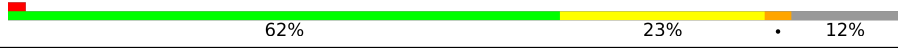
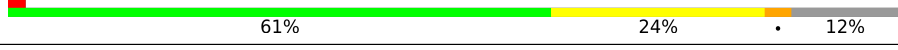
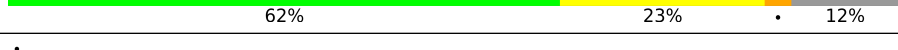
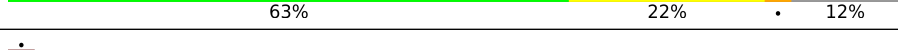
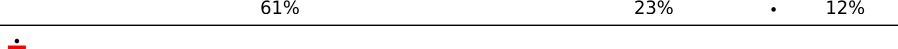
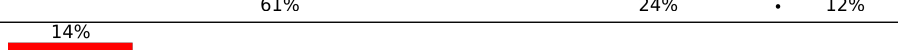
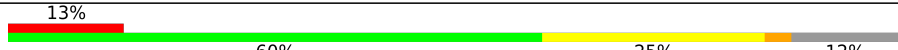
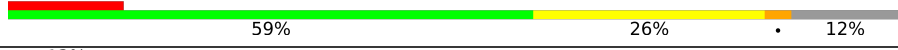
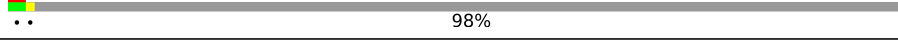
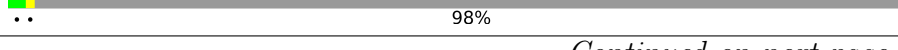
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Mol	Chain	Length	Quality of chain
1	A13	204	
1	A2	204	
1	A3	204	
1	A4	204	
1	A5	204	
1	A6	204	
1	A7	204	
1	A8	204	
1	A9	204	
1	B1	204	
1	B10	204	
1	B11	204	
1	B12	204	
1	B13	204	
1	B2	204	
1	B3	204	
1	B4	204	
1	B5	204	
1	B6	204	
1	B7	204	
1	B8	204	
1	B9	204	
2	C1	246	
2	C10	246	
2	C11	246	

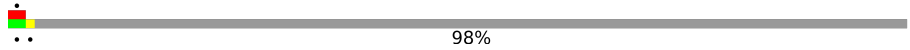
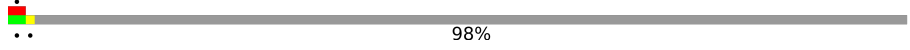
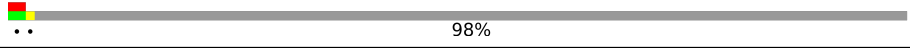
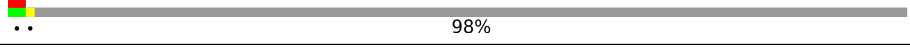
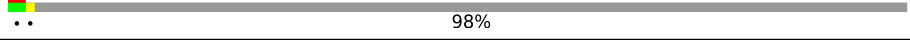
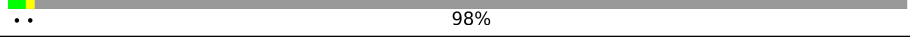
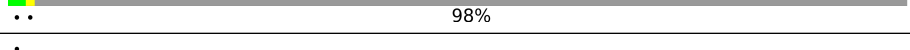
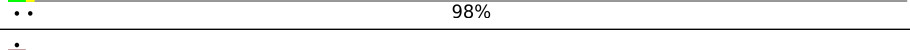
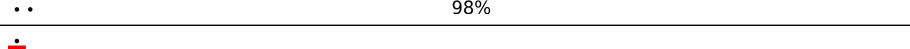
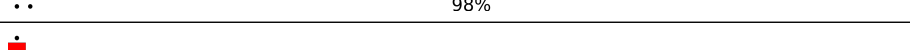
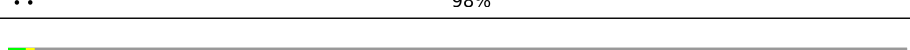
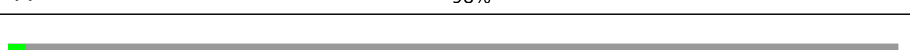
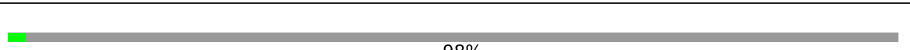
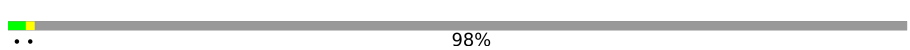
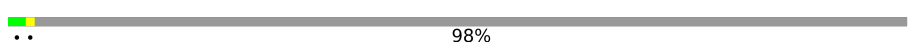
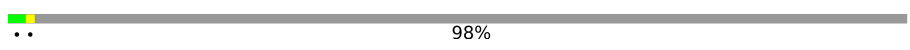
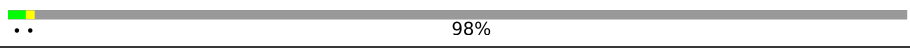
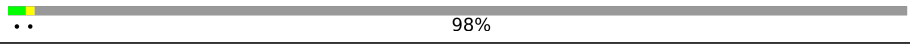
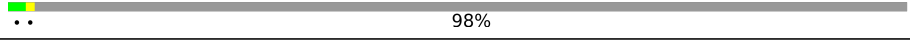
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Mol	Chain	Length	Quality of chain
2	C12	246	
2	C13	246	
2	C2	246	
2	C3	246	
2	C4	246	
2	C5	246	
2	C6	246	
2	C7	246	
2	C8	246	
2	C9	246	
2	D1	246	
2	D10	246	
2	D11	246	
2	D12	246	
2	D13	246	
2	D2	246	
2	D3	246	
2	D4	246	
2	D5	246	
2	D6	246	
2	D7	246	
2	D8	246	
2	D9	246	
3	E1	453	
3	E10	453	

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Mol	Chain	Length	Quality of chain
3	E11	453	 98%
3	E12	453	 98%
3	E13	453	 98%
3	E2	453	 98%
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

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 498	C 314	N 92	O 91	S 1	0	0
1	B6	65	Total 498	C 314	N 92	O 91	S 1	0	0
1	B7	65	Total 498	C 314	N 92	O 91	S 1	0	0
1	B8	65	Total 498	C 314	N 92	O 91	S 1	0	0
1	B9	65	Total 498	C 314	N 92	O 91	S 1	0	0
1	B10	65	Total 498	C 314	N 92	O 91	S 1	0	0
1	B11	65	Total 498	C 314	N 92	O 91	S 1	0	0
1	B12	65	Total 498	C 314	N 92	O 91	S 1	0	0
1	B13	65	Total 498	C 314	N 92	O 91	S 1	0	0

- Molecule 2 is a protein called TraK.

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

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

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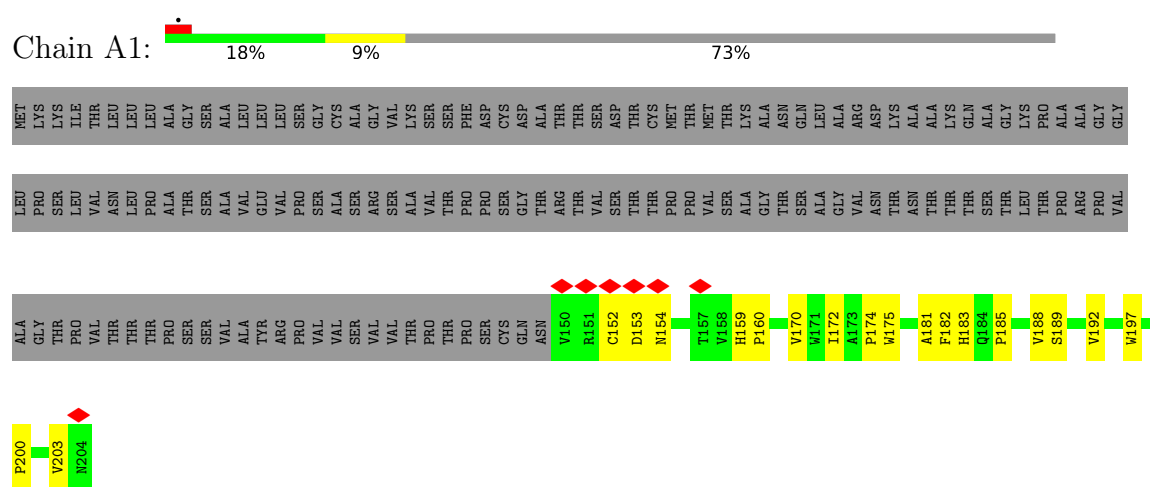
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Mol	Chain	Residues	Atoms					AltConf	Trace
3	F12	11	Total	C	N	O	S	0	0
			87	52	15	18	2		
3	F13	11	Total	C	N	O	S	0	0
			87	52	15	18	2		

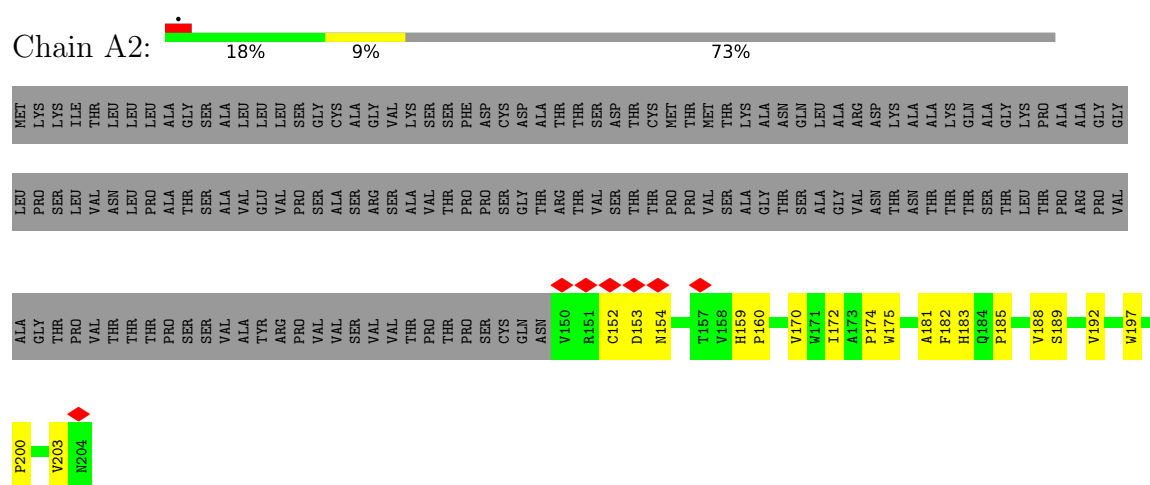
3 Residue-property plots

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.

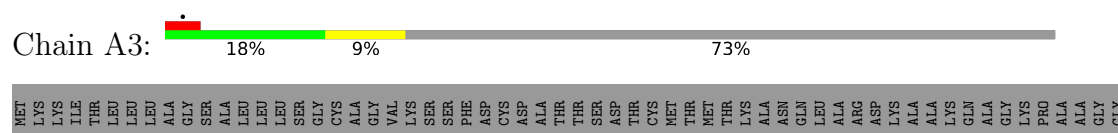
• Molecule 1: TraV

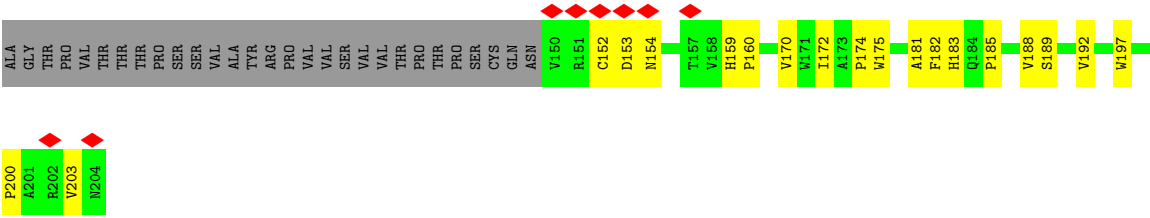


• Molecule 1: TraV

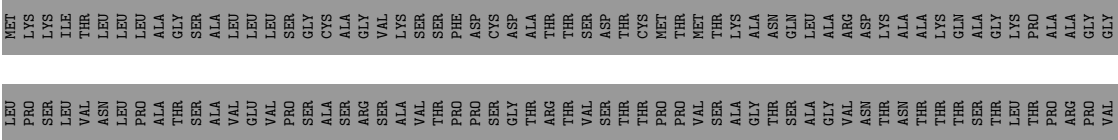


• Molecule 1: TraV

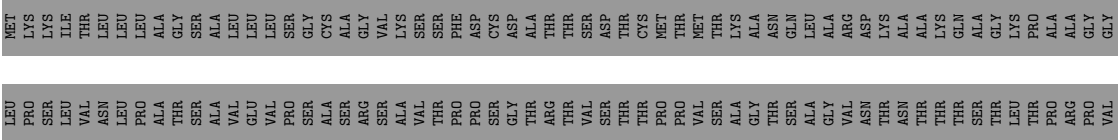




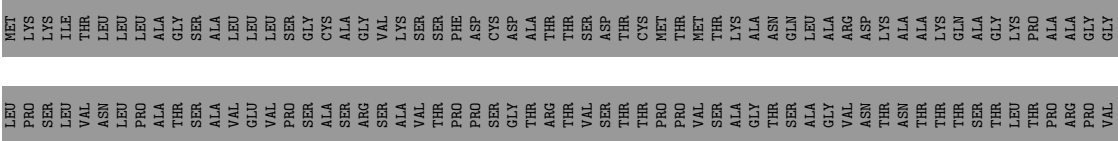
• Molecule 1: TraV

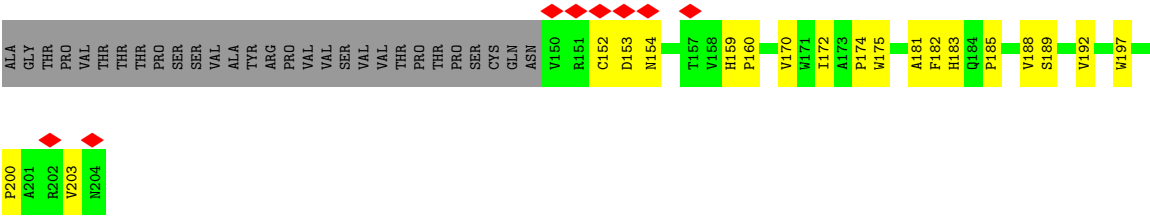


• Molecule 1: TraV



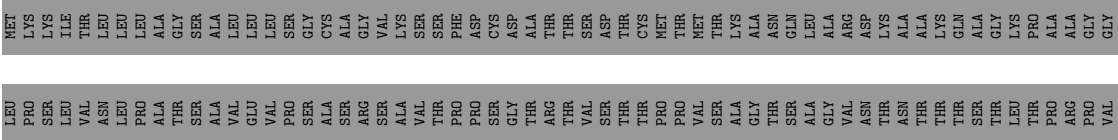
• Molecule 1: TraV





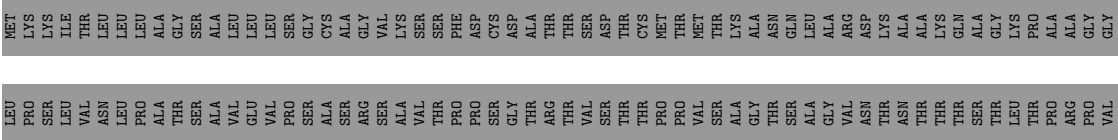
• Molecule 1: TraV

Chain A10: 18% 9% 73%



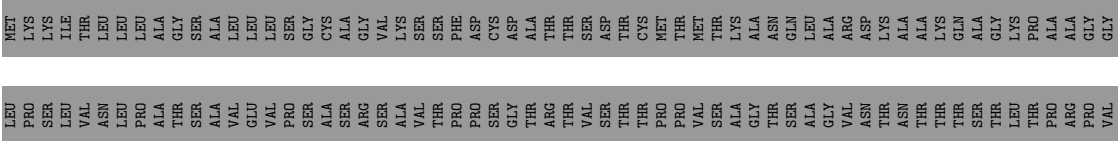
• Molecule 1: TraV

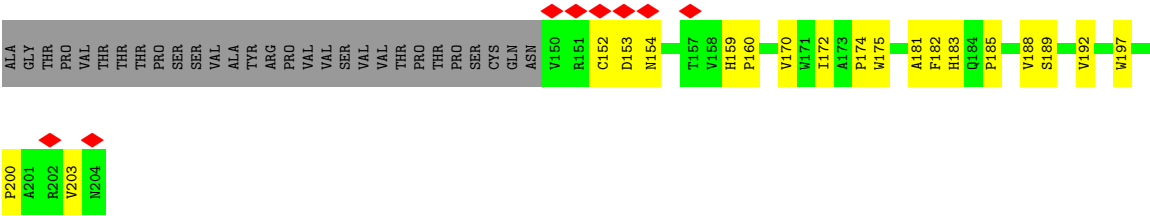
Chain A11: 18% 9% 73%



• Molecule 1: TraV

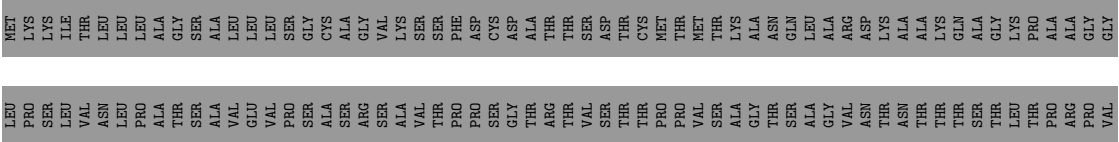
Chain A12: 18% 9% 73%





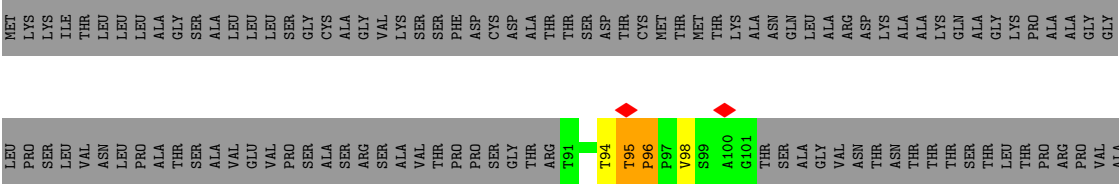
• Molecule 1: TraV

Chain A13: 18% 9% 73%



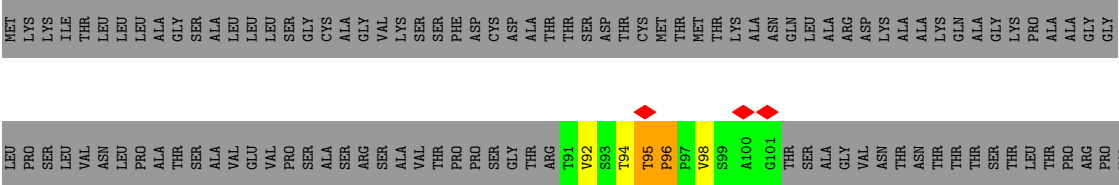
• Molecule 1: TraV

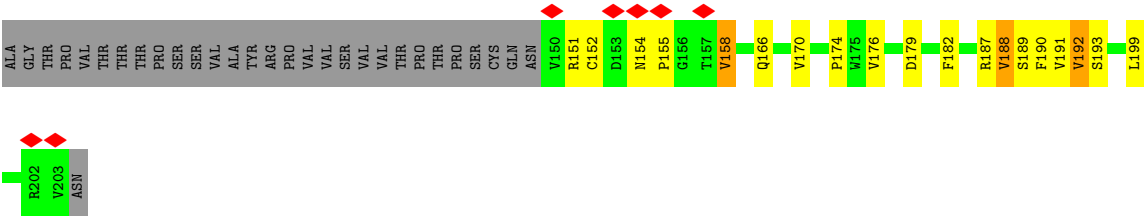
Chain B1: 21% 9% 68%



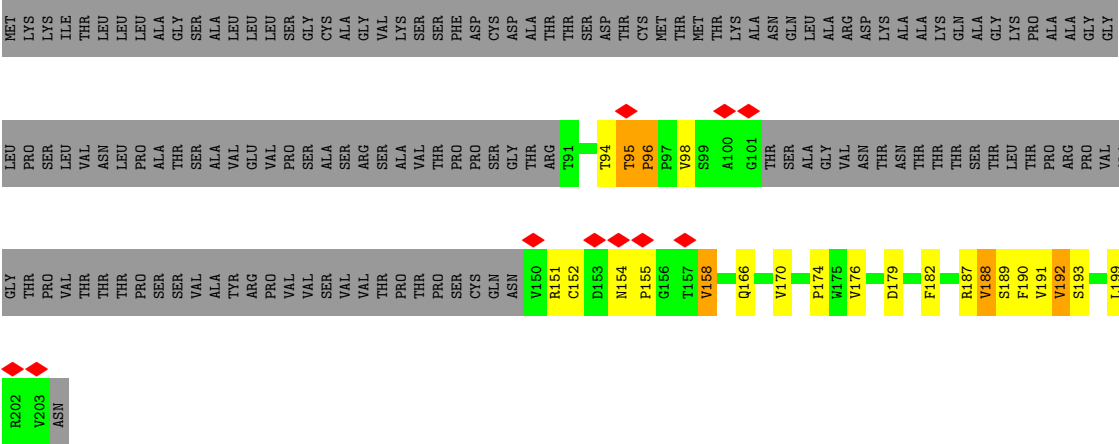
• Molecule 1: TraV

Chain B2: 5% 20% 9% 68%

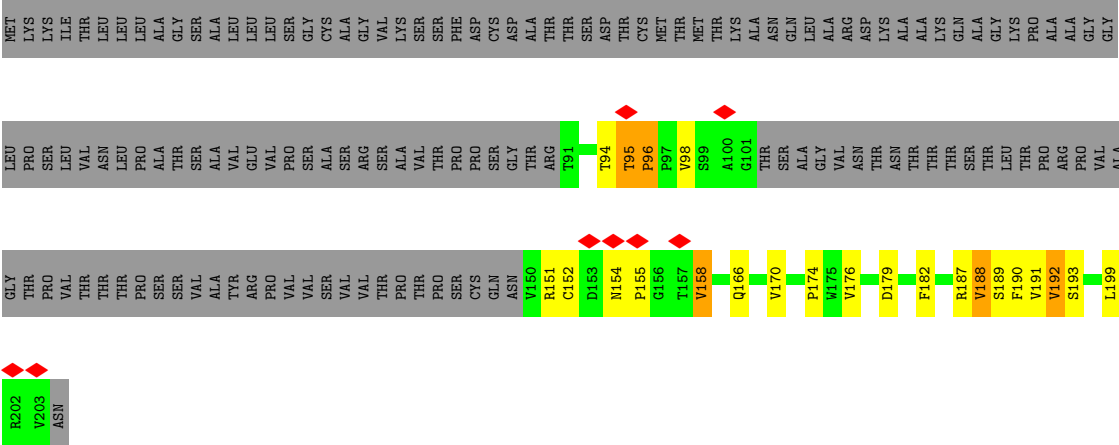




• Molecule 1: TraV

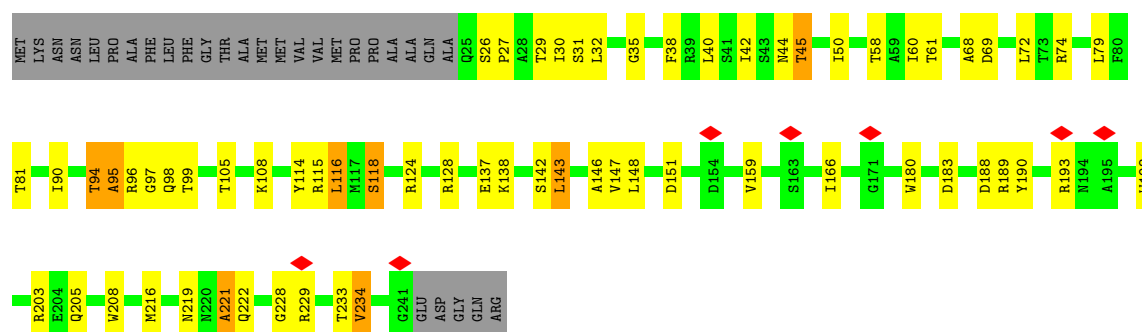


• Molecule 1: TraV

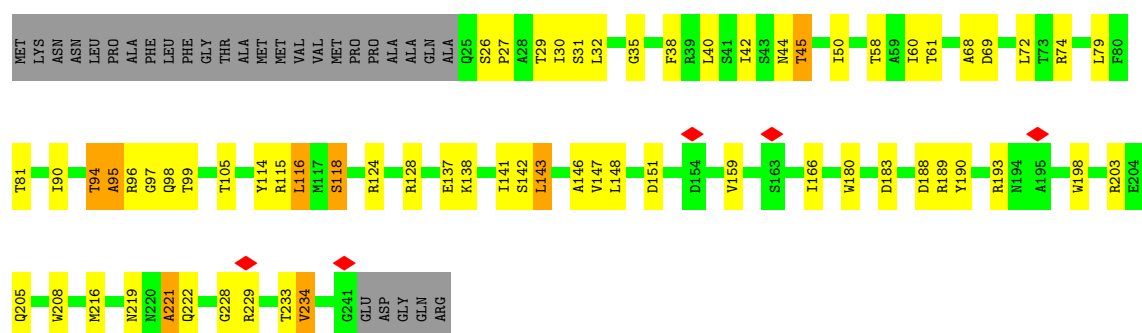


• Molecule 1: TraV

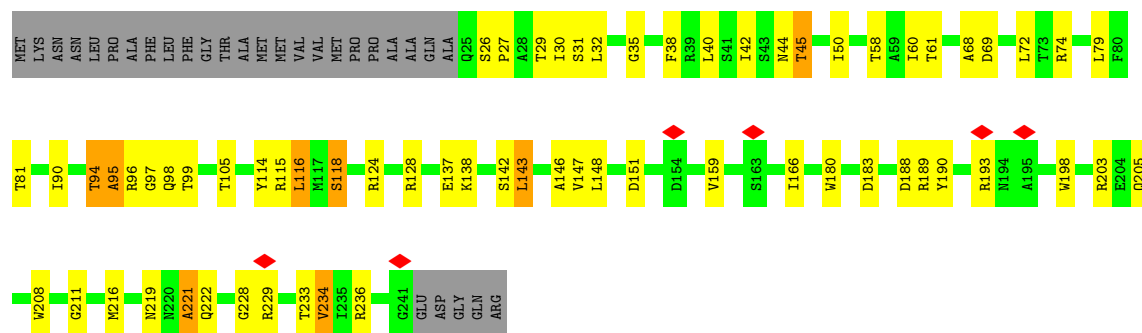




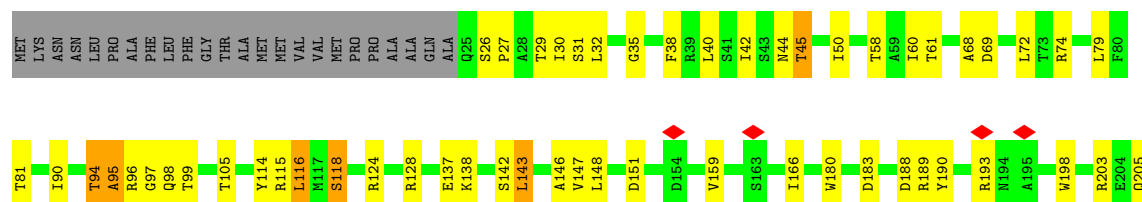
• Molecule 2: TraK

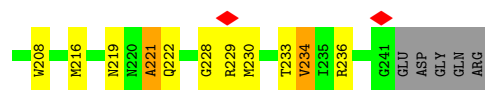


• Molecule 2: TraK

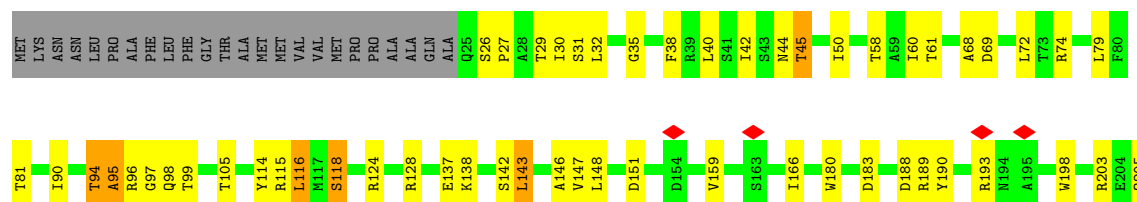


• Molecule 2: TraK

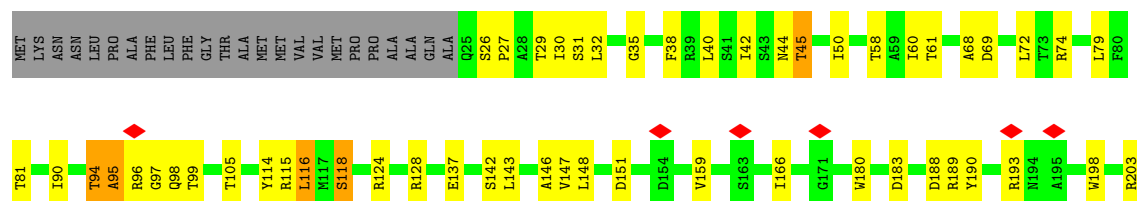




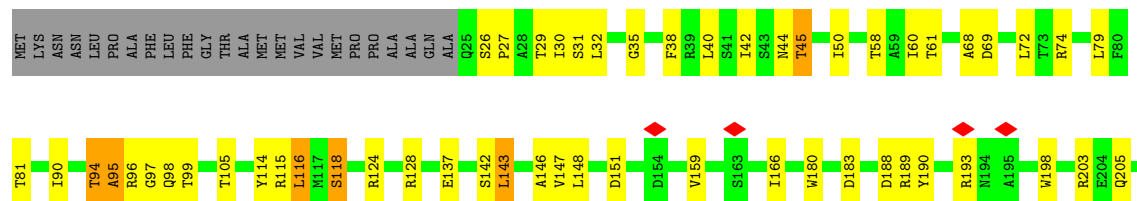
• Molecule 2: TraK



• Molecule 2: TraK

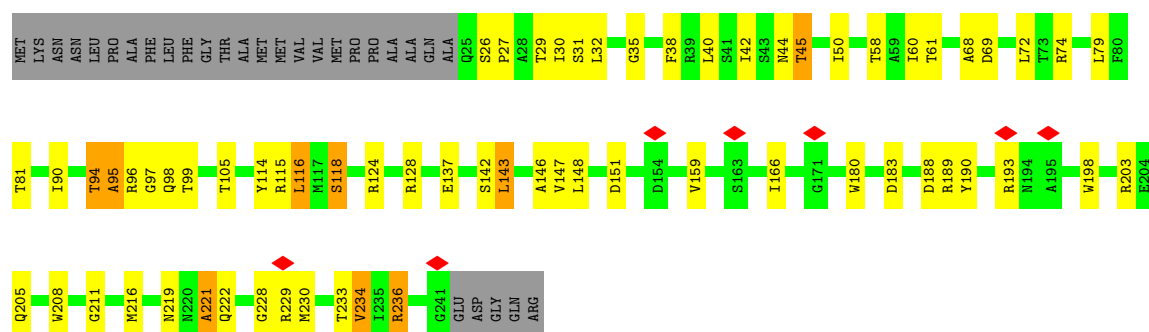


• Molecule 2: TraK



• Molecule 2: TraK





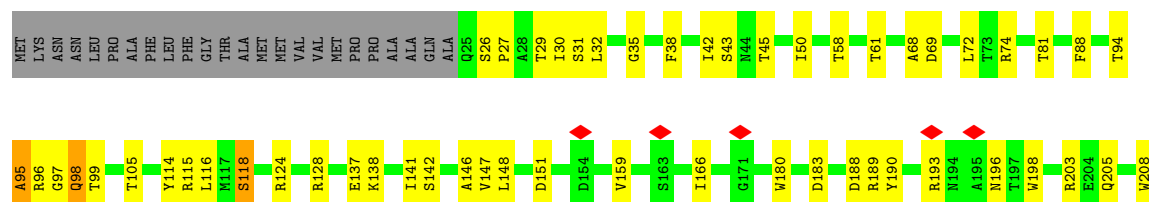
• Molecule 2: TraK

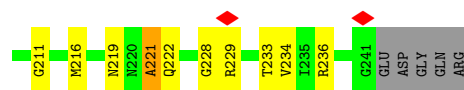


• Molecule 2: TraK

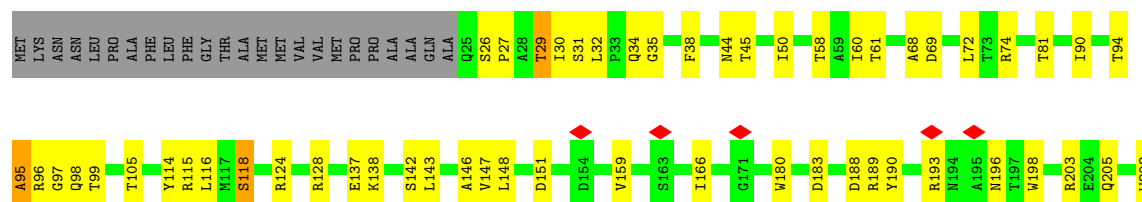


• Molecule 2: TraK

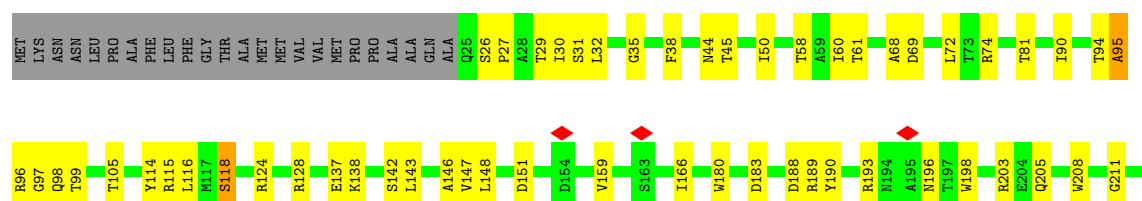




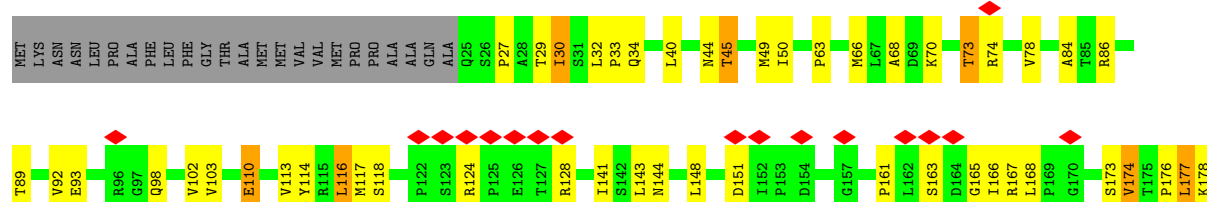
• Molecule 2: TraK



• Molecule 2: TraK

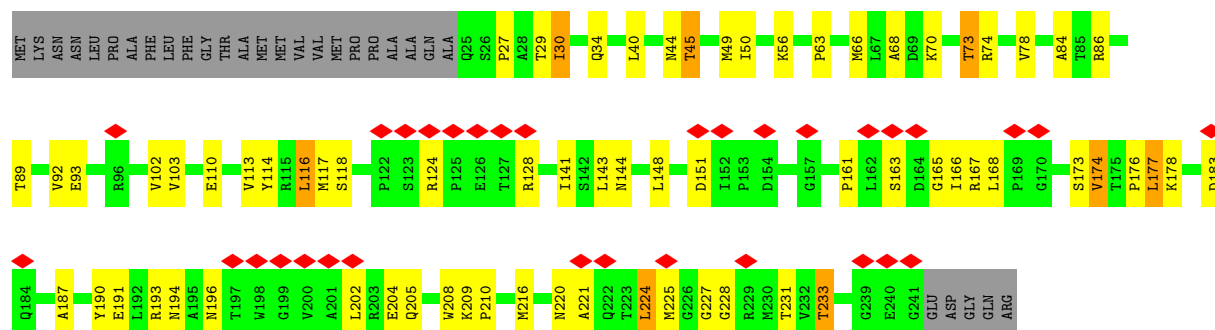


• Molecule 2: TraK

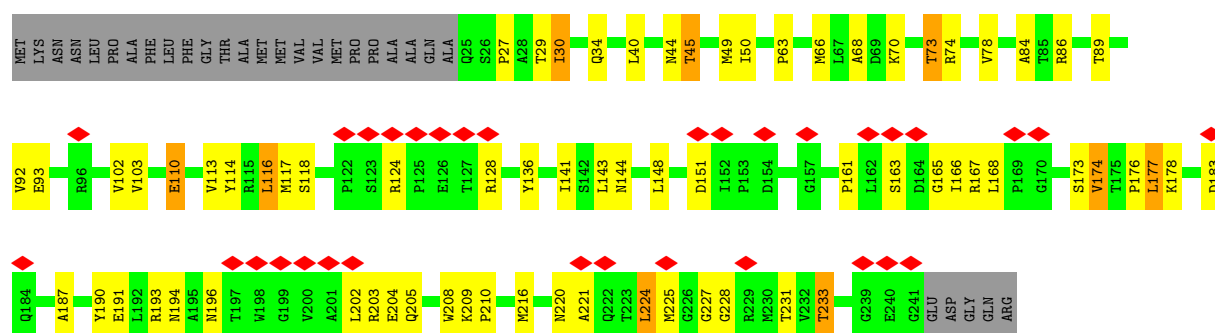


• Molecule 2: TraK

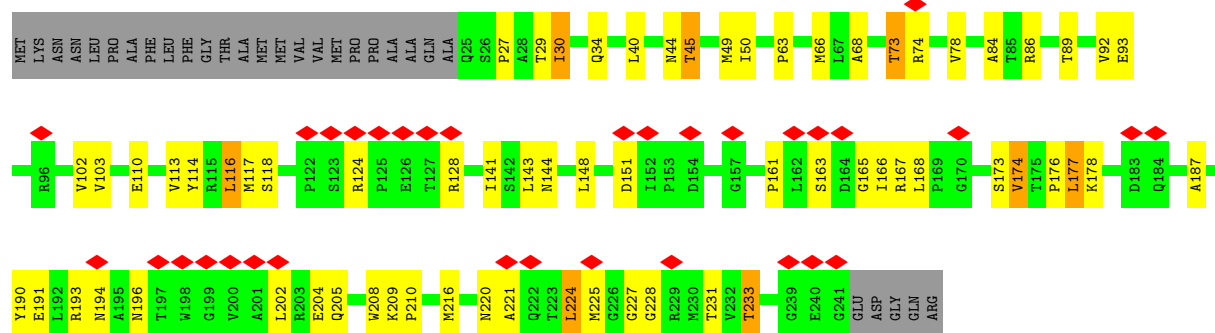




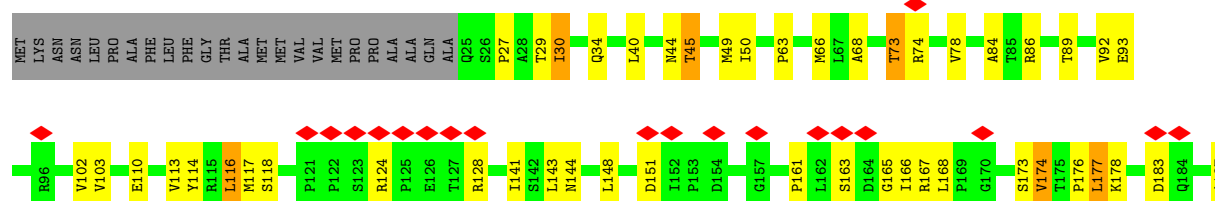
• Molecule 2: TraK

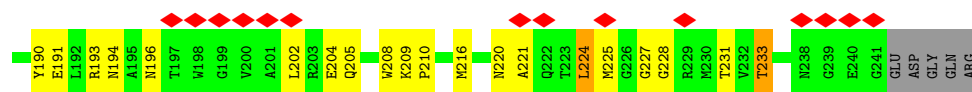


• Molecule 2: TraK

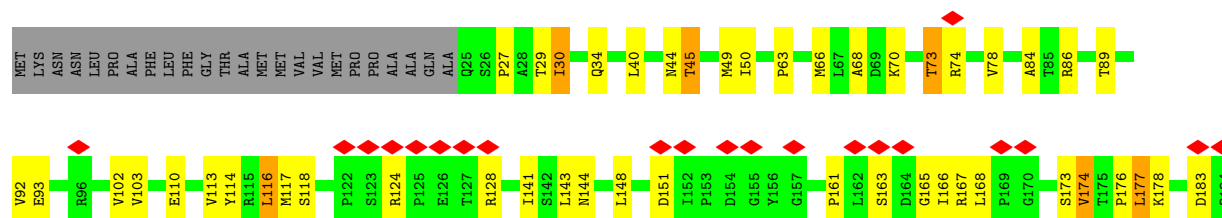


• Molecule 2: TraK

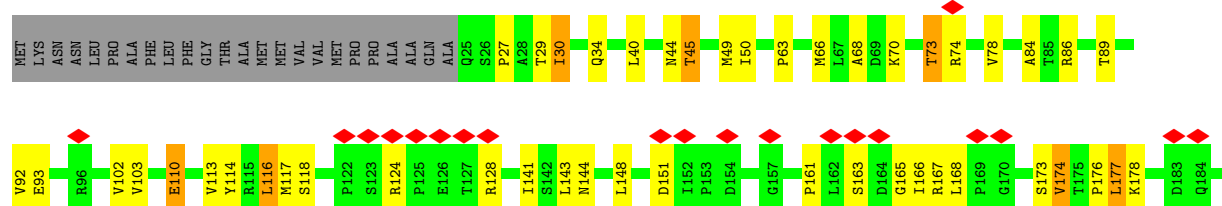




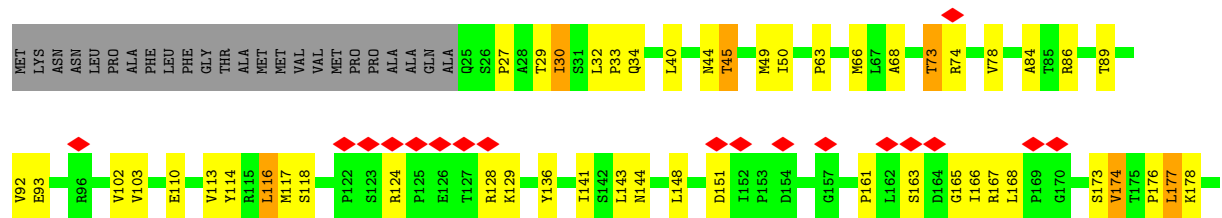
- Molecule 2: TraK



- Molecule 2: TraK



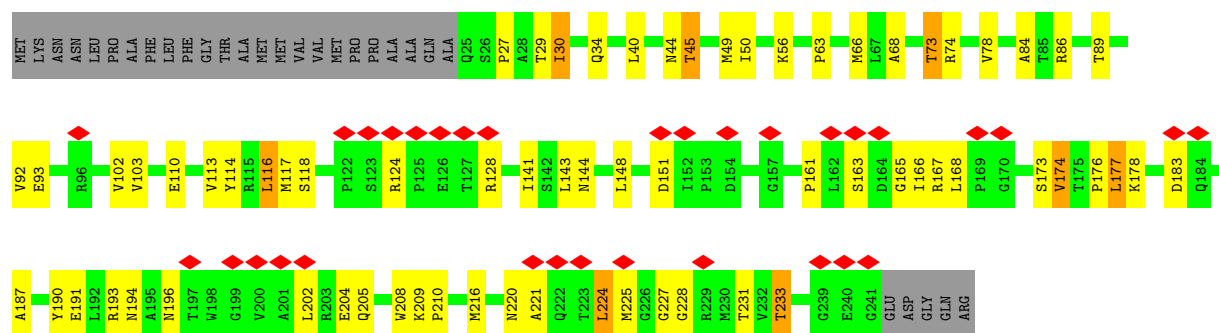
- Molecule 2: TraK



- Molecule 2: TraK

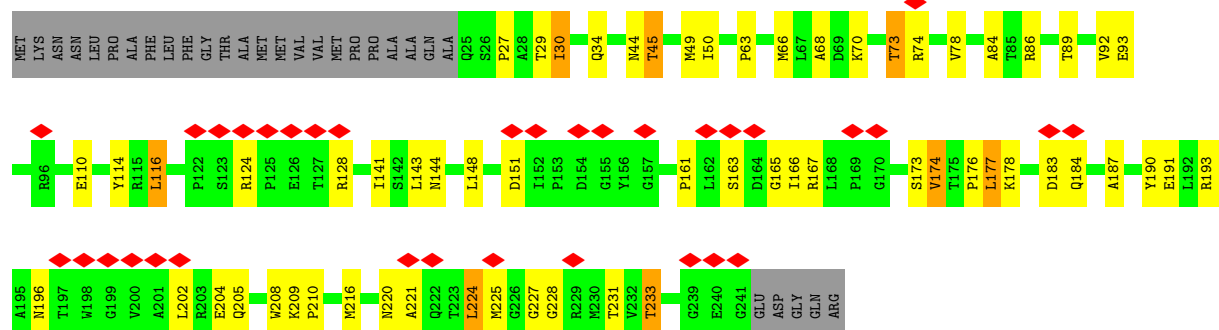


Chain D9: 



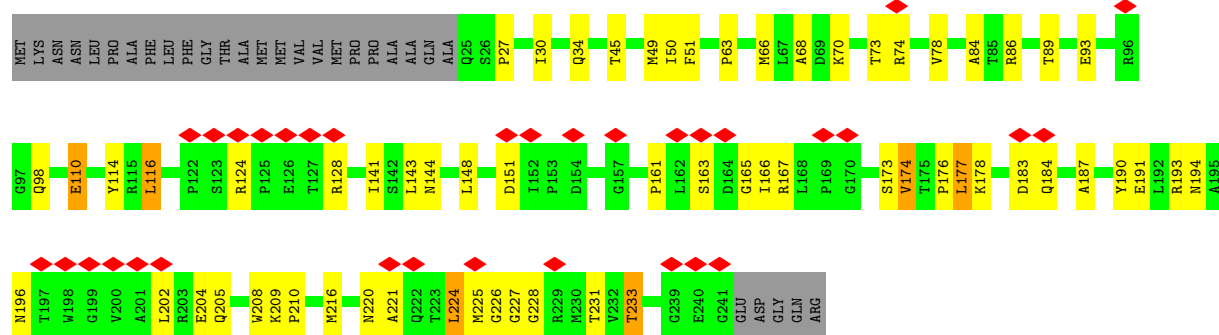
• Molecule 2: TraK

Chain D10: 



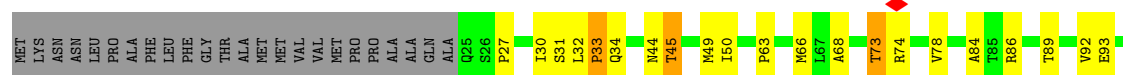
• Molecule 2: TraK

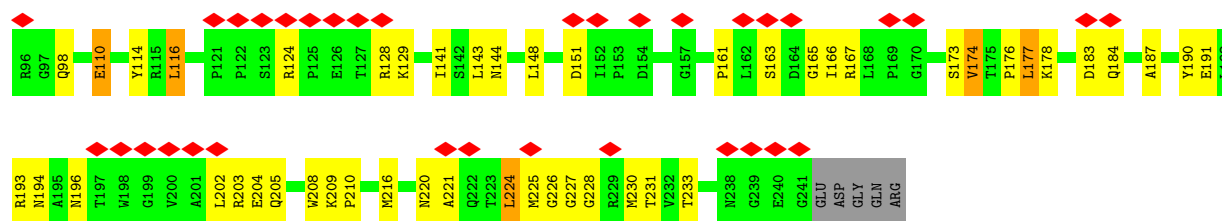
Chain D11: 



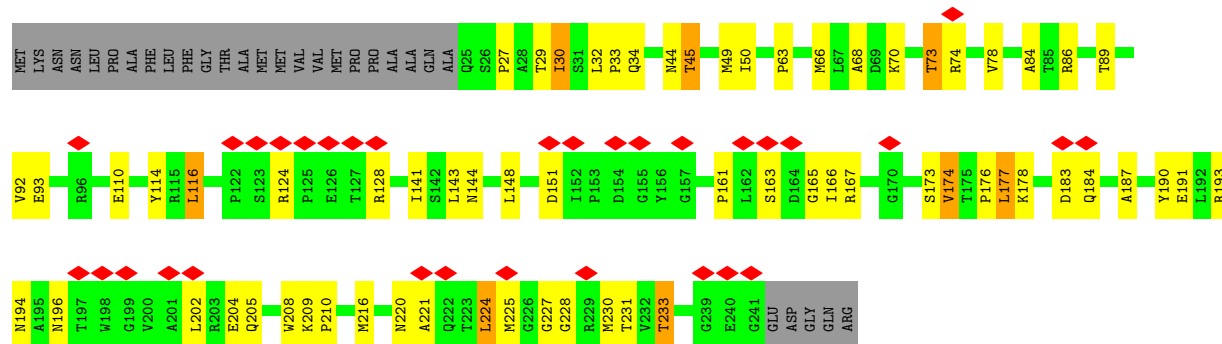
• Molecule 2: TraK

Chain D12: 

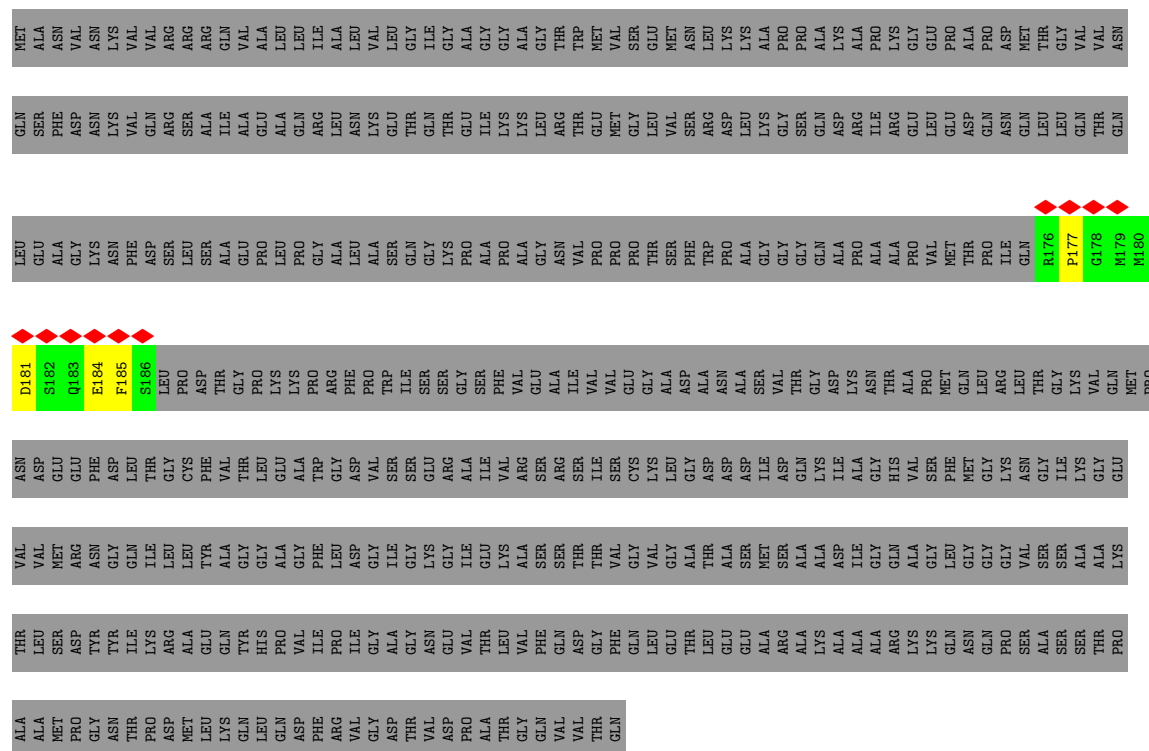




• Molecule 2: TraK



• Molecule 3: TraB



• Molecule 3: TraB

98%

D181	S182	Q183	E184	F185	S186	LEU	PRO	PRO	ASP	THR	GLY	PRO	LYS	LYS	PRO	ARG	PHE	PRO	TRP	ILE	SER	SER	GLY	PHE	VAL	GLU	ALA	ILE	VAL	VAL	GLU	GLY	ALA	ASP	ASN	ALA	SER	VAL	THR	GLY	ASP	LYS	ASN	THR	ALA	PRO	MET	GLN	LEU	ARG	LEU	THR	GLY	LYS	VAL	GLN	MET	PRO
------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 3: TraB

98%

D181	S182	Q183	E184	F185	S186	LEU	PRO	PRO	ASP	THR	GLY	PRO	LYS	LYS	PRO	ARG	PHE	PRO	TRP	ILE	SER	GLY	SER	PHE	VAL	GLU	ALA	ILE	VAL	VAL	GLU	GLY	ALA	ASP	ALA	ASN	ALA	SER	VAL	THR	GLY	ASP	LYS	ASN	THR	ALA	PRO	MET	GLN	LEU	ARG	LEU	THR	GLY	LYS	VAL	GLN	MET	PRO
------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Chain E4: 98%



Chain E6: 98%

Chain E7: 98%



Chain E8:

Chain E9:  98%



WORLD WIDE
PDB
PROTEIN DATA BANK

Chain E10: 98%

Chain E11: 98%

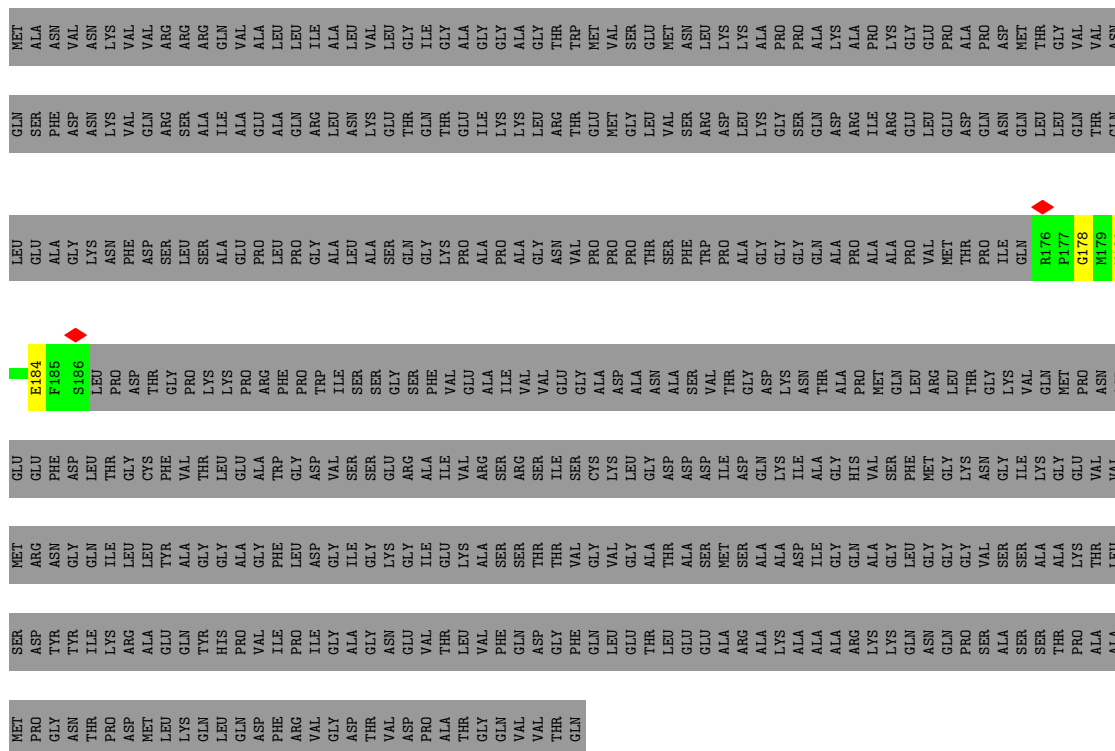


Chain E12: 98%



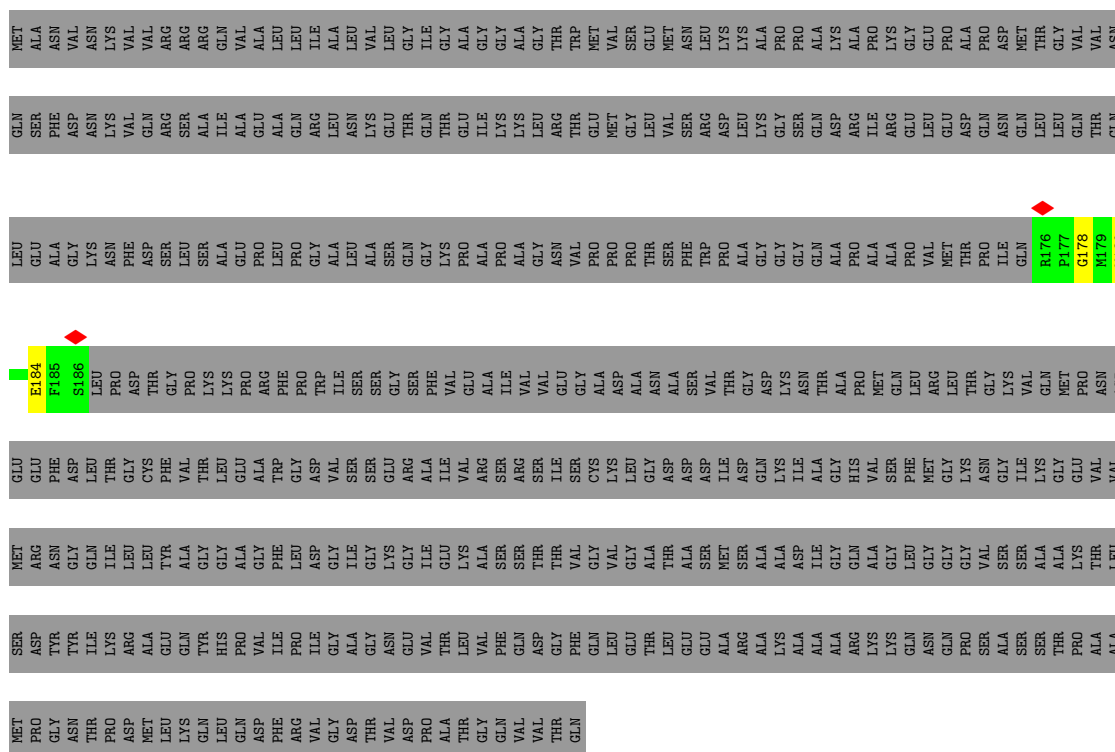
- Molecule 3: TraB

Chain F7: 98%



- Molecule 3: TraB

Chain F8: 98%



[illegible]

Chain F13: 98%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C13	Depositor
Number of particles used	148000	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 ($e^-/\text{\AA}^2$)	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	3.160	Depositor
Minimum map value	-1.854	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.060	Depositor
Recommended contour level	0.25	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 ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A1	0.52	0/451	1.05	3/622 (0.5%)
1	A10	0.52	0/451	1.05	3/622 (0.5%)
1	A11	0.52	0/451	1.05	3/622 (0.5%)
1	A12	0.52	0/451	1.05	3/622 (0.5%)
1	A13	0.52	0/451	1.05	3/622 (0.5%)
1	A2	0.52	0/451	1.05	3/622 (0.5%)
1	A3	0.52	0/451	1.05	3/622 (0.5%)
1	A4	0.52	0/451	1.05	3/622 (0.5%)
1	A5	0.52	0/451	1.04	3/622 (0.5%)
1	A6	0.52	0/451	1.04	3/622 (0.5%)
1	A7	0.52	0/451	1.05	3/622 (0.5%)
1	A8	0.52	0/451	1.05	3/622 (0.5%)
1	A9	0.52	0/451	1.05	3/622 (0.5%)
1	B1	0.59	0/514	1.06	6/710 (0.8%)
1	B10	0.59	0/514	1.06	6/710 (0.8%)
1	B11	0.59	0/514	1.06	6/710 (0.8%)
1	B12	0.59	0/514	1.06	6/710 (0.8%)
1	B13	0.59	0/514	1.06	6/710 (0.8%)
1	B2	0.59	0/514	1.06	6/710 (0.8%)
1	B3	0.59	0/514	1.06	6/710 (0.8%)
1	B4	0.59	0/514	1.06	6/710 (0.8%)
1	B5	0.59	0/514	1.06	6/710 (0.8%)
1	B6	0.59	0/514	1.06	6/710 (0.8%)
1	B7	0.59	0/514	1.06	6/710 (0.8%)
1	B8	0.59	0/514	1.06	6/710 (0.8%)
1	B9	0.59	0/514	1.06	6/710 (0.8%)
2	C1	0.83	1/1688 (0.1%)	1.03	8/2290 (0.3%)
2	C10	0.83	1/1688 (0.1%)	1.03	8/2290 (0.3%)
2	C11	0.83	1/1688 (0.1%)	1.03	8/2290 (0.3%)
2	C12	0.83	2/1688 (0.1%)	1.03	8/2290 (0.3%)
2	C13	0.83	1/1688 (0.1%)	1.03	8/2290 (0.3%)
2	C2	0.83	1/1688 (0.1%)	1.03	8/2290 (0.3%)
2	C3	0.83	1/1688 (0.1%)	1.03	8/2290 (0.3%)
2	C4	0.83	2/1688 (0.1%)	1.03	8/2290 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	C5	0.83	1/1688 (0.1%)	1.03	8/2290 (0.3%)
2	C6	0.83	2/1688 (0.1%)	1.03	8/2290 (0.3%)
2	C7	0.83	1/1688 (0.1%)	1.03	8/2290 (0.3%)
2	C8	0.83	2/1688 (0.1%)	1.03	8/2290 (0.3%)
2	C9	0.83	1/1688 (0.1%)	1.03	8/2290 (0.3%)
2	D1	0.61	0/1688	1.07	11/2290 (0.5%)
2	D10	0.62	0/1688	1.07	11/2290 (0.5%)
2	D11	0.61	0/1688	1.07	11/2290 (0.5%)
2	D12	0.61	0/1688	1.07	11/2290 (0.5%)
2	D13	0.62	0/1688	1.07	11/2290 (0.5%)
2	D2	0.62	0/1688	1.07	11/2290 (0.5%)
2	D3	0.62	0/1688	1.07	11/2290 (0.5%)
2	D4	0.62	0/1688	1.07	11/2290 (0.5%)
2	D5	0.61	0/1688	1.07	11/2290 (0.5%)
2	D6	0.61	0/1688	1.07	11/2290 (0.5%)
2	D7	0.62	0/1688	1.07	11/2290 (0.5%)
2	D8	0.62	0/1688	1.07	11/2290 (0.5%)
2	D9	0.62	0/1688	1.07	11/2290 (0.5%)
3	E1	0.66	0/88	0.83	0/115
3	E10	0.66	0/88	0.83	0/115
3	E11	0.67	0/88	0.83	0/115
3	E12	0.66	0/88	0.84	0/115
3	E13	0.66	0/88	0.83	0/115
3	E2	0.67	0/88	0.84	0/115
3	E3	0.66	0/88	0.83	0/115
3	E4	0.67	0/88	0.83	0/115
3	E5	0.67	0/88	0.83	0/115
3	E6	0.67	0/88	0.83	0/115
3	E7	0.67	0/88	0.83	0/115
3	E8	0.67	0/88	0.84	0/115
3	E9	0.66	0/88	0.84	0/115
3	F1	0.68	0/88	1.21	0/115
3	F10	0.68	0/88	1.20	0/115
3	F11	0.68	0/88	1.21	0/115
3	F12	0.68	0/88	1.20	0/115
3	F13	0.68	0/88	1.21	0/115
3	F2	0.68	0/88	1.20	0/115
3	F3	0.68	0/88	1.21	0/115
3	F4	0.68	0/88	1.20	0/115
3	F5	0.69	0/88	1.21	0/115
3	F6	0.68	0/88	1.21	0/115
3	F7	0.67	0/88	1.21	0/115
3	F8	0.68	0/88	1.21	0/115

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	F9	0.68	0/88	1.20	0/115
All	All	0.69	17/58721 (0.0%)	1.05	364/79846 (0.5%)

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C11	180	TRP	CA-C	-5.12	1.46	1.52
2	C7	180	TRP	CA-C	-5.09	1.46	1.52
2	C4	180	TRP	CA-C	-5.09	1.46	1.52
2	C5	180	TRP	CA-C	-5.09	1.46	1.52
2	C8	180	TRP	CA-C	-5.09	1.46	1.52

The worst 5 of 364 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D5	165	GLY	N-CA-C	9.81	124.51	112.73
2	D2	165	GLY	N-CA-C	9.80	124.50	112.73
2	D7	165	GLY	N-CA-C	9.80	124.49	112.73
2	D10	165	GLY	N-CA-C	9.80	124.49	112.73
2	D4	165	GLY	N-CA-C	9.79	124.48	112.73

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A1	436	0	414	26	0
1	A10	436	0	414	26	0
1	A11	436	0	414	26	0
1	A12	436	0	414	26	0
1	A13	436	0	414	26	0
1	A2	436	0	414	26	0
1	A3	436	0	414	25	0
1	A4	436	0	414	26	0
1	A5	436	0	414	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A6	436	0	414	26	0
1	A7	436	0	414	26	0
1	A8	436	0	414	26	0
1	A9	436	0	414	26	0
1	B1	498	0	478	67	0
1	B10	498	0	478	69	0
1	B11	498	0	478	69	0
1	B12	498	0	478	69	0
1	B13	498	0	478	69	0
1	B2	498	0	478	69	0
1	B3	498	0	478	69	0
1	B4	498	0	478	69	0
1	B5	498	0	478	68	0
1	B6	498	0	478	67	0
1	B7	498	0	478	69	0
1	B8	498	0	478	69	0
1	B9	498	0	478	69	0
2	C1	1654	0	1664	65	0
2	C10	1654	0	1664	64	0
2	C11	1654	0	1664	65	0
2	C12	1654	0	1664	64	0
2	C13	1654	0	1664	66	0
2	C2	1654	0	1664	65	0
2	C3	1654	0	1664	63	0
2	C4	1654	0	1664	65	0
2	C5	1654	0	1664	65	0
2	C6	1654	0	1664	64	0
2	C7	1654	0	1664	62	0
2	C8	1654	0	1664	63	0
2	C9	1654	0	1664	64	0
2	D1	1654	0	1664	61	0
2	D10	1654	0	1664	56	0
2	D11	1654	0	1664	59	0
2	D12	1654	0	1664	63	0
2	D13	1654	0	1664	59	0
2	D2	1654	0	1664	58	0
2	D3	1654	0	1664	59	0
2	D4	1654	0	1664	52	0
2	D5	1654	0	1664	54	0
2	D6	1654	0	1664	56	0
2	D7	1654	0	1664	57	0
2	D8	1654	0	1664	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D9	1654	0	1664	55	0
3	E1	87	0	77	25	0
3	E10	87	0	77	25	0
3	E11	87	0	77	25	0
3	E12	87	0	77	25	0
3	E13	87	0	77	25	0
3	E2	87	0	77	25	0
3	E3	87	0	77	23	0
3	E4	87	0	77	25	0
3	E5	87	0	77	25	0
3	E6	87	0	77	25	0
3	E7	87	0	77	25	0
3	E8	87	0	77	24	0
3	E9	87	0	77	24	0
3	F1	87	0	77	2	0
3	F10	87	0	77	2	0
3	F11	87	0	77	2	0
3	F12	87	0	77	2	0
3	F13	87	0	77	2	0
3	F2	87	0	77	2	0
3	F3	87	0	77	2	0
3	F4	87	0	77	2	0
3	F5	87	0	77	2	0
3	F6	87	0	77	2	0
3	F7	87	0	77	2	0
3	F8	87	0	77	2	0
3	F9	87	0	77	2	0
All	All	57408	0	56862	1945	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 17.

The worst 5 of 1945 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C10:72:LEU:HD22	3:E10:185:PHE:CB	1.77	1.15
2:C9:72:LEU:HD22	3:E9:185:PHE:CB	1.77	1.14
2:C11:72:LEU:HD22	3:E11:185:PHE:CB	1.77	1.14
2:C1:72:LEU:HD22	3:E1:185:PHE:CB	1.77	1.14
2:C2:72:LEU:HD22	3:E2:185:PHE:CB	1.77	1.14

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	21/204 (10%)	21 (100%)	0	0	100	100
1	A10	53/204 (26%)	53 (100%)	0	0	100	100
1	A11	53/204 (26%)	53 (100%)	0	0	100	100
1	A12	53/204 (26%)	53 (100%)	0	0	100	100
1	A13	53/204 (26%)	53 (100%)	0	0	100	100
1	A3	38/204 (19%)	38 (100%)	0	0	100	100
1	A4	53/204 (26%)	53 (100%)	0	0	100	100
1	A5	31/204 (15%)	31 (100%)	0	0	100	100
1	A6	50/204 (24%)	50 (100%)	0	0	100	100
1	A7	53/204 (26%)	53 (100%)	0	0	100	100
1	A8	53/204 (26%)	53 (100%)	0	0	100	100
1	A9	53/204 (26%)	53 (100%)	0	0	100	100
1	B1	61/204 (30%)	58 (95%)	2 (3%)	1 (2%)	7	31
1	B10	61/204 (30%)	58 (95%)	2 (3%)	1 (2%)	7	31
1	B11	61/204 (30%)	58 (95%)	2 (3%)	1 (2%)	7	31
1	B12	61/204 (30%)	58 (95%)	2 (3%)	1 (2%)	7	31
1	B13	61/204 (30%)	58 (95%)	2 (3%)	1 (2%)	7	31
1	B2	61/204 (30%)	58 (95%)	2 (3%)	1 (2%)	7	31
1	B3	61/204 (30%)	58 (95%)	2 (3%)	1 (2%)	7	31
1	B4	61/204 (30%)	58 (95%)	2 (3%)	1 (2%)	7	31
1	B5	61/204 (30%)	58 (95%)	2 (3%)	1 (2%)	7	31
1	B6	61/204 (30%)	58 (95%)	2 (3%)	1 (2%)	7	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B7	61/204 (30%)	58 (95%)	2 (3%)	1 (2%)	7	31
1	B8	61/204 (30%)	58 (95%)	2 (3%)	1 (2%)	7	31
1	B9	61/204 (30%)	58 (95%)	2 (3%)	1 (2%)	7	31
2	C1	215/246 (87%)	198 (92%)	16 (7%)	1 (0%)	24	58
2	C10	215/246 (87%)	197 (92%)	17 (8%)	1 (0%)	24	58
2	C11	215/246 (87%)	198 (92%)	16 (7%)	1 (0%)	24	58
2	C12	215/246 (87%)	198 (92%)	16 (7%)	1 (0%)	24	58
2	C13	215/246 (87%)	197 (92%)	17 (8%)	1 (0%)	24	58
2	C2	215/246 (87%)	197 (92%)	17 (8%)	1 (0%)	24	58
2	C3	215/246 (87%)	198 (92%)	16 (7%)	1 (0%)	24	58
2	C4	215/246 (87%)	197 (92%)	17 (8%)	1 (0%)	24	58
2	C5	215/246 (87%)	196 (91%)	18 (8%)	1 (0%)	24	58
2	C6	215/246 (87%)	198 (92%)	16 (7%)	1 (0%)	24	58
2	C7	215/246 (87%)	198 (92%)	16 (7%)	1 (0%)	24	58
2	C8	215/246 (87%)	197 (92%)	17 (8%)	1 (0%)	24	58
2	C9	215/246 (87%)	198 (92%)	16 (7%)	1 (0%)	24	58
2	D1	215/246 (87%)	202 (94%)	12 (6%)	1 (0%)	24	58
2	D10	215/246 (87%)	202 (94%)	12 (6%)	1 (0%)	24	58
2	D11	215/246 (87%)	202 (94%)	12 (6%)	1 (0%)	24	58
2	D12	215/246 (87%)	202 (94%)	12 (6%)	1 (0%)	24	58
2	D13	215/246 (87%)	202 (94%)	12 (6%)	1 (0%)	24	58
2	D2	215/246 (87%)	202 (94%)	12 (6%)	1 (0%)	24	58
2	D3	215/246 (87%)	202 (94%)	12 (6%)	1 (0%)	24	58
2	D4	215/246 (87%)	202 (94%)	12 (6%)	1 (0%)	24	58
2	D5	215/246 (87%)	202 (94%)	12 (6%)	1 (0%)	24	58
2	D6	215/246 (87%)	202 (94%)	12 (6%)	1 (0%)	24	58
2	D7	215/246 (87%)	202 (94%)	12 (6%)	1 (0%)	24	58
2	D8	215/246 (87%)	202 (94%)	12 (6%)	1 (0%)	24	58
2	D9	215/246 (87%)	202 (94%)	12 (6%)	1 (0%)	24	58
3	E1	9/453 (2%)	8 (89%)	0	1 (11%)	0	1
3	E10	9/453 (2%)	8 (89%)	0	1 (11%)	0	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	E11	9/453 (2%)	8 (89%)	0	1 (11%)	0	1
3	E12	9/453 (2%)	8 (89%)	0	1 (11%)	0	1
3	E13	9/453 (2%)	8 (89%)	0	1 (11%)	0	1
3	E2	9/453 (2%)	8 (89%)	0	1 (11%)	0	1
3	E3	9/453 (2%)	8 (89%)	0	1 (11%)	0	1
3	E4	9/453 (2%)	8 (89%)	0	1 (11%)	0	1
3	E5	9/453 (2%)	8 (89%)	0	1 (11%)	0	1
3	E6	9/453 (2%)	8 (89%)	0	1 (11%)	0	1
3	E7	9/453 (2%)	8 (89%)	0	1 (11%)	0	1
3	E8	9/453 (2%)	8 (89%)	0	1 (11%)	0	1
3	E9	9/453 (2%)	8 (89%)	0	1 (11%)	0	1
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	7181/23274 (31%)	6732 (94%)	397 (6%)	52 (1%)	20	50

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D1	196	ASN
2	D2	196	ASN
2	D3	196	ASN
2	D4	196	ASN
2	D5	196	ASN

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%)	47	74
1	A10	48/168 (29%)	47 (98%)	1 (2%)	47	74
1	A11	48/168 (29%)	47 (98%)	1 (2%)	47	74
1	A12	48/168 (29%)	47 (98%)	1 (2%)	47	74
1	A13	48/168 (29%)	47 (98%)	1 (2%)	47	74
1	A2	48/168 (29%)	47 (98%)	1 (2%)	47	74
1	A3	48/168 (29%)	47 (98%)	1 (2%)	47	74
1	A4	48/168 (29%)	47 (98%)	1 (2%)	47	74
1	A5	48/168 (29%)	47 (98%)	1 (2%)	47	74
1	A6	48/168 (29%)	47 (98%)	1 (2%)	47	74
1	A7	48/168 (29%)	47 (98%)	1 (2%)	47	74
1	A8	48/168 (29%)	47 (98%)	1 (2%)	47	74
1	A9	48/168 (29%)	47 (98%)	1 (2%)	47	74
1	B1	56/168 (33%)	51 (91%)	5 (9%)	9	32
1	B10	56/168 (33%)	55 (98%)	1 (2%)	51	76
1	B11	56/168 (33%)	54 (96%)	2 (4%)	31	63
1	B12	56/168 (33%)	55 (98%)	1 (2%)	51	76
1	B13	56/168 (33%)	55 (98%)	1 (2%)	51	76
1	B2	56/168 (33%)	51 (91%)	5 (9%)	9	32
1	B3	56/168 (33%)	51 (91%)	5 (9%)	9	32
1	B4	56/168 (33%)	51 (91%)	5 (9%)	9	32
1	B5	56/168 (33%)	51 (91%)	5 (9%)	9	32
1	B6	56/168 (33%)	51 (91%)	5 (9%)	9	32
1	B7	56/168 (33%)	51 (91%)	5 (9%)	9	32
1	B8	56/168 (33%)	51 (91%)	5 (9%)	9	32
1	B9	56/168 (33%)	51 (91%)	5 (9%)	9	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C1	173/195 (89%)	157 (91%)	16 (9%)	8	31
2	C10	173/195 (89%)	164 (95%)	9 (5%)	21	53
2	C11	173/195 (89%)	163 (94%)	10 (6%)	18	49
2	C12	173/195 (89%)	162 (94%)	11 (6%)	16	45
2	C13	173/195 (89%)	164 (95%)	9 (5%)	21	53
2	C2	173/195 (89%)	157 (91%)	16 (9%)	8	31
2	C3	173/195 (89%)	157 (91%)	16 (9%)	8	31
2	C4	173/195 (89%)	157 (91%)	16 (9%)	8	31
2	C5	173/195 (89%)	157 (91%)	16 (9%)	8	31
2	C6	173/195 (89%)	157 (91%)	16 (9%)	8	31
2	C7	173/195 (89%)	157 (91%)	16 (9%)	8	31
2	C8	173/195 (89%)	157 (91%)	16 (9%)	8	31
2	C9	173/195 (89%)	157 (91%)	16 (9%)	8	31
2	D1	173/195 (89%)	151 (87%)	22 (13%)	4	18
2	D10	173/195 (89%)	157 (91%)	16 (9%)	8	31
2	D11	173/195 (89%)	162 (94%)	11 (6%)	16	45
2	D12	173/195 (89%)	157 (91%)	16 (9%)	8	31
2	D13	173/195 (89%)	157 (91%)	16 (9%)	8	31
2	D2	173/195 (89%)	151 (87%)	22 (13%)	4	18
2	D3	173/195 (89%)	151 (87%)	22 (13%)	4	18
2	D4	173/195 (89%)	151 (87%)	22 (13%)	4	18
2	D5	173/195 (89%)	151 (87%)	22 (13%)	4	18
2	D6	173/195 (89%)	151 (87%)	22 (13%)	4	18
2	D7	173/195 (89%)	151 (87%)	22 (13%)	4	18
2	D8	173/195 (89%)	151 (87%)	22 (13%)	4	18
2	D9	173/195 (89%)	151 (87%)	22 (13%)	4	18
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	9 (90%)	1 (10%)	7	27
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
3	F2	10/353 (3%)	9 (90%)	1 (10%)	7	27
3	F3	10/353 (3%)	9 (90%)	1 (10%)	7	27
3	F4	10/353 (3%)	9 (90%)	1 (10%)	7	27
3	F5	10/353 (3%)	9 (90%)	1 (10%)	7	27
3	F6	10/353 (3%)	9 (90%)	1 (10%)	7	27
3	F7	10/353 (3%)	9 (90%)	1 (10%)	7	27
3	F8	10/353 (3%)	9 (90%)	1 (10%)	7	27
3	F9	10/353 (3%)	9 (90%)	1 (10%)	7	27
All	All	6110/18616 (33%)	5598 (92%)	512 (8%)	12	35

5 of 512 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D11	116	LEU
2	D12	78	VAL
2	D11	110	GLU
2	C9	45	THR
2	C8	229	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
2	D3	144	ASN
2	D7	222	GLN
2	D3	222	GLN
2	D5	222	GLN
2	D9	144	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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.

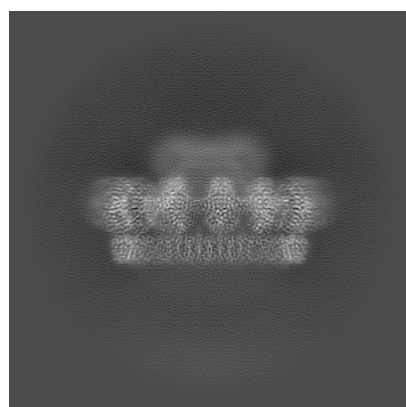
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24771. These allow visual inspection of the internal detail of the map and identification of artifacts.

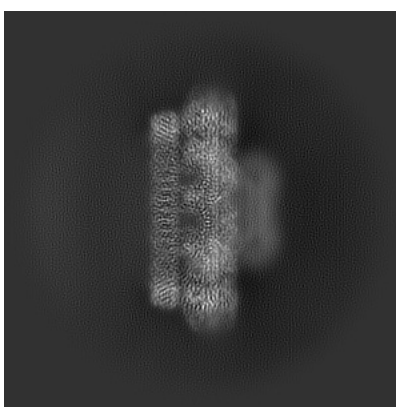
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

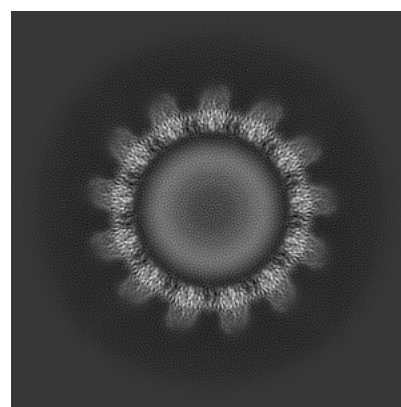
6.1.1 Primary map



X



Y

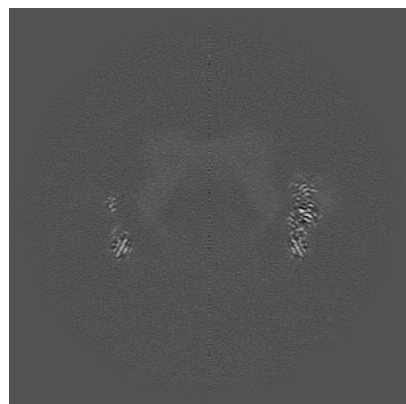


Z

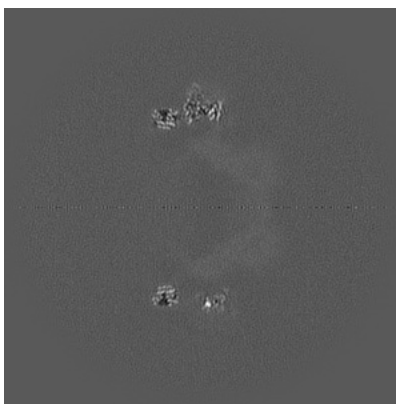
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

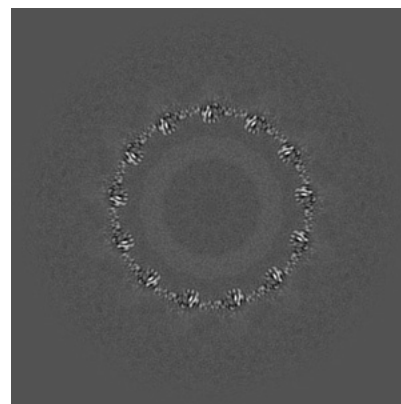
6.2.1 Primary map



X Index: 200



Y Index: 200

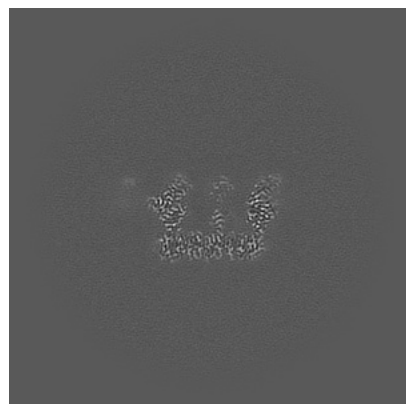


Z Index: 200

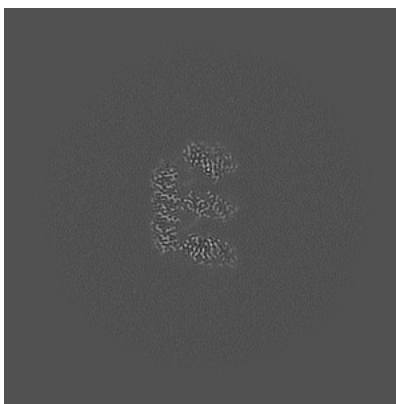
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

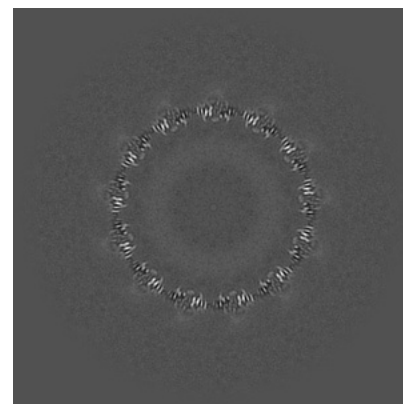
6.3.1 Primary map



X Index: 283



Y Index: 288

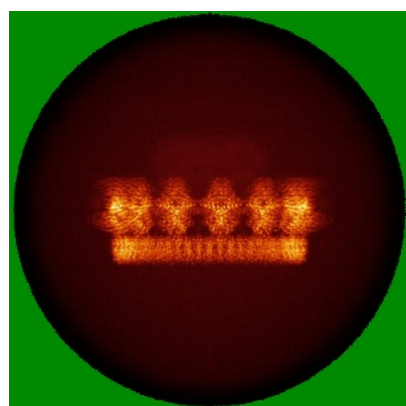


Z Index: 204

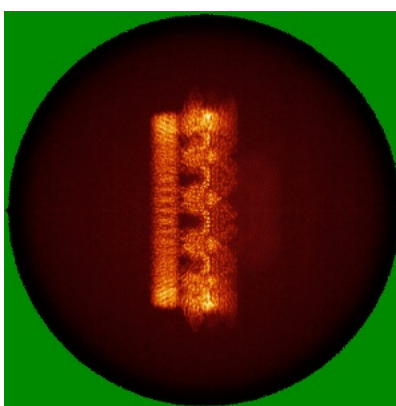
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

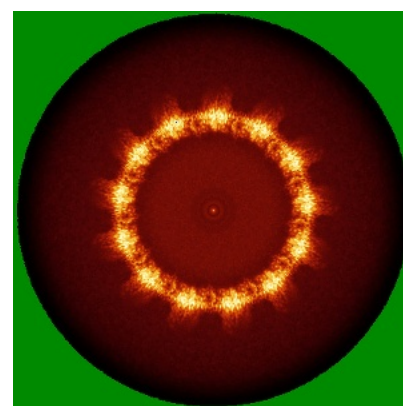
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

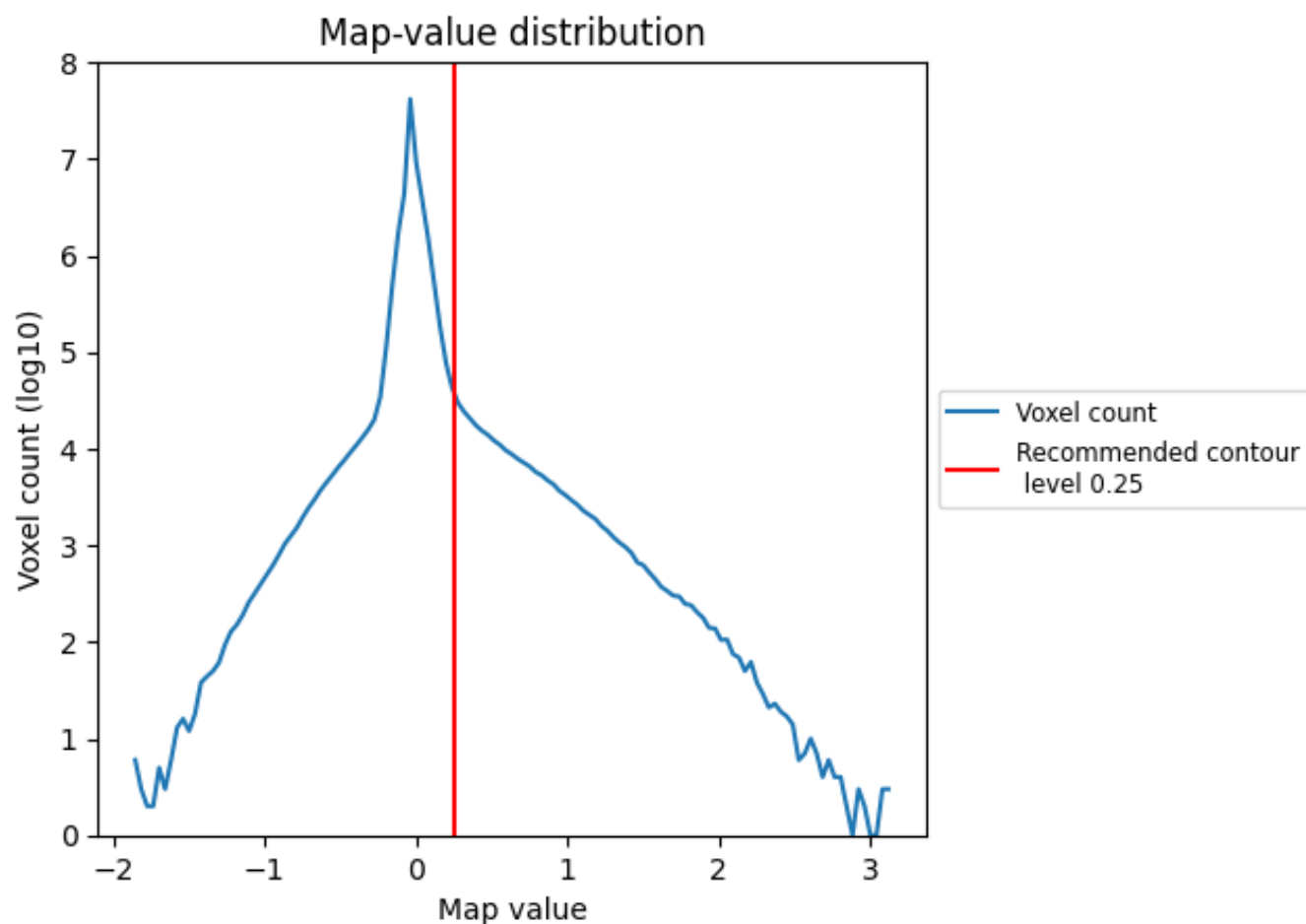
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

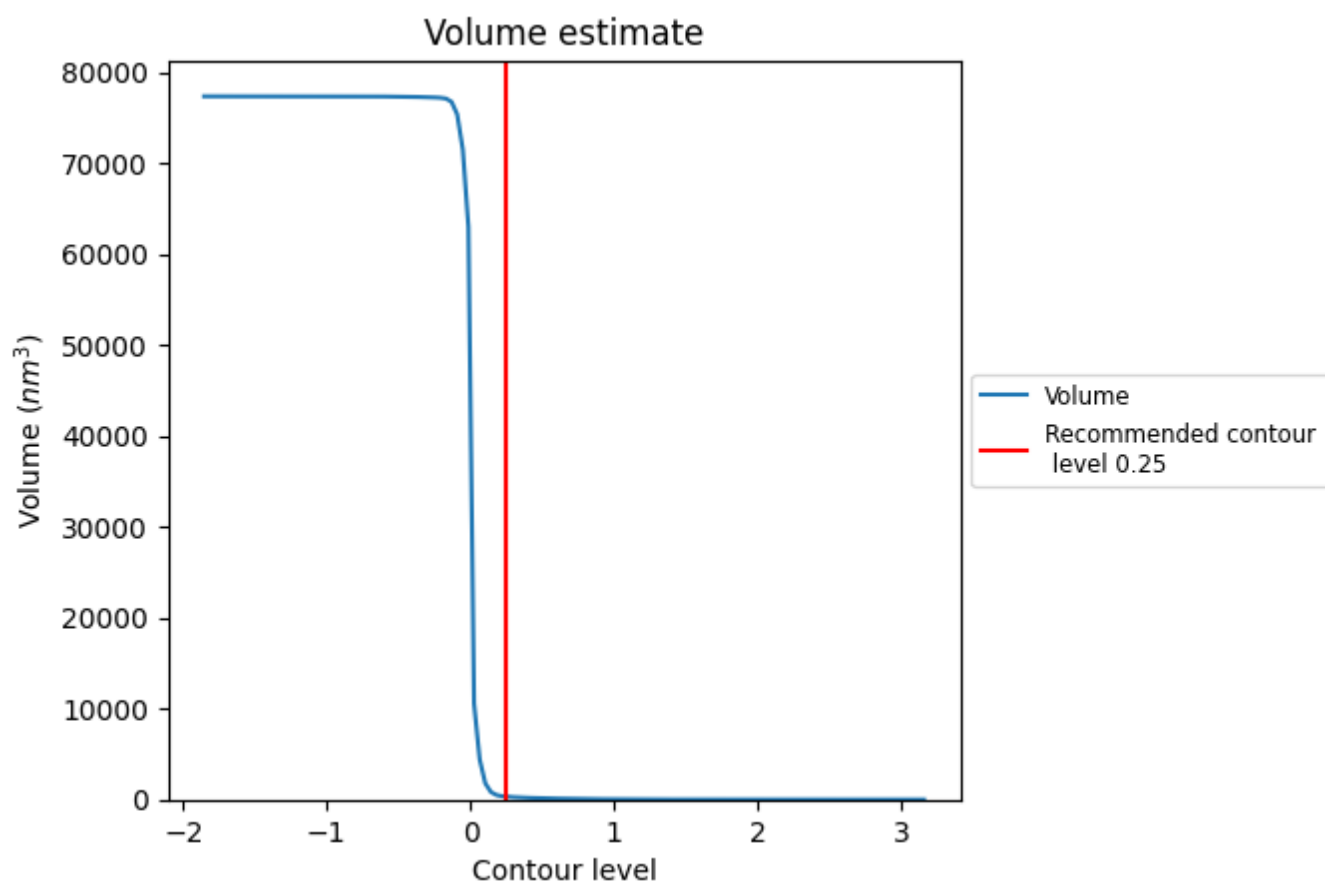
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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.

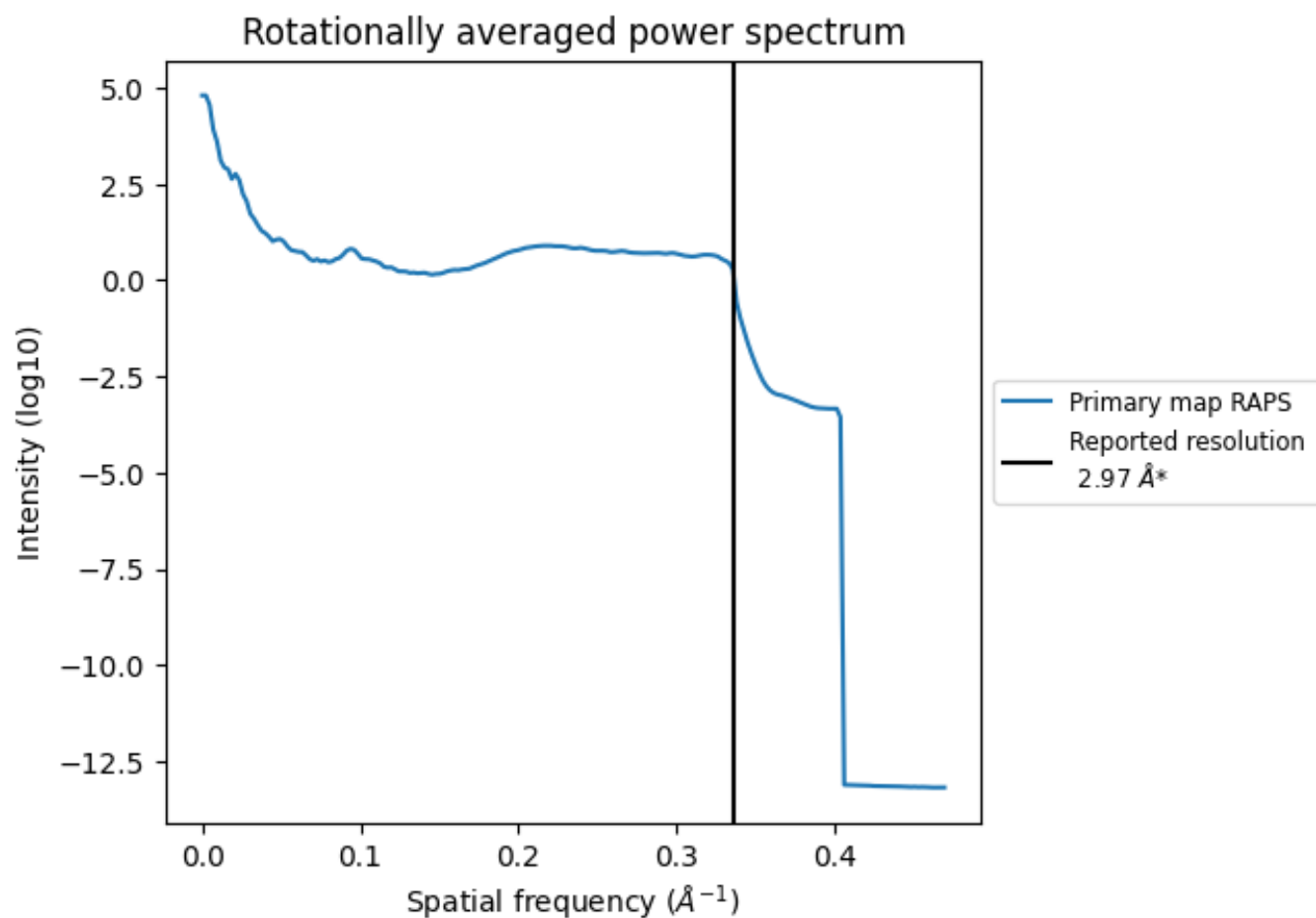
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 322 nm³; this corresponds to an approximate mass of 291 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.337 Å⁻¹

8 Fourier-Shell correlation

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

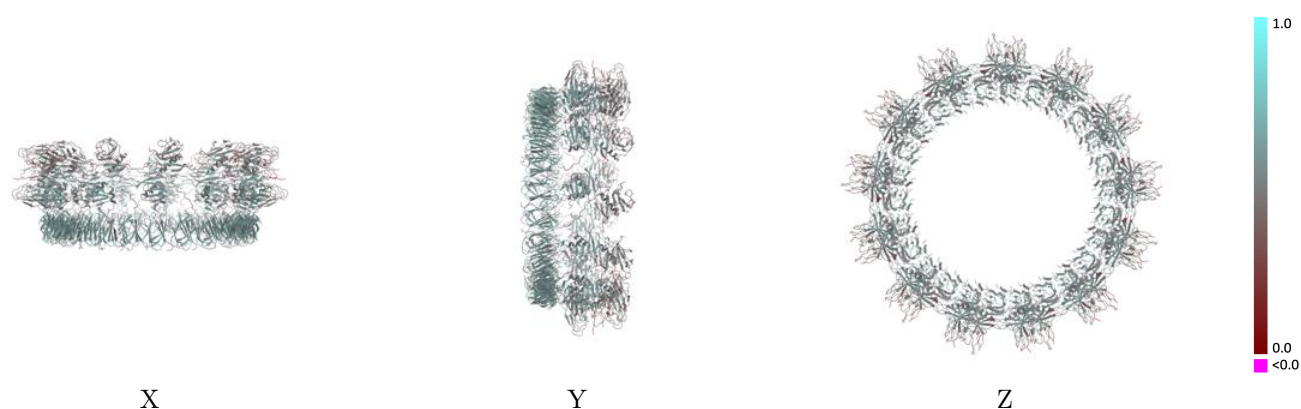
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24771 and PDB model 7SPI. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

This section was not generated.

9.2 Q-score mapped to coordinate model [i](#)

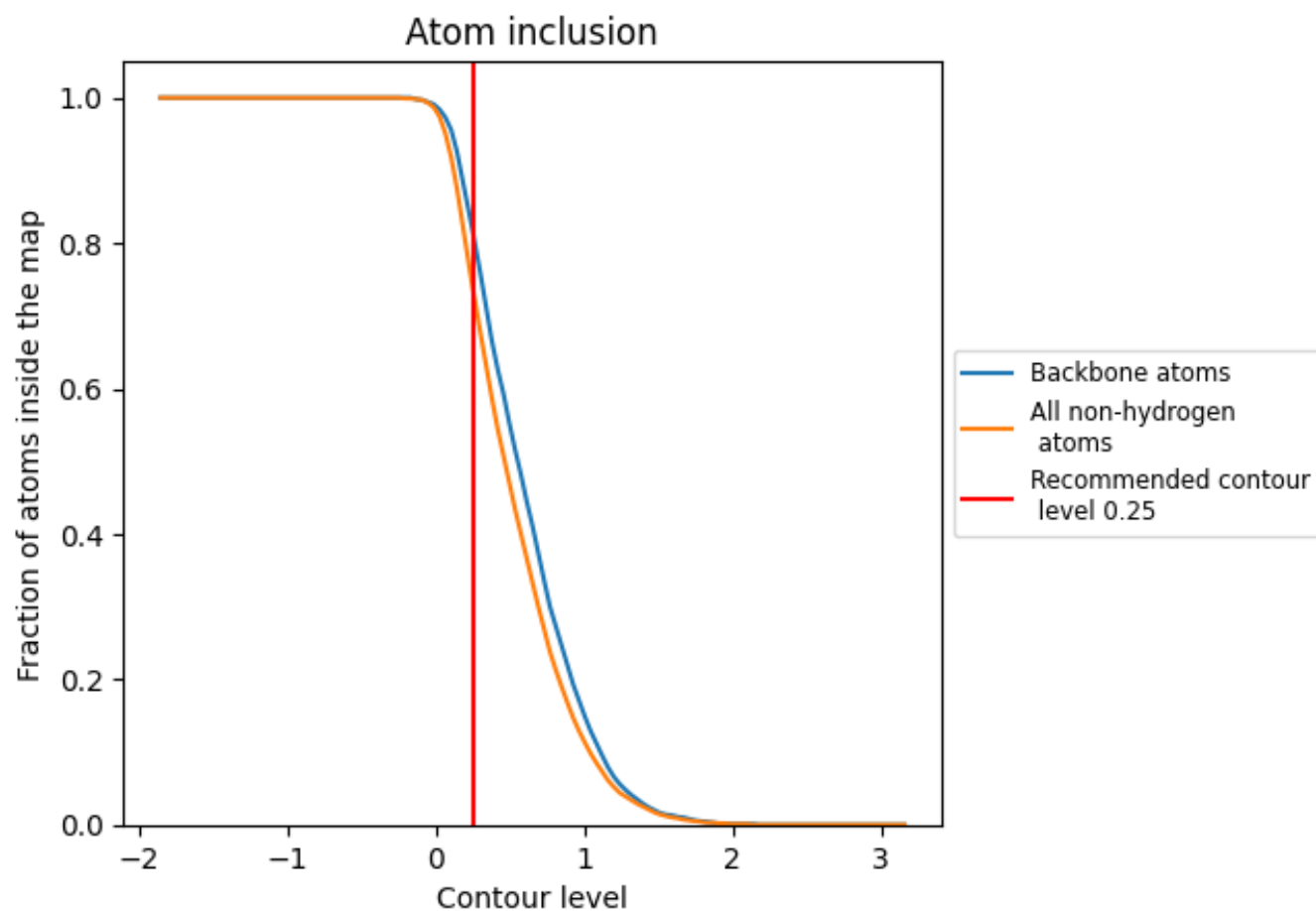


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 74% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7370	 0.5020
A1	 0.7450	 0.4910
A10	 0.7330	 0.4930
A11	 0.7280	 0.4860
A12	 0.7420	 0.4900
A13	 0.7450	 0.4910
A2	 0.7520	 0.4910
A3	 0.7350	 0.4910
A4	 0.7400	 0.4910
A5	 0.7400	 0.4910
A6	 0.7400	 0.4920
A7	 0.7420	 0.4940
A8	 0.7400	 0.4900
A9	 0.7400	 0.4900
B1	 0.6950	 0.4650
B10	 0.6970	 0.4650
B11	 0.6930	 0.4630
B12	 0.7010	 0.4640
B13	 0.6950	 0.4640
B2	 0.7010	 0.4630
B3	 0.6990	 0.4620
B4	 0.7010	 0.4650
B5	 0.7010	 0.4640
B6	 0.6930	 0.4660
B7	 0.6970	 0.4650
B8	 0.7030	 0.4660
B9	 0.6990	 0.4670
C1	 0.8210	 0.5400
C10	 0.8190	 0.5370
C11	 0.8200	 0.5380
C12	 0.8180	 0.5380
C13	 0.8230	 0.5390
C2	 0.8220	 0.5380
C3	 0.8220	 0.5390
C4	 0.8170	 0.5390



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Chain	Atom inclusion	Q-score
C5	 0.8200	 0.5380
C6	 0.8210	 0.5380
C7	 0.8180	 0.5370
C8	 0.8220	 0.5370
C9	 0.8160	 0.5370
D1	 0.7060	 0.4890
D10	 0.7030	 0.4840
D11	 0.7030	 0.4860
D12	 0.7030	 0.4870
D13	 0.7060	 0.4850
D2	 0.7010	 0.4880
D3	 0.7070	 0.4860
D4	 0.7060	 0.4890
D5	 0.7040	 0.4880
D6	 0.7050	 0.4880
D7	 0.7030	 0.4860
D8	 0.7040	 0.4860
D9	 0.7080	 0.4860
E1	 0.1060	 0.3830
E10	 0.1180	 0.3690
E11	 0.1180	 0.3860
E12	 0.1180	 0.3770
E13	 0.1180	 0.3820
E2	 0.1060	 0.3820
E3	 0.1180	 0.3860
E4	 0.1180	 0.3830
E5	 0.1290	 0.3780
E6	 0.1180	 0.3810
E7	 0.1060	 0.3770
E8	 0.1290	 0.3760
E9	 0.0820	 0.3710
F1	 0.6240	 0.5220
F10	 0.6000	 0.5090
F11	 0.6350	 0.5170
F12	 0.6240	 0.5100
F13	 0.6240	 0.5220
F2	 0.6120	 0.5080
F3	 0.6350	 0.5110
F4	 0.6120	 0.5080
F5	 0.6240	 0.5160
F6	 0.6350	 0.5150
F7	 0.6350	 0.5120

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Chain	Atom inclusion	Q-score
F8	0.6470	0.5070
F9	0.6350	0.5190