



## Full wwPDB EM Validation Report ⓘ

Nov 20, 2022 – 10:47 AM EST

PDB ID : 7RD1  
EMDB ID : EMD-24408  
Title : The Capsid Structure of the ChAdOx1 viral vector/chimpanzee adenovirus Y25  
Authors : Baker, A.T.; Boyd, R.J.; Sarkar, D.; Vermaas, J.V.; Williams, D.; Singharoy, A.  
Deposited on : 2021-07-08  
Resolution : 3.07 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](mailto: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>.

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

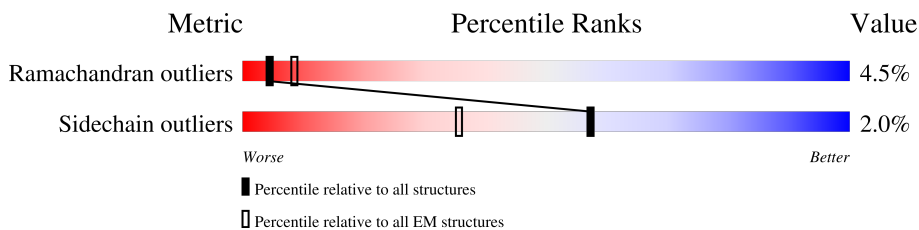
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

# 1 Overall quality at a glance

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

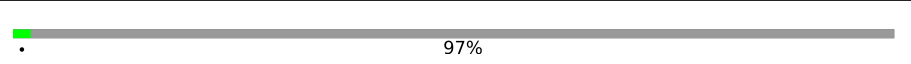
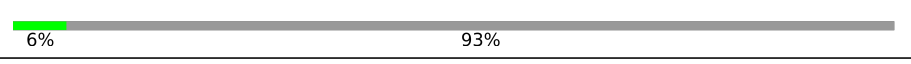
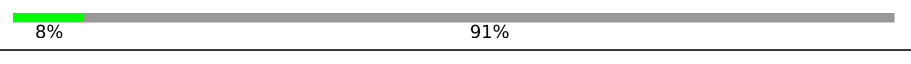
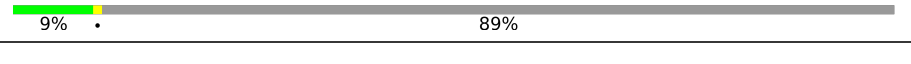
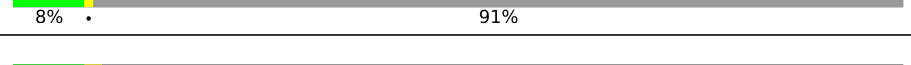
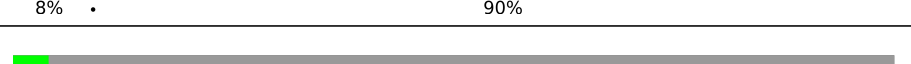
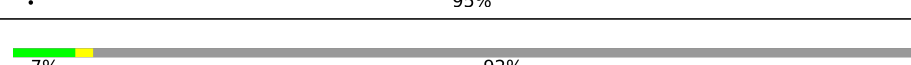
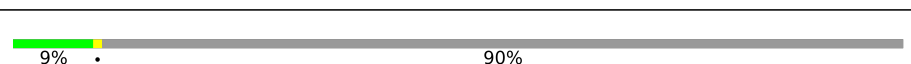


The reported resolution of this entry is 3.07 Å.

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.




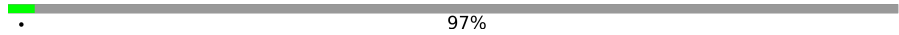
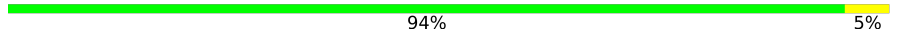

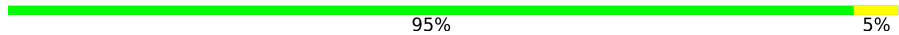
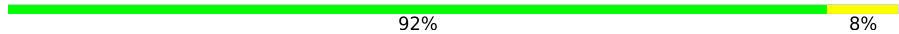
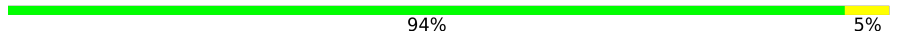
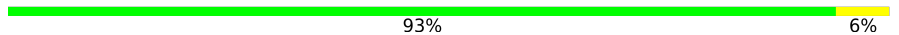
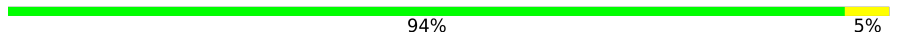
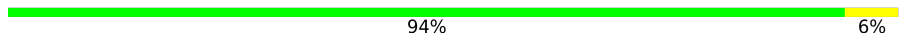
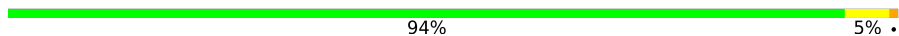
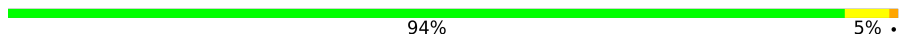
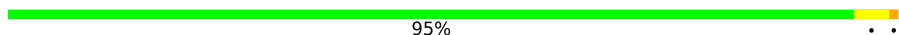
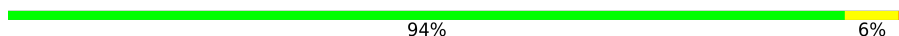


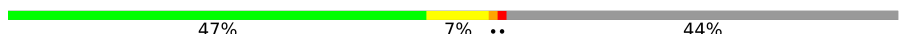





Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	0	243	 97%
1	1	243	 93%
1	2	243	 91%
1	3	243	 89%
1	4	243	 91%
1	8	243	 90%
1	U	243	 95%
1	V	243	 92%
1	W	243	 90%
1	X	243	 89%

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Mol	Chain	Length	Quality of chain
1	Y	243	 10% . 89%
1	Z	243	 . 97%
2	A	942	 94% 5%
2	B	942	 90% 9% .
2	C	942	 95% 5%
2	D	942	 92% 8%
2	E	942	 94% 5%
2	F	942	 93% 6%
2	G	942	 94% 5%
2	H	942	 94% 6%
2	I	942	 94% 5% .
2	J	942	 94% 5% .
2	K	942	 95% . .
2	L	942	 94% 6% .
3	M	532	 78% . 18%
4	N	142	 52% 9% . 37%
4	O	142	 47% 7% . . 44%
4	P	142	 58% 8% . 32%
4	Q	142	 47% . . 49%
5	R	589	 18% . 81%
6	S	227	 70% 7% . 23%
6	T	227	 69% 8% . 22%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 197782 atoms, of which 96589 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 Pre-protein VI.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			
1	0	7	Total	C	H	N	O	0	0	
			106	35	51	8	12			
1	U	11	Total	C	H	N	O	0	0	
			171	55	83	17	16			
1	1	17	Total	C	H	N	O	0	0	
			245	77	118	23	27			
1	V	20	Total	C	H	N	O	S	0	0
			286	96	136	22	31	1		
1	2	21	Total	C	H	N	O	S	0	0
			323	106	156	31	29	1		
1	W	24	Total	C	H	N	O	S	0	0
			361	118	174	34	34	1		
1	3	26	Total	C	H	N	O	S	0	0
			386	125	186	36	38	1		
1	X	26	Total	C	H	N	O	S	0	0
			386	125	186	36	38	1		
1	4	22	Total	C	H	N	O	S	0	0
			335	110	160	32	32	1		
1	Y	26	Total	C	H	N	O	S	0	0
			386	125	186	36	38	1		
1	8	24	Total	C	H	N	O	S	0	0
			363	118	177	34	33	1		
1	Z	7	Total	C	H	N	O	0	0	
			106	35	51	8	12			

- Molecule 2 is a protein called Hexon protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			
2	A	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	B	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	C	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		

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Mol	Chain	Residues	Atoms						AltConf	Trace
2	D	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	E	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	F	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	G	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	H	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	I	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	J	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	K	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	L	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		

- Molecule 3 is a protein called Penton protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	M	435	Total	C	H	N	O	S	0	0
			6923	2219	3423	596	672	13		

- Molecule 4 is a protein called Hexon-interlacing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	N	89	Total	C	H	N	O	S	0	0
			1328	412	664	114	135	3		
4	O	79	Total	C	H	N	O	S	0	0
			1187	368	595	102	119	3		
4	P	96	Total	C	H	N	O	S	0	0
			1435	443	720	125	144	3		
4	Q	73	Total	C	H	N	O	S	0	0
			1108	342	560	99	104	3		

- Molecule 5 is a protein called Pre-hexon-linking protein IIIa.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	R	114	Total	C	H	N	O	S	0	0
			1767	539	885	167	173	3		

- Molecule 6 is a protein called Pre-hexon-linking protein VIII.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
6	S	175	Total	C	H	N	O	S	0	0
			2673	861	1308	234	265	5		
6	T	177	Total	C	H	N	O	S	0	0
			2695	867	1318	236	269	5		













- Molecule 2: Hexon protein

Chain C: 95% 5%



- Molecule 2: Hexon protein

Chain D: 92% 8%



- Molecule 2: Hexon protein

Chain E: 94% 5%

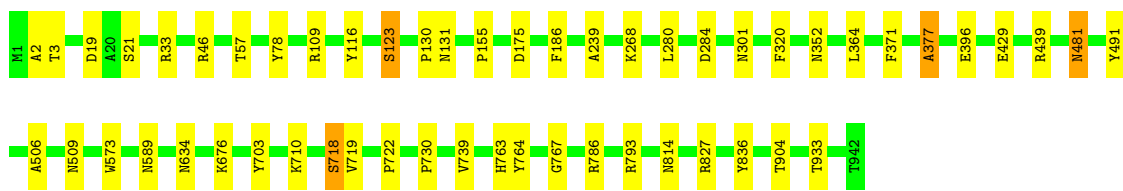


- Molecule 2: Hexon protein

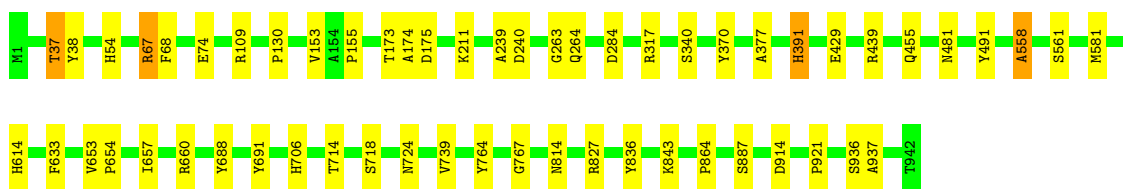
Chain F: 93% 6%



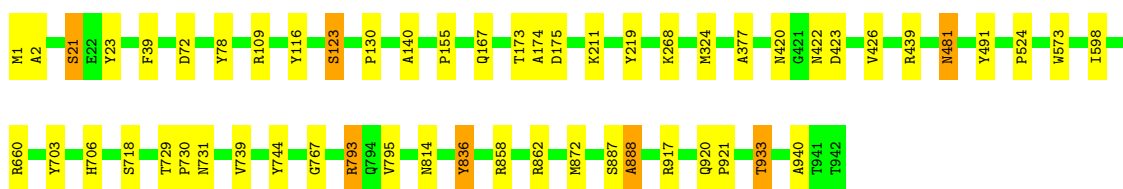
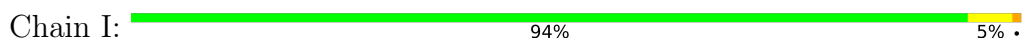
• Molecule 2: Hexon protein



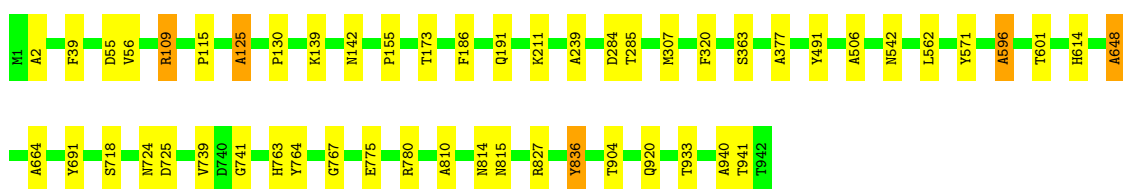
• Molecule 2: Hexon protein



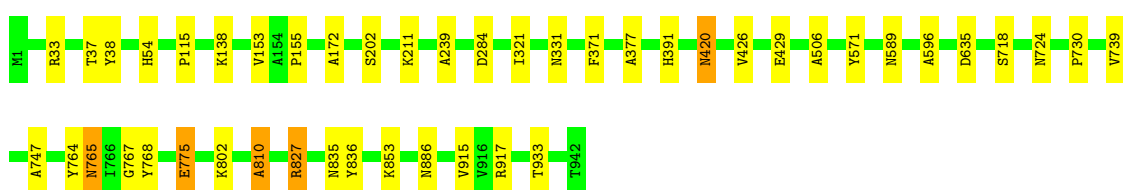
• Molecule 2: Hexon protein



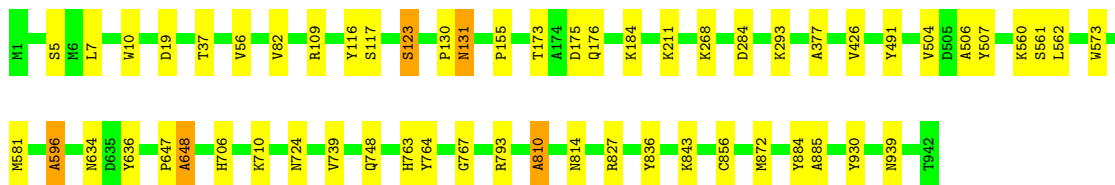
• Molecule 2: Hexon protein



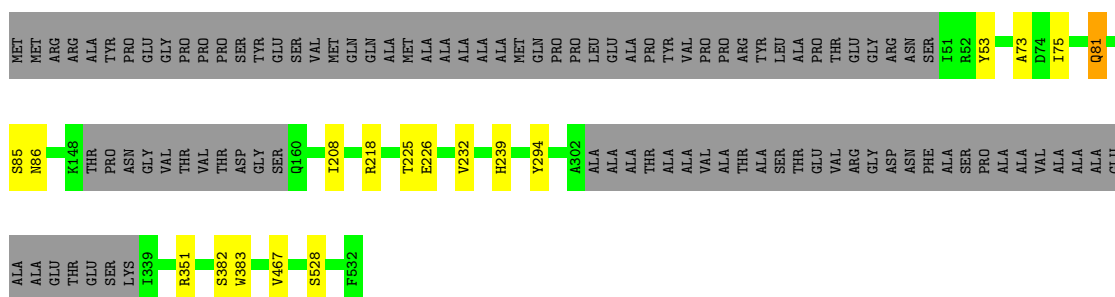
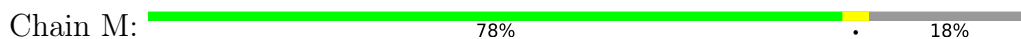
• Molecule 2: Hexon protein



• Molecule 2: Hexon protein



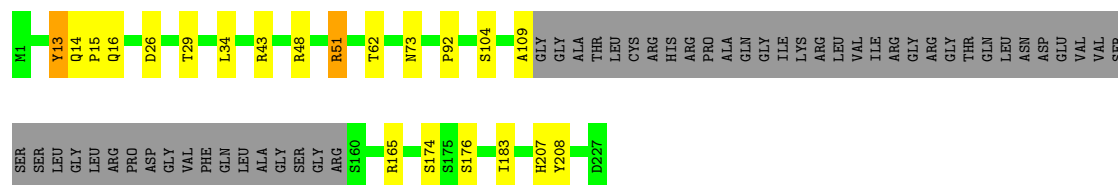
• Molecule 3: Penton protein





• Molecule 6: Pre-hexon-linking protein VIII

Chain T:  69% 8% 22%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5748	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.1802	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	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	0	0.95	0/55	1.06	0/73
1	1	0.81	0/128	1.22	1/171 (0.6%)
1	2	0.88	0/173	1.21	1/234 (0.4%)
1	3	0.79	0/206	1.30	1/279 (0.4%)
1	4	0.76	0/181	1.24	1/245 (0.4%)
1	8	0.91	0/192	1.18	0/260
1	U	0.85	0/90	1.27	1/121 (0.8%)
1	V	0.84	0/153	1.25	0/206
1	W	0.79	0/193	1.22	1/261 (0.4%)
1	X	0.93	0/206	1.17	1/279 (0.4%)
1	Y	0.75	0/206	1.26	1/279 (0.4%)
1	Z	0.91	0/55	0.79	0/73
2	A	0.90	0/7683	1.07	8/10460 (0.1%)
2	B	0.91	0/7683	1.11	10/10460 (0.1%)
2	C	0.90	0/7683	1.06	4/10460 (0.0%)
2	D	0.89	0/7683	1.11	8/10460 (0.1%)
2	E	0.90	0/7683	1.07	8/10460 (0.1%)
2	F	0.91	0/7683	1.07	4/10460 (0.0%)
2	G	0.91	0/7683	1.08	9/10460 (0.1%)
2	H	0.91	0/7683	1.07	4/10460 (0.0%)
2	I	0.90	0/7683	1.07	9/10460 (0.1%)
2	J	0.90	0/7683	1.08	13/10460 (0.1%)
2	K	0.91	0/7683	1.07	10/10460 (0.1%)
2	L	0.91	0/7683	1.08	9/10460 (0.1%)
3	M	0.91	0/3580	1.05	3/4872 (0.1%)
4	N	0.92	0/672	1.19	5/909 (0.6%)
4	O	0.87	0/597	1.18	4/803 (0.5%)
4	P	0.92	0/723	1.11	3/979 (0.3%)
4	Q	0.90	0/554	1.04	0/746
5	R	0.94	0/892	0.98	0/1213
6	S	0.87	0/1403	1.14	8/1917 (0.4%)
6	T	0.89	0/1415	1.14	5/1933 (0.3%)
All	All	0.90	0/103870	1.08	132/141373 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A	0	2
2	B	0	5
2	D	0	6
2	E	0	4
2	F	0	2
2	G	0	1
2	H	0	3
2	I	0	6
2	J	0	2
2	K	0	1
2	L	0	5
3	M	0	1
4	O	0	1
4	Q	0	1
5	R	0	1
6	T	0	2
All	All	0	43

There are no bond length outliers.

All (132) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	571	TYR	CB-CG-CD2	-7.83	116.30	121.00
2	L	116	TYR	CB-CG-CD2	-7.82	116.31	121.00
2	E	571	TYR	CB-CG-CD2	-7.53	116.48	121.00
1	U	12	ARG	NE-CZ-NH1	7.51	124.06	120.30
2	L	116	TYR	CB-CG-CD1	7.36	125.42	121.00
1	Y	12	ARG	NE-CZ-NH1	7.35	123.97	120.30
2	E	836	TYR	CB-CG-CD2	-7.30	116.62	121.00
2	E	836	TYR	CB-CG-CD1	7.17	125.30	121.00
2	A	571	TYR	CB-CG-CD2	-7.11	116.73	121.00
2	D	571	TYR	CB-CG-CD2	-6.97	116.82	121.00
2	J	648	ALA	N-CA-CB	6.90	119.77	110.10
2	G	116	TYR	CB-CG-CD2	-6.89	116.86	121.00
2	B	46	ARG	NE-CZ-NH2	6.83	123.72	120.30
2	K	571	TYR	CB-CG-CD2	-6.82	116.91	121.00
4	O	133	ARG	NE-CZ-NH2	6.82	123.71	120.30
2	G	33	ARG	NE-CZ-NH2	6.79	123.70	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	T	165	ARG	NE-CZ-NH2	6.75	123.67	120.30
2	K	836	TYR	CB-CG-CD2	-6.66	117.00	121.00
4	O	7	PHE	CB-CG-CD1	6.51	125.36	120.80
2	E	571	TYR	CB-CG-CD1	6.50	124.90	121.00
2	J	780	ARG	NE-CZ-NH1	-6.36	117.12	120.30
6	S	208	TYR	CB-CG-CD2	-6.33	117.20	121.00
2	J	571	TYR	CB-CG-CD1	6.31	124.78	121.00
2	D	571	TYR	CB-CG-CD1	6.27	124.76	121.00
1	2	16	ARG	NE-CZ-NH1	6.26	123.43	120.30
2	I	888	ALA	N-CA-CB	6.24	118.83	110.10
2	E	602	SER	N-CA-CB	6.23	119.85	110.50
2	K	836	TYR	CB-CG-CD1	6.23	124.74	121.00
2	J	836	TYR	CB-CG-CD2	-6.22	117.27	121.00
2	B	685	PHE	CB-CG-CD2	6.19	125.14	120.80
2	J	780	ARG	NE-CZ-NH2	6.15	123.38	120.30
2	L	648	ALA	N-CA-CB	6.13	118.68	110.10
2	G	123	SER	N-CA-CB	6.11	119.67	110.50
1	W	16	ARG	NE-CZ-NH1	6.11	123.35	120.30
2	C	109	ARG	NE-CZ-NH2	6.08	123.34	120.30
2	B	663	ALA	N-CA-CB	6.08	118.61	110.10
2	K	765	ASN	N-CA-CB	6.08	121.54	110.60
2	A	370	TYR	CB-CG-CD2	-6.04	117.38	121.00
2	G	116	TYR	CB-CG-CD1	5.95	124.57	121.00
2	A	571	TYR	CB-CG-CD1	5.95	124.57	121.00
6	T	208	TYR	CB-CG-CD1	-5.94	117.44	121.00
2	D	2	ALA	N-CA-CB	5.94	118.41	110.10
6	S	93	ARG	NE-CZ-NH1	5.90	123.25	120.30
1	4	16	ARG	NE-CZ-NH1	5.89	123.25	120.30
6	S	13	TYR	CB-CG-CD1	-5.89	117.47	121.00
6	S	13	TYR	CB-CG-CD2	5.84	124.50	121.00
1	1	12	ARG	NE-CZ-NH2	5.80	123.20	120.30
2	G	109	ARG	NE-CZ-NH1	-5.79	117.41	120.30
2	J	836	TYR	CB-CG-CD1	5.79	124.47	121.00
4	P	15	TYR	CB-CG-CD1	5.77	124.46	121.00
2	J	596	ALA	N-CA-CB	5.74	118.13	110.10
4	P	15	TYR	CB-CG-CD2	-5.74	117.56	121.00
2	B	131	ASN	N-CA-CB	5.72	120.89	110.60
2	G	109	ARG	NE-CZ-NH2	5.72	123.16	120.30
3	M	351	ARG	NE-CZ-NH2	5.71	123.16	120.30
2	K	420	ASN	N-CA-CB	5.68	120.83	110.60
6	S	208	TYR	CB-CG-CD1	5.67	124.40	121.00
2	F	131	ASN	N-CA-CB	5.67	120.80	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	836	TYR	CB-CG-CD2	-5.66	117.61	121.00
2	G	131	ASN	N-CA-CB	5.66	120.78	110.60
2	B	685	PHE	CB-CG-CD1	-5.63	116.86	120.80
2	D	737	ARG	NE-CZ-NH2	5.63	123.11	120.30
3	M	53	TYR	CB-CG-CD1	-5.63	117.62	121.00
2	K	775	GLU	N-CA-CB	5.61	120.69	110.60
2	H	558	ALA	N-CA-CB	5.56	117.89	110.10
2	A	377	ALA	N-CA-CB	5.54	117.86	110.10
2	H	109	ARG	NE-CZ-NH2	5.53	123.07	120.30
2	I	744	TYR	CB-CG-CD2	-5.53	117.68	121.00
2	I	21	SER	N-CA-CB	5.52	118.78	110.50
2	A	370	TYR	CB-CG-CD1	5.50	124.30	121.00
1	3	12	ARG	NE-CZ-NH1	5.50	123.05	120.30
2	B	836	TYR	CB-CG-CD2	-5.49	117.71	121.00
2	J	664	ALA	N-CA-CB	5.49	117.78	110.10
2	L	131	ASN	N-CA-CB	5.47	120.45	110.60
2	L	596	ALA	N-CA-CB	5.45	117.74	110.10
6	S	35	SER	N-CA-CB	5.45	118.68	110.50
2	J	691	TYR	CB-CG-CD1	-5.44	117.73	121.00
2	K	764	TYR	CB-CG-CD2	-5.44	117.74	121.00
2	G	718	SER	N-CA-CB	5.40	118.60	110.50
2	E	815	ASN	N-CA-CB	5.40	120.31	110.60
4	O	7	PHE	CB-CG-CD2	-5.39	117.03	120.80
2	A	810	ALA	N-CA-CB	5.39	117.64	110.10
4	N	18	GLY	N-CA-C	-5.38	99.65	113.10
2	B	109	ARG	NE-CZ-NH2	5.38	122.99	120.30
2	F	884	TYR	CB-CG-CD2	-5.38	117.78	121.00
2	C	131	ASN	N-CA-CB	5.36	120.24	110.60
2	I	123	SER	N-CA-CB	5.36	118.54	110.50
2	J	125	ALA	N-CA-CB	5.35	117.59	110.10
2	A	344	ALA	N-CA-CB	5.34	117.57	110.10
2	D	513	ARG	NE-CZ-NH2	5.32	122.96	120.30
2	D	131	ASN	N-CA-CB	5.32	120.17	110.60
2	J	109	ARG	NE-CZ-NH2	5.31	122.95	120.30
2	E	89	GLY	N-CA-C	-5.30	99.85	113.10
2	L	123	SER	N-CA-CB	5.30	118.45	110.50
4	P	43	ALA	N-CA-CB	5.30	117.52	110.10
4	N	15	TYR	CB-CG-CD1	-5.27	117.84	121.00
2	A	862	ARG	NE-CZ-NH2	5.26	122.93	120.30
2	K	810	ALA	N-CA-CB	5.25	117.46	110.10
2	L	561	SER	N-CA-CB	5.24	118.36	110.50
2	H	581	MET	CG-SD-CE	-5.23	91.83	100.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	370	TYR	CB-CG-CD2	-5.20	117.88	121.00
2	K	827	ARG	NE-CZ-NH2	5.20	122.90	120.30
6	T	51	ARG	NE-CZ-NH1	5.19	122.90	120.30
2	E	367	ARG	NE-CZ-NH2	5.18	122.89	120.30
4	N	13	SER	CA-C-N	5.16	131.55	117.10
3	M	218	ARG	NE-CZ-NH1	5.14	122.87	120.30
2	K	571	TYR	CB-CG-CD1	5.14	124.08	121.00
2	G	377	ALA	N-CA-CB	5.13	117.29	110.10
4	O	14	PRO	N-CA-C	5.13	125.45	112.10
4	N	13	SER	CB-CA-C	5.13	119.85	110.10
2	B	33	ARG	NE-CZ-NH2	5.12	122.86	120.30
2	I	793	ARG	NE-CZ-NH2	5.12	122.86	120.30
2	D	672	ARG	NE-CZ-NH1	-5.12	117.74	120.30
1	X	10	ALA	N-CA-CB	5.12	117.26	110.10
2	B	680	SER	N-CA-CB	5.11	118.17	110.50
2	C	370	TYR	CB-CG-CD2	-5.11	117.94	121.00
2	F	320	PHE	N-CA-CB	5.11	119.79	110.60
2	F	815	ASN	N-CA-CB	5.10	119.78	110.60
2	J	815	ASN	N-CA-CB	5.09	119.77	110.60
2	I	324	MET	CG-SD-CE	-5.09	92.05	100.20
2	I	744	TYR	CB-CG-CD1	5.09	124.05	121.00
2	I	862	ARG	NE-CZ-NH2	5.08	122.84	120.30
2	B	370	TYR	CB-CG-CD2	-5.08	117.95	121.00
2	D	88	VAL	N-CA-C	-5.07	97.30	111.00
2	L	581	MET	CG-SD-CE	-5.05	92.12	100.20
2	L	810	ALA	N-CA-CB	5.05	117.17	110.10
6	T	208	TYR	CB-CG-CD2	5.04	124.02	121.00
6	S	212	PHE	CB-CG-CD2	-5.03	117.28	120.80
6	S	197	TYR	CB-CG-CD2	-5.02	117.99	121.00
2	C	12	TYR	CB-CG-CD2	-5.02	117.99	121.00
4	N	46	SER	N-CA-CB	5.01	118.02	110.50
6	T	109	ALA	N-CA-C	5.01	124.53	111.00

There are no chirality outliers.

All (43) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	109	ARG	Sidechain
2	A	207	ARG	Sidechain
2	B	219	TYR	Sidechain
2	B	507	TYR	Sidechain
2	B	571	TYR	Sidechain

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>Group</b>
2	B	654	PRO	Peptide
2	B	676	LYS	Peptide
2	D	187	GLN	Peptide
2	D	219	TYR	Sidechain
2	D	325	TYR	Sidechain
2	D	400	TYR	Sidechain
2	D	507	TYR	Sidechain
2	D	722	PRO	Peptide
2	E	219	TYR	Sidechain
2	E	470	TYR	Sidechain
2	E	625	ARG	Sidechain
2	E	68	PHE	Peptide
2	F	219	TYR	Sidechain
2	F	507	TYR	Sidechain
2	G	491	TYR	Sidechain
2	H	491	TYR	Sidechain
2	H	653	VAL	Peptide
2	H	691	TYR	Sidechain
2	I	109	ARG	Sidechain
2	I	116	TYR	Sidechain
2	I	23	TYR	Sidechain
2	I	491	TYR	Sidechain
2	I	729	THR	Peptide
2	I	917	ARG	Sidechain
2	J	109	ARG	Sidechain
2	J	491	TYR	Sidechain
2	K	768	TYR	Sidechain
2	L	109	ARG	Sidechain
2	L	491	TYR	Sidechain
2	L	507	TYR	Sidechain
2	L	636	TYR	Sidechain
2	L	930	TYR	Sidechain
3	M	294	TYR	Sidechain
4	O	20	LEU	Peptide
4	Q	27	ARG	Sidechain
5	R	54	ARG	Sidechain
6	T	13	TYR	Sidechain
6	T	14	GLN	Peptide

## 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	0	55	51	50	0	0
1	1	127	118	116	0	0
1	2	167	156	155	0	0
1	3	200	186	185	0	0
1	4	175	160	159	0	0
1	8	186	177	176	0	0
1	U	88	83	82	0	0
1	V	150	136	134	0	0
1	W	187	174	173	0	0
1	X	200	186	185	0	0
1	Y	200	186	185	0	0
1	Z	55	51	50	0	0
2	A	7480	7121	7121	0	0
2	B	7480	7121	7121	0	0
2	C	7480	7121	7121	0	0
2	D	7480	7121	7121	0	0
2	E	7480	7121	7121	0	0
2	F	7480	7121	7121	0	0
2	G	7480	7121	7121	0	0
2	H	7480	7121	7121	0	0
2	I	7480	7121	7121	0	0
2	J	7480	7121	7121	0	0
2	K	7480	7121	7121	0	0
2	L	7480	7121	7121	0	0
3	M	3500	3423	3420	0	0
4	N	664	664	663	0	0
4	O	592	595	593	0	0
4	P	715	720	719	0	0
4	Q	548	560	559	0	0
5	R	882	885	884	0	0
6	S	1365	1308	1307	0	0
6	T	1377	1318	1317	0	0
All	All	101193	96589	96564	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

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	0	5/243 (2%)	4 (80%)	0	1 (20%)	0	0
1	1	13/243 (5%)	9 (69%)	3 (23%)	1 (8%)	1	5
1	2	19/243 (8%)	15 (79%)	2 (10%)	2 (10%)	0	2
1	3	24/243 (10%)	16 (67%)	7 (29%)	1 (4%)	3	15
1	4	20/243 (8%)	14 (70%)	3 (15%)	3 (15%)	0	0
1	8	22/243 (9%)	13 (59%)	5 (23%)	4 (18%)	0	0
1	U	9/243 (4%)	7 (78%)	2 (22%)	0	100	100
1	V	16/243 (7%)	13 (81%)	2 (12%)	1 (6%)	1	7
1	W	22/243 (9%)	12 (54%)	8 (36%)	2 (9%)	1	3
1	X	24/243 (10%)	16 (67%)	3 (12%)	5 (21%)	0	0
1	Y	24/243 (10%)	18 (75%)	5 (21%)	1 (4%)	3	15
1	Z	5/243 (2%)	5 (100%)	0	0	100	100
2	A	940/942 (100%)	822 (87%)	80 (8%)	38 (4%)	3	15
2	B	940/942 (100%)	771 (82%)	99 (10%)	70 (7%)	1	5
2	C	940/942 (100%)	824 (88%)	85 (9%)	31 (3%)	4	19
2	D	940/942 (100%)	819 (87%)	75 (8%)	46 (5%)	2	12
2	E	940/942 (100%)	826 (88%)	79 (8%)	35 (4%)	3	17
2	F	940/942 (100%)	834 (89%)	67 (7%)	39 (4%)	3	15
2	G	940/942 (100%)	824 (88%)	82 (9%)	34 (4%)	3	18
2	H	940/942 (100%)	811 (86%)	89 (10%)	40 (4%)	2	14
2	I	940/942 (100%)	827 (88%)	79 (8%)	34 (4%)	3	18
2	J	940/942 (100%)	829 (88%)	75 (8%)	36 (4%)	3	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	K	940/942 (100%)	816 (87%)	95 (10%)	29 (3%)	4	21
2	L	940/942 (100%)	827 (88%)	75 (8%)	38 (4%)	3	15
3	M	429/532 (81%)	390 (91%)	28 (6%)	11 (3%)	5	24
4	N	85/142 (60%)	65 (76%)	9 (11%)	11 (13%)	0	1
4	O	73/142 (51%)	54 (74%)	9 (12%)	10 (14%)	0	1
4	P	92/142 (65%)	69 (75%)	11 (12%)	12 (13%)	0	1
4	Q	69/142 (49%)	57 (83%)	9 (13%)	3 (4%)	2	14
5	R	112/589 (19%)	94 (84%)	13 (12%)	5 (4%)	2	13
6	S	171/227 (75%)	141 (82%)	20 (12%)	10 (6%)	1	9
6	T	173/227 (76%)	143 (83%)	18 (10%)	12 (7%)	1	6
All	All	12687/16363 (78%)	10985 (87%)	1137 (9%)	565 (4%)	4	13

All (565) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	V	6	PHE
1	W	10	ALA
1	8	25	ILE
2	A	21	SER
2	A	76	ASN
2	A	232	GLN
2	A	344	ALA
2	A	377	ALA
2	A	676	LYS
2	A	686	ASP
2	A	810	ALA
2	B	59	ASP
2	B	70	PRO
2	B	219	TYR
2	B	342	LEU
2	B	645	PRO
2	B	650	ALA
2	B	651	THR
2	B	661	ASN
2	B	663	ALA
2	B	717	SER
2	B	724	ASN
2	B	836	TYR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	B	936	SER
2	C	5	SER
2	C	11	ALA
2	C	187	GLN
2	C	339	ALA
2	C	377	ALA
2	C	558	ALA
2	C	706	HIS
2	C	836	TYR
2	D	2	ALA
2	D	4	PRO
2	D	175	ASP
2	D	197	TRP
2	D	198	GLN
2	D	377	ALA
2	D	425	ASP
2	D	689	PHE
2	D	866	SER
2	D	889	HIS
2	D	890	ALA
2	D	891	LEU
2	D	903	SER
2	E	7	LEU
2	E	172	ALA
2	E	239	ALA
2	E	377	ALA
2	E	558	ALA
2	E	886	ASN
2	F	21	SER
2	F	175	ASP
2	F	202	SER
2	F	284	ASP
2	F	377	ALA
2	F	716	ASP
2	F	836	TYR
2	F	885	ALA
2	F	933	THR
2	F	940	ALA
2	G	46	ARG
2	G	123	SER
2	G	506	ALA
2	G	718	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	G	786	ARG
2	G	836	TYR
2	G	933	THR
2	H	174	ALA
2	H	175	ASP
2	H	239	ALA
2	H	377	ALA
2	H	391	HIS
2	H	558	ALA
2	H	654	PRO
2	H	657	ILE
2	H	660	ARG
2	H	724	ASN
2	H	937	ALA
2	I	2	ALA
2	I	21	SER
2	I	140	ALA
2	I	175	ASP
2	I	219	TYR
2	I	706	HIS
2	I	836	TYR
2	J	125	ALA
2	J	506	ALA
2	J	596	ALA
2	J	648	ALA
2	J	810	ALA
2	J	836	TYR
2	K	377	ALA
2	K	420	ASN
2	K	724	ASN
2	K	765	ASN
2	K	775	GLU
2	K	810	ALA
2	K	933	THR
2	L	5	SER
2	L	123	SER
2	L	175	ASP
2	L	560	LYS
2	L	648	ALA
2	L	706	HIS
2	L	724	ASN
2	L	810	ALA

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	L	939	ASN
3	M	75	ILE
3	M	85	SER
3	M	239	HIS
3	M	382	SER
4	N	4	SER
4	N	6	SER
4	N	11	VAL
4	N	12	PHE
4	N	13	SER
4	N	26	VAL
4	O	13	SER
4	P	7	PHE
4	P	43	ALA
6	S	36	ALA
1	1	6	PHE
1	2	4	ILE
1	X	7	SER
1	X	19	MET
1	Y	8	SER
2	A	331	ASN
2	A	426	VAL
2	A	516	LEU
2	B	68	PHE
2	B	73	ARG
2	B	155	PRO
2	B	173	THR
2	B	176	GLN
2	B	338	GLN
2	B	339	ALA
2	B	377	ALA
2	B	631	GLN
2	B	647	PRO
2	B	649	ASN
2	B	680	SER
2	B	711	VAL
2	C	155	PRO
2	C	175	ASP
2	C	506	ALA
2	C	933	THR
2	D	130	PRO
2	D	188	PRO

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	D	202	SER
2	D	268	LYS
2	D	284	ASP
2	D	426	VAL
2	D	676	LYS
2	D	836	TYR
2	D	884	TYR
2	D	939	ASN
2	D	940	ALA
2	E	56	VAL
2	E	59	ASP
2	E	130	PRO
2	E	155	PRO
2	E	268	LYS
2	E	426	VAL
2	E	474	SER
2	E	742	GLU
2	E	836	TYR
2	E	933	THR
2	F	155	PRO
2	F	214	SER
2	F	296	ALA
2	F	426	VAL
2	F	815	ASN
2	G	239	ALA
2	G	320	PHE
2	G	364	LEU
2	G	377	ALA
2	G	481	ASN
2	G	589	ASN
2	G	764	TYR
2	H	130	PRO
2	H	240	ASP
2	H	340	SER
2	H	439	ARG
2	H	481	ASN
2	H	706	HIS
2	H	718	SER
2	H	739	VAL
2	I	123	SER
2	I	377	ALA
2	I	420	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	I	426	VAL
2	I	739	VAL
2	I	888	ALA
2	I	933	THR
2	J	2	ALA
2	J	173	THR
2	J	191	GLN
2	J	363	SER
2	J	377	ALA
2	J	718	SER
2	J	940	ALA
2	K	155	PRO
2	K	202	SER
2	K	426	VAL
2	L	10	TRP
2	L	19	ASP
2	L	56	VAL
2	L	155	PRO
2	L	173	THR
2	L	377	ALA
2	L	426	VAL
2	L	562	LEU
2	L	596	ALA
2	L	764	TYR
2	L	836	TYR
2	L	872	MET
2	L	884	TYR
2	L	885	ALA
3	M	81	GLN
3	M	208	ILE
4	N	22	SER
4	N	46	SER
4	N	54	SER
4	O	6	SER
4	O	11	VAL
4	O	30	VAL
4	P	27	ARG
4	P	47	THR
4	Q	19	ARG
4	Q	134	ALA
5	R	23	ASN
5	R	27	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
5	R	52	ALA
6	T	176	SER
1	X	10	ALA
1	4	12	ARG
1	8	12	ARG
1	8	20	GLY
2	A	78	TYR
2	A	155	PRO
2	A	210	LYS
2	A	240	ASP
2	A	439	ARG
2	A	558	ALA
2	A	692	SER
2	A	718	SER
2	A	836	TYR
2	B	5	SER
2	B	16	ALA
2	B	210	LYS
2	B	220	GLY
2	B	262	ASN
2	B	330	GLY
2	B	560	LYS
2	B	659	SER
2	B	691	TYR
2	B	800	ASN
2	B	906	LEU
2	B	939	ASN
2	C	130	PRO
2	C	210	LYS
2	C	240	ASP
2	C	815	ASN
2	C	842	GLY
2	C	887	SER
2	C	939	ASN
2	D	36	ASP
2	D	78	TYR
2	D	291	PRO
2	D	364	LEU
2	D	506	ALA
2	D	703	TYR
2	D	814	ASN
2	D	901	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	E	16	ALA
2	E	43	ASN
2	E	71	VAL
2	E	198	GLN
2	E	341	GLN
2	E	422	ASN
2	E	718	SER
2	E	815	ASN
2	F	36	ASP
2	F	59	ASP
2	F	219	TYR
2	F	718	SER
2	G	2	ALA
2	G	175	ASP
2	G	186	PHE
2	G	710	LYS
2	G	767	GLY
2	H	37	THR
2	H	173	THR
2	H	263	GLY
2	H	264	GLN
2	H	688	TYR
2	H	764	TYR
2	H	767	GLY
2	H	814	ASN
2	H	836	TYR
2	H	887	SER
2	H	936	SER
2	I	39	PHE
2	I	130	PRO
2	I	174	ALA
2	I	422	ASN
2	I	481	ASN
2	I	767	GLY
2	I	887	SER
2	I	940	ALA
2	J	55	ASP
2	J	142	ASN
2	J	239	ALA
2	J	284	ASP
2	J	562	LEU
2	J	724	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	J	741	GLY
2	J	763	HIS
2	J	764	TYR
2	J	767	GLY
2	K	33	ARG
2	K	54	HIS
2	K	391	HIS
2	K	718	SER
2	K	767	GLY
2	L	7	LEU
2	L	117	SER
2	L	268	LYS
2	L	284	ASP
2	L	767	GLY
2	L	814	ASN
3	M	73	ALA
3	M	86	ASN
4	O	9	GLY
4	O	22	SER
4	O	133	ARG
4	P	119	GLY
4	P	131	GLN
6	S	43	ARG
6	S	73	ASN
6	S	176	SER
6	T	15	PRO
6	T	29	THR
6	T	34	LEU
6	T	73	ASN
6	T	174	SER
1	0	4	ILE
1	2	16	ARG
2	A	38	TYR
2	A	188	PRO
2	A	345	VAL
2	A	674	LYS
2	A	689	PHE
2	A	690	VAL
2	A	703	TYR
2	B	74	GLU
2	B	130	PRO
2	B	175	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	B	340	SER
2	B	426	VAL
2	B	648	ALA
2	B	692	SER
2	B	716	ASP
2	B	843	LYS
2	B	886	ASN
2	C	37	THR
2	C	202	SER
2	C	439	ARG
2	C	764	TYR
2	C	798	GLU
2	D	155	PRO
2	D	186	PHE
2	D	219	TYR
2	D	239	ALA
2	D	439	ARG
2	D	472	PRO
2	D	868	ASN
2	E	86	LEU
2	E	124	LEU
2	E	219	TYR
2	E	284	ASP
2	E	692	SER
2	E	739	VAL
2	F	159	GLU
2	F	168	ILE
2	F	201	GLU
2	F	240	ASP
2	F	291	PRO
2	F	320	PHE
2	F	739	VAL
2	F	814	ASN
2	G	78	TYR
2	G	155	PRO
2	G	268	LYS
2	G	429	GLU
2	G	439	ARG
2	G	730	PRO
2	G	739	VAL
2	G	763	HIS
2	H	38	TYR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	H	67	ARG
2	H	317	ARG
2	I	78	TYR
2	I	703	TYR
2	I	718	SER
2	I	814	ASN
2	J	39	PHE
2	J	155	PRO
2	J	320	PHE
2	J	941	THR
2	K	37	THR
2	K	38	TYR
2	K	239	ALA
2	K	331	ASN
2	K	506	ALA
2	K	835	ASN
2	L	130	PRO
2	L	176	GLN
2	L	293	LYS
2	L	763	HIS
3	M	226	GLU
3	M	528	SER
4	N	33	SER
4	O	18	GLY
4	O	21	PRO
4	P	13	SER
4	P	51	ALA
4	P	56	SER
4	P	133	ARG
4	Q	35	VAL
5	R	25	SER
5	R	42	ASN
6	S	4	GLU
6	S	32	ASN
6	S	35	SER
6	S	96	GLN
6	S	215	ASN
6	T	16	GLN
6	T	26	ASP
6	T	183	ILE
6	T	207	HIS
1	3	23	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	X	24	ASP
1	4	16	ARG
2	A	130	PRO
2	A	166	LEU
2	A	284	ASP
2	A	602	SER
2	A	726	ARG
2	A	739	VAL
2	A	940	ALA
2	B	60	ARG
2	B	64	LEU
2	B	72	ASP
2	B	131	ASN
2	B	166	LEU
2	B	284	ASP
2	B	291	PRO
2	B	602	SER
2	B	739	VAL
2	B	903	SER
2	C	185	THR
2	C	331	ASN
2	C	685	PHE
2	C	703	TYR
2	C	739	VAL
2	C	940	ALA
2	D	38	TYR
2	D	407	SER
2	E	186	PHE
2	E	291	PRO
2	E	706	HIS
2	E	814	ASN
2	F	123	SER
2	F	130	PRO
2	F	429	GLU
2	F	439	ARG
2	F	602	SER
2	F	717	SER
2	F	740	ASP
2	G	130	PRO
2	G	284	ASP
2	G	814	ASN
2	H	155	PRO

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	H	429	GLU
2	H	561	SER
2	I	155	PRO
2	I	423	ASP
2	I	439	ARG
2	I	730	PRO
2	I	731	ASN
2	I	858	ARG
2	J	130	PRO
2	J	139	LYS
2	J	186	PHE
2	J	739	VAL
2	J	775	GLU
2	J	814	ASN
2	K	172	ALA
2	K	284	ASP
2	K	429	GLU
2	K	596	ALA
2	K	739	VAL
2	K	747	ALA
2	L	131	ASN
2	L	506	ALA
2	L	739	VAL
3	M	383	TRP
4	O	14	PRO
4	P	20	LEU
4	P	134	ALA
6	S	31	MET
1	W	19	MET
2	A	678	THR
2	B	75	ASP
2	B	242	VAL
2	B	268	LYS
2	B	341	GLN
2	B	429	GLU
2	B	439	ARG
2	B	658	PRO
2	B	703	TYR
2	B	921	PRO
2	D	201	GLU
2	D	658	PRO
2	D	679	PRO

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	D	933	THR
2	E	876	THR
2	F	39	PHE
2	F	314	ILE
2	F	703	TYR
2	F	705	ASN
2	G	396	GLU
2	G	703	TYR
2	G	719	VAL
2	G	722	PRO
2	H	54	HIS
2	H	284	ASP
2	J	115	PRO
2	J	725	ASP
2	K	115	PRO
6	T	104	SER
2	A	933	THR
2	B	261	VAL
2	C	56	VAL
2	I	524	PRO
2	J	56	VAL
2	L	504	VAL
1	X	11	PRO
1	8	11	PRO
2	A	115	PRO
2	B	504	VAL
2	H	864	PRO
2	H	921	PRO
2	K	730	PRO
6	T	92	PRO
2	A	114	LYS
2	B	934	PRO
2	D	283	PRO
2	I	921	PRO
4	N	20	LEU
2	F	472	PRO
2	L	647	PRO
1	4	14	GLY

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	0	7/203 (3%)	7 (100%)	0	100	100
1	1	15/203 (7%)	14 (93%)	1 (7%)	16	45
1	2	18/203 (9%)	17 (94%)	1 (6%)	21	51
1	3	22/203 (11%)	19 (86%)	3 (14%)	3	15
1	4	19/203 (9%)	18 (95%)	1 (5%)	22	53
1	8	20/203 (10%)	19 (95%)	1 (5%)	24	55
1	U	10/203 (5%)	9 (90%)	1 (10%)	7	27
1	V	17/203 (8%)	14 (82%)	3 (18%)	2	8
1	W	20/203 (10%)	19 (95%)	1 (5%)	24	55
1	X	22/203 (11%)	22 (100%)	0	100	100
1	Y	22/203 (11%)	22 (100%)	0	100	100
1	Z	7/203 (3%)	7 (100%)	0	100	100
2	A	810/810 (100%)	798 (98%)	12 (2%)	65	84
2	B	810/810 (100%)	787 (97%)	23 (3%)	43	71
2	C	810/810 (100%)	791 (98%)	19 (2%)	50	75
2	D	810/810 (100%)	790 (98%)	20 (2%)	47	74
2	E	810/810 (100%)	795 (98%)	15 (2%)	57	79
2	F	810/810 (100%)	790 (98%)	20 (2%)	47	74
2	G	810/810 (100%)	794 (98%)	16 (2%)	55	78
2	H	810/810 (100%)	796 (98%)	14 (2%)	60	82
2	I	810/810 (100%)	795 (98%)	15 (2%)	57	79
2	J	810/810 (100%)	800 (99%)	10 (1%)	71	87
2	K	810/810 (100%)	797 (98%)	13 (2%)	62	83
2	L	810/810 (100%)	798 (98%)	12 (2%)	65	84
3	M	393/461 (85%)	389 (99%)	4 (1%)	76	89
4	N	74/105 (70%)	72 (97%)	2 (3%)	44	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	O	64/105 (61%)	63 (98%)	1 (2%)	62	83
4	P	79/105 (75%)	76 (96%)	3 (4%)	33	64
4	Q	58/105 (55%)	55 (95%)	3 (5%)	23	54
5	R	96/502 (19%)	93 (97%)	3 (3%)	40	69
6	S	149/189 (79%)	146 (98%)	3 (2%)	55	78
6	T	151/189 (80%)	146 (97%)	5 (3%)	38	68
All	All	10983/13917 (79%)	10758 (98%)	225 (2%)	57	78

All (225) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	U	12	ARG
1	1	12	ARG
1	V	19	MET
1	V	22	TRP
1	V	24	ASP
1	2	16	ARG
1	W	16	ARG
1	3	5	ASN
1	3	12	ARG
1	3	16	ARG
1	4	16	ARG
1	8	4	ILE
2	A	153	VAL
2	A	178	LYS
2	A	245	LYS
2	A	319	ASN
2	A	332	MET
2	A	536	ARG
2	A	560	LYS
2	A	690	VAL
2	A	714	THR
2	A	827	ARG
2	A	835	ASN
2	A	843	LYS
2	B	44	LYS
2	B	58	THR
2	B	64	LEU
2	B	153	VAL
2	B	185	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	B	211	LYS
2	B	342	LEU
2	B	343	ASN
2	B	390	ASN
2	B	574	ASN
2	B	593	THR
2	B	633	PHE
2	B	644	TYR
2	B	646	ILE
2	B	651	THR
2	B	653	VAL
2	B	689	PHE
2	B	710	LYS
2	B	800	ASN
2	B	827	ARG
2	B	841	ILE
2	B	894	ASN
2	B	904	THR
2	C	37	THR
2	C	53	THR
2	C	65	THR
2	C	138	LYS
2	C	185	THR
2	C	211	LYS
2	C	281	GLU
2	C	319	ASN
2	C	404	LEU
2	C	560	LYS
2	C	566	PRO
2	C	573	TRP
2	C	634	ASN
2	C	653	VAL
2	C	802	LYS
2	C	826	MET
2	C	827	ARG
2	C	870	MET
2	C	933	THR
2	D	10	TRP
2	D	53	THR
2	D	138	LYS
2	D	197	TRP
2	D	211	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	D	293	LYS
2	D	352	ASN
2	D	373	MET
2	D	450	MET
2	D	572	GLU
2	D	573	TRP
2	D	643	LEU
2	D	710	LYS
2	D	869	PHE
2	D	872	MET
2	D	882	MET
2	D	900	MET
2	D	904	THR
2	D	905	LEU
2	D	933	THR
2	E	67	ARG
2	E	109	ARG
2	E	146	MET
2	E	211	LYS
2	E	229	LYS
2	E	503	LEU
2	E	566	PRO
2	E	571	TYR
2	E	573	TRP
2	E	589	ASN
2	E	793	ARG
2	E	827	ARG
2	E	836	TYR
2	E	904	THR
2	E	919	HIS
2	F	1	MET
2	F	41	LEU
2	F	53	THR
2	F	82	VAL
2	F	109	ARG
2	F	146	MET
2	F	153	VAL
2	F	211	LYS
2	F	264	GLN
2	F	285	THR
2	F	321	ILE
2	F	373	MET

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	F	417	LYS
2	F	450	MET
2	F	487	ASN
2	F	589	ASN
2	F	614	HIS
2	F	746	VAL
2	F	827	ARG
2	F	843	LYS
2	G	3	THR
2	G	19	ASP
2	G	21	SER
2	G	57	THR
2	G	280	LEU
2	G	301	ASN
2	G	352	ASN
2	G	371	PHE
2	G	481	ASN
2	G	509	ASN
2	G	573	TRP
2	G	634	ASN
2	G	676	LYS
2	G	793	ARG
2	G	827	ARG
2	G	904	THR
2	H	37	THR
2	H	67	ARG
2	H	68	PHE
2	H	74	GLU
2	H	153	VAL
2	H	211	LYS
2	H	391	HIS
2	H	455	GLN
2	H	614	HIS
2	H	633	PHE
2	H	714	THR
2	H	827	ARG
2	H	843	LYS
2	H	914	ASP
2	I	1	MET
2	I	72	ASP
2	I	167	GLN
2	I	173	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	I	211	LYS
2	I	268	LYS
2	I	481	ASN
2	I	573	TRP
2	I	598	ILE
2	I	660	ARG
2	I	793	ARG
2	I	795	VAL
2	I	872	MET
2	I	920	GLN
2	I	933	THR
2	J	211	LYS
2	J	285	THR
2	J	307	MET
2	J	542	ASN
2	J	601	THR
2	J	614	HIS
2	J	827	ARG
2	J	904	THR
2	J	920	GLN
2	J	933	THR
2	K	138	LYS
2	K	153	VAL
2	K	211	LYS
2	K	321	ILE
2	K	371	PHE
2	K	589	ASN
2	K	635	ASP
2	K	802	LYS
2	K	827	ARG
2	K	853	LYS
2	K	886	ASN
2	K	915	VAL
2	K	917	ARG
2	L	37	THR
2	L	82	VAL
2	L	184	LYS
2	L	211	LYS
2	L	573	TRP
2	L	634	ASN
2	L	710	LYS
2	L	748	GLN

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Mol	Chain	Res	Type
2	L	793	ARG
2	L	827	ARG
2	L	843	LYS
2	L	856	CYS
3	M	81	GLN
3	M	225	THR
3	M	232	VAL
3	M	467	VAL
4	N	17	THR
4	N	41	GLN
4	O	14	PRO
4	P	27	ARG
4	P	103	LYS
4	P	131	GLN
4	Q	15	TYR
4	Q	23	TRP
4	Q	27	ARG
5	R	23	ASN
5	R	58	ILE
5	R	81	LEU
6	S	96	GLN
6	S	165	ARG
6	S	179	ARG
6	T	13	TYR
6	T	43	ARG
6	T	48	ARG
6	T	51	ARG
6	T	62	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 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-24408. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections

This section was not generated.

### 6.2 Central slices

This section was not generated.

### 6.3 Largest variance slices

This section was not generated.

### 6.4 Orthogonal surface views

This section was not generated.

### 6.5 Mask visualisation

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

This section was not generated.

### 7.2 Volume estimate versus contour level

This section was not generated.

### 7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.



## 8 Fourier-Shell correlation

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

## 9 Map-model fit

This section was not generated.