



Full wwPDB/EMDataBank EM Map/Model Validation Report ⓘ

Nov 2, 2017 – 06:39 AM EDT

PDB ID : 5W9L
EMDB ID: : EMD-8787
Title : MERS S ectodomain trimer in complex with variable domain of neutralizing antibody G4
Authors : Pallesen, J.; Ward, A.B.
Deposited on : unknown
Resolution : 4.80 Å(reported)

This is a Full wwPDB/EMDataBank EM Map/Model Validation Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

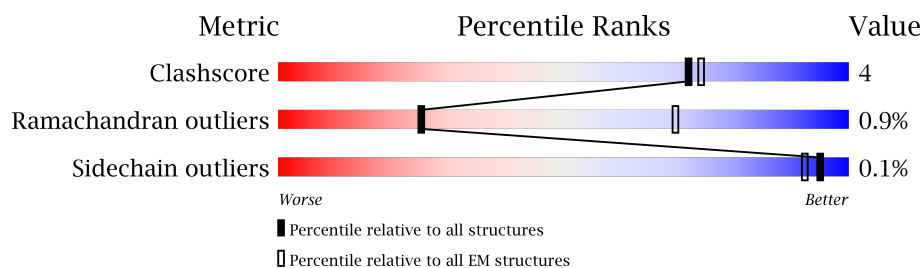
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	1329	
1	B	1329	
1	C	1329	
1	D	1329	
1	G	1329	
1	J	1329	
2	E	233	
2	H	233	
3	F	218	

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Mol	Chain	Length	Quality of chain
3	I	218	<div>49%</div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 31118 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	456	Total	C	N	O	S	0	0
			3488	2210	588	673	17		
1	D	463	Total	C	N	O	S	0	0
			3545	2243	600	685	17		
1	G	463	Total	C	N	O	S	0	0
			3545	2243	600	685	17		
1	B	726	Total	C	N	O	S	0	0
			5658	3601	926	1097	34		
1	C	726	Total	C	N	O	S	0	0
			5658	3601	926	1097	34		
1	J	726	Total	C	N	O	S	0	0
			5658	3601	926	1097	34		

There are 258 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	506	PHE	LEU	conflict	UNP W5ZZF5
A	748	ALA	ARG	conflict	UNP W5ZZF5
A	751	GLY	ARG	conflict	UNP W5ZZF5
A	1060	PRO	VAL	engineered mutation	UNP W5ZZF5
A	1061	PRO	LEU	engineered mutation	UNP W5ZZF5
A	1292	GLY	-	expression tag	UNP W5ZZF5
A	1293	SER	-	expression tag	UNP W5ZZF5
A	1294	GLY	-	expression tag	UNP W5ZZF5
A	1295	TYR	-	expression tag	UNP W5ZZF5
A	1296	ILE	-	expression tag	UNP W5ZZF5
A	1297	PRO	-	expression tag	UNP W5ZZF5
A	1298	GLU	-	expression tag	UNP W5ZZF5
A	1299	ALA	-	expression tag	UNP W5ZZF5
A	1300	PRO	-	expression tag	UNP W5ZZF5
A	1301	ARG	-	expression tag	UNP W5ZZF5
A	1302	ASP	-	expression tag	UNP W5ZZF5
A	1303	GLY	-	expression tag	UNP W5ZZF5
A	1304	GLN	-	expression tag	UNP W5ZZF5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1305	ALA	-	expression tag	UNP W5ZZF5
A	1306	TYR	-	expression tag	UNP W5ZZF5
A	1307	VAL	-	expression tag	UNP W5ZZF5
A	1308	ARG	-	expression tag	UNP W5ZZF5
A	1309	LYS	-	expression tag	UNP W5ZZF5
A	1310	ASP	-	expression tag	UNP W5ZZF5
A	1311	GLY	-	expression tag	UNP W5ZZF5
A	1312	GLU	-	expression tag	UNP W5ZZF5
A	1313	TRP	-	expression tag	UNP W5ZZF5
A	1314	VAL	-	expression tag	UNP W5ZZF5
A	1315	LEU	-	expression tag	UNP W5ZZF5
A	1316	LEU	-	expression tag	UNP W5ZZF5
A	1317	SER	-	expression tag	UNP W5ZZF5
A	1318	THR	-	expression tag	UNP W5ZZF5
A	1319	PHE	-	expression tag	UNP W5ZZF5
A	1320	LEU	-	expression tag	UNP W5ZZF5
A	1321	GLY	-	expression tag	UNP W5ZZF5
A	1322	ARG	-	expression tag	UNP W5ZZF5
A	1323	SER	-	expression tag	UNP W5ZZF5
A	1324	LEU	-	expression tag	UNP W5ZZF5
A	1325	GLU	-	expression tag	UNP W5ZZF5
A	1326	VAL	-	expression tag	UNP W5ZZF5
A	1327	LEU	-	expression tag	UNP W5ZZF5
A	1328	PHE	-	expression tag	UNP W5ZZF5
A	1329	GLN	-	expression tag	UNP W5ZZF5
D	506	PHE	LEU	conflict	UNP W5ZZF5
D	748	ALA	ARG	conflict	UNP W5ZZF5
D	751	GLY	ARG	conflict	UNP W5ZZF5
D	1060	PRO	VAL	engineered mutation	UNP W5ZZF5
D	1061	PRO	LEU	engineered mutation	UNP W5ZZF5
D	1292	GLY	-	expression tag	UNP W5ZZF5
D	1293	SER	-	expression tag	UNP W5ZZF5
D	1294	GLY	-	expression tag	UNP W5ZZF5
D	1295	TYR	-	expression tag	UNP W5ZZF5
D	1296	ILE	-	expression tag	UNP W5ZZF5
D	1297	PRO	-	expression tag	UNP W5ZZF5
D	1298	GLU	-	expression tag	UNP W5ZZF5
D	1299	ALA	-	expression tag	UNP W5ZZF5
D	1300	PRO	-	expression tag	UNP W5ZZF5
D	1301	ARG	-	expression tag	UNP W5ZZF5
D	1302	ASP	-	expression tag	UNP W5ZZF5
D	1303	GLY	-	expression tag	UNP W5ZZF5

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1304	GLN	-	expression tag	UNP W5ZZF5
D	1305	ALA	-	expression tag	UNP W5ZZF5
D	1306	TYR	-	expression tag	UNP W5ZZF5
D	1307	VAL	-	expression tag	UNP W5ZZF5
D	1308	ARG	-	expression tag	UNP W5ZZF5
D	1309	LYS	-	expression tag	UNP W5ZZF5
D	1310	ASP	-	expression tag	UNP W5ZZF5
D	1311	GLY	-	expression tag	UNP W5ZZF5
D	1312	GLU	-	expression tag	UNP W5ZZF5
D	1313	TRP	-	expression tag	UNP W5ZZF5
D	1314	VAL	-	expression tag	UNP W5ZZF5
D	1315	LEU	-	expression tag	UNP W5ZZF5
D	1316	LEU	-	expression tag	UNP W5ZZF5
D	1317	SER	-	expression tag	UNP W5ZZF5
D	1318	THR	-	expression tag	UNP W5ZZF5
D	1319	PHE	-	expression tag	UNP W5ZZF5
D	1320	LEU	-	expression tag	UNP W5ZZF5
D	1321	GLY	-	expression tag	UNP W5ZZF5
D	1322	ARG	-	expression tag	UNP W5ZZF5
D	1323	SER	-	expression tag	UNP W5ZZF5
D	1324	LEU	-	expression tag	UNP W5ZZF5
D	1325	GLU	-	expression tag	UNP W5ZZF5
D	1326	VAL	-	expression tag	UNP W5ZZF5
D	1327	LEU	-	expression tag	UNP W5ZZF5
D	1328	PHE	-	expression tag	UNP W5ZZF5
D	1329	GLN	-	expression tag	UNP W5ZZF5
G	506	PHE	LEU	conflict	UNP W5ZZF5
G	748	ALA	ARG	conflict	UNP W5ZZF5
G	751	GLY	ARG	conflict	UNP W5ZZF5
G	1060	PRO	VAL	engineered mutation	UNP W5ZZF5
G	1061	PRO	LEU	engineered mutation	UNP W5ZZF5
G	1292	GLY	-	expression tag	UNP W5ZZF5
G	1293	SER	-	expression tag	UNP W5ZZF5
G	1294	GLY	-	expression tag	UNP W5ZZF5
G	1295	TYR	-	expression tag	UNP W5ZZF5
G	1296	ILE	-	expression tag	UNP W5ZZF5
G	1297	PRO	-	expression tag	UNP W5ZZF5
G	1298	GLU	-	expression tag	UNP W5ZZF5
G	1299	ALA	-	expression tag	UNP W5ZZF5
G	1300	PRO	-	expression tag	UNP W5ZZF5
G	1301	ARG	-	expression tag	UNP W5ZZF5
G	1302	ASP	-	expression tag	UNP W5ZZF5

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1303	GLY	-	expression tag	UNP W5ZZF5
G	1304	GLN	-	expression tag	UNP W5ZZF5
G	1305	ALA	-	expression tag	UNP W5ZZF5
G	1306	TYR	-	expression tag	UNP W5ZZF5
G	1307	VAL	-	expression tag	UNP W5ZZF5
G	1308	ARG	-	expression tag	UNP W5ZZF5
G	1309	LYS	-	expression tag	UNP W5ZZF5
G	1310	ASP	-	expression tag	UNP W5ZZF5
G	1311	GLY	-	expression tag	UNP W5ZZF5
G	1312	GLU	-	expression tag	UNP W5ZZF5
G	1313	TRP	-	expression tag	UNP W5ZZF5
G	1314	VAL	-	expression tag	UNP W5ZZF5
G	1315	LEU	-	expression tag	UNP W5ZZF5
G	1316	LEU	-	expression tag	UNP W5ZZF5
G	1317	SER	-	expression tag	UNP W5ZZF5
G	1318	THR	-	expression tag	UNP W5ZZF5
G	1319	PHE	-	expression tag	UNP W5ZZF5
G	1320	LEU	-	expression tag	UNP W5ZZF5
G	1321	GLY	-	expression tag	UNP W5ZZF5
G	1322	ARG	-	expression tag	UNP W5ZZF5
G	1323	SER	-	expression tag	UNP W5ZZF5
G	1324	LEU	-	expression tag	UNP W5ZZF5
G	1325	GLU	-	expression tag	UNP W5ZZF5
G	1326	VAL	-	expression tag	UNP W5ZZF5
G	1327	LEU	-	expression tag	UNP W5ZZF5
G	1328	PHE	-	expression tag	UNP W5ZZF5
G	1329	GLN	-	expression tag	UNP W5ZZF5
B	506	PHE	LEU	conflict	UNP W5ZZF5
B	748	ALA	ARG	conflict	UNP W5ZZF5
B	751	GLY	ARG	conflict	UNP W5ZZF5
B	1060	PRO	VAL	engineered mutation	UNP W5ZZF5
B	1061	PRO	LEU	engineered mutation	UNP W5ZZF5
B	1292	GLY	-	expression tag	UNP W5ZZF5
B	1293	SER	-	expression tag	UNP W5ZZF5
B	1294	GLY	-	expression tag	UNP W5ZZF5
B	1295	TYR	-	expression tag	UNP W5ZZF5
B	1296	ILE	-	expression tag	UNP W5ZZF5
B	1297	PRO	-	expression tag	UNP W5ZZF5
B	1298	GLU	-	expression tag	UNP W5ZZF5
B	1299	ALA	-	expression tag	UNP W5ZZF5
B	1300	PRO	-	expression tag	UNP W5ZZF5
B	1301	ARG	-	expression tag	UNP W5ZZF5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1302	ASP	-	expression tag	UNP W5ZZF5
B	1303	GLY	-	expression tag	UNP W5ZZF5
B	1304	GLN	-	expression tag	UNP W5ZZF5
B	1305	ALA	-	expression tag	UNP W5ZZF5
B	1306	TYR	-	expression tag	UNP W5ZZF5
B	1307	VAL	-	expression tag	UNP W5ZZF5
B	1308	ARG	-	expression tag	UNP W5ZZF5
B	1309	LYS	-	expression tag	UNP W5ZZF5
B	1310	ASP	-	expression tag	UNP W5ZZF5
B	1311	GLY	-	expression tag	UNP W5ZZF5
B	1312	GLU	-	expression tag	UNP W5ZZF5
B	1313	TRP	-	expression tag	UNP W5ZZF5
B	1314	VAL	-	expression tag	UNP W5ZZF5
B	1315	LEU	-	expression tag	UNP W5ZZF5
B	1316	LEU	-	expression tag	UNP W5ZZF5
B	1317	SER	-	expression tag	UNP W5ZZF5
B	1318	THR	-	expression tag	UNP W5ZZF5
B	1319	PHE	-	expression tag	UNP W5ZZF5
B	1320	LEU	-	expression tag	UNP W5ZZF5
B	1321	GLY	-	expression tag	UNP W5ZZF5
B	1322	ARG	-	expression tag	UNP W5ZZF5
B	1323	SER	-	expression tag	UNP W5ZZF5
B	1324	LEU	-	expression tag	UNP W5ZZF5
B	1325	GLU	-	expression tag	UNP W5ZZF5
B	1326	VAL	-	expression tag	UNP W5ZZF5
B	1327	LEU	-	expression tag	UNP W5ZZF5
B	1328	PHE	-	expression tag	UNP W5ZZF5
B	1329	GLN	-	expression tag	UNP W5ZZF5
C	506	PHE	LEU	conflict	UNP W5ZZF5
C	748	ALA	ARG	conflict	UNP W5ZZF5
C	751	GLY	ARG	conflict	UNP W5ZZF5
C	1060	PRO	VAL	engineered mutation	UNP W5ZZF5
C	1061	PRO	LEU	engineered mutation	UNP W5ZZF5
C	1292	GLY	-	expression tag	UNP W5ZZF5
C	1293	SER	-	expression tag	UNP W5ZZF5
C	1294	GLY	-	expression tag	UNP W5ZZF5
C	1295	TYR	-	expression tag	UNP W5ZZF5
C	1296	ILE	-	expression tag	UNP W5ZZF5
C	1297	PRO	-	expression tag	UNP W5ZZF5
C	1298	GLU	-	expression tag	UNP W5ZZF5
C	1299	ALA	-	expression tag	UNP W5ZZF5
C	1300	PRO	-	expression tag	UNP W5ZZF5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1301	ARG	-	expression tag	UNP W5ZZF5
C	1302	ASP	-	expression tag	UNP W5ZZF5
C	1303	GLY	-	expression tag	UNP W5ZZF5
C	1304	GLN	-	expression tag	UNP W5ZZF5
C	1305	ALA	-	expression tag	UNP W5ZZF5
C	1306	TYR	-	expression tag	UNP W5ZZF5
C	1307	VAL	-	expression tag	UNP W5ZZF5
C	1308	ARG	-	expression tag	UNP W5ZZF5
C	1309	LYS	-	expression tag	UNP W5ZZF5
C	1310	ASP	-	expression tag	UNP W5ZZF5
C	1311	GLY	-	expression tag	UNP W5ZZF5
C	1312	GLU	-	expression tag	UNP W5ZZF5
C	1313	TRP	-	expression tag	UNP W5ZZF5
C	1314	VAL	-	expression tag	UNP W5ZZF5
C	1315	LEU	-	expression tag	UNP W5ZZF5
C	1316	LEU	-	expression tag	UNP W5ZZF5
C	1317	SER	-	expression tag	UNP W5ZZF5
C	1318	THR	-	expression tag	UNP W5ZZF5
C	1319	PHE	-	expression tag	UNP W5ZZF5
C	1320	LEU	-	expression tag	UNP W5ZZF5
C	1321	GLY	-	expression tag	UNP W5ZZF5
C	1322	ARG	-	expression tag	UNP W5ZZF5
C	1323	SER	-	expression tag	UNP W5ZZF5
C	1324	LEU	-	expression tag	UNP W5ZZF5
C	1325	GLU	-	expression tag	UNP W5ZZF5
C	1326	VAL	-	expression tag	UNP W5ZZF5
C	1327	LEU	-	expression tag	UNP W5ZZF5
C	1328	PHE	-	expression tag	UNP W5ZZF5
C	1329	GLN	-	expression tag	UNP W5ZZF5
J	506	PHE	LEU	conflict	UNP W5ZZF5
J	748	ALA	ARG	conflict	UNP W5ZZF5
J	751	GLY	ARG	conflict	UNP W5ZZF5
J	1060	PRO	VAL	engineered mutation	UNP W5ZZF5
J	1061	PRO	LEU	engineered mutation	UNP W5ZZF5
J	1292	GLY	-	expression tag	UNP W5ZZF5
J	1293	SER	-	expression tag	UNP W5ZZF5
J	1294	GLY	-	expression tag	UNP W5ZZF5
J	1295	TYR	-	expression tag	UNP W5ZZF5
J	1296	ILE	-	expression tag	UNP W5ZZF5
J	1297	PRO	-	expression tag	UNP W5ZZF5
J	1298	GLU	-	expression tag	UNP W5ZZF5
J	1299	ALA	-	expression tag	UNP W5ZZF5

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Chain	Residue	Modelled	Actual	Comment	Reference
J	1300	PRO	-	expression tag	UNP W5ZZF5
J	1301	ARG	-	expression tag	UNP W5ZZF5
J	1302	ASP	-	expression tag	UNP W5ZZF5
J	1303	GLY	-	expression tag	UNP W5ZZF5
J	1304	GLN	-	expression tag	UNP W5ZZF5
J	1305	ALA	-	expression tag	UNP W5ZZF5
J	1306	TYR	-	expression tag	UNP W5ZZF5
J	1307	VAL	-	expression tag	UNP W5ZZF5
J	1308	ARG	-	expression tag	UNP W5ZZF5
J	1309	LYS	-	expression tag	UNP W5ZZF5
J	1310	ASP	-	expression tag	UNP W5ZZF5
J	1311	GLY	-	expression tag	UNP W5ZZF5
J	1312	GLU	-	expression tag	UNP W5ZZF5
J	1313	TRP	-	expression tag	UNP W5ZZF5
J	1314	VAL	-	expression tag	UNP W5ZZF5
J	1315	LEU	-	expression tag	UNP W5ZZF5
J	1316	LEU	-	expression tag	UNP W5ZZF5
J	1317	SER	-	expression tag	UNP W5ZZF5
J	1318	THR	-	expression tag	UNP W5ZZF5
J	1319	PHE	-	expression tag	UNP W5ZZF5
J	1320	LEU	-	expression tag	UNP W5ZZF5
J	1321	GLY	-	expression tag	UNP W5ZZF5
J	1322	ARG	-	expression tag	UNP W5ZZF5
J	1323	SER	-	expression tag	UNP W5ZZF5
J	1324	LEU	-	expression tag	UNP W5ZZF5
J	1325	GLU	-	expression tag	UNP W5ZZF5
J	1326	VAL	-	expression tag	UNP W5ZZF5
J	1327	LEU	-	expression tag	UNP W5ZZF5
J	1328	PHE	-	expression tag	UNP W5ZZF5
J	1329	GLN	-	expression tag	UNP W5ZZF5

- Molecule 2 is a protein called G4 VH.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	119	Total	C	N	O	S	0	0
			948	602	156	185	5		
2	H	119	Total	C	N	O	S	0	0
			948	602	156	185	5		

- Molecule 3 is a protein called G4 VL.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	111	Total 835	C 522	N 143	O 166	S 4	0	0
3	I	111	Total 835	C 522	N 143	O 166	S 4	0	0

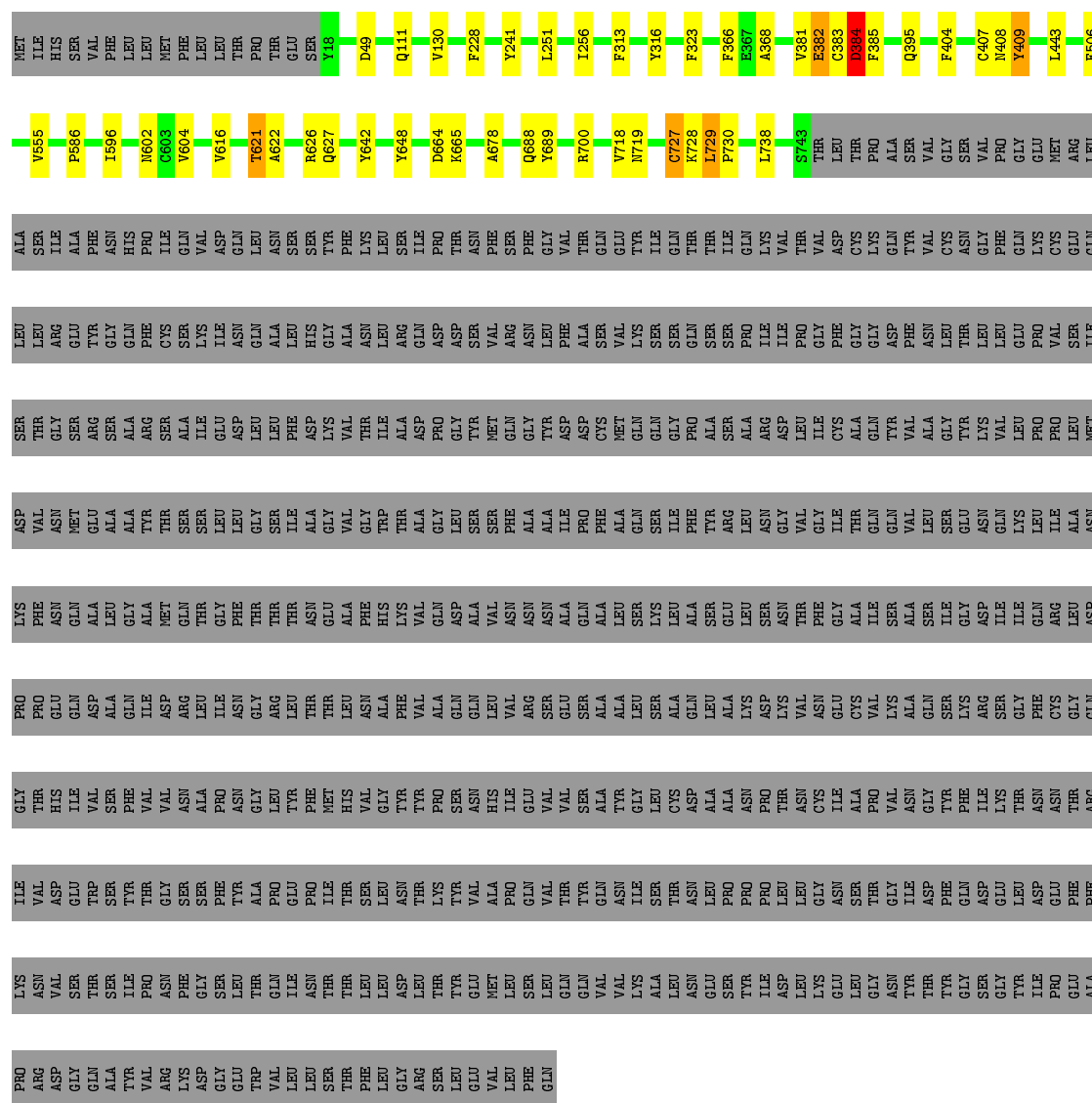
- Molecule 1: Spike glycoprotein

Chain G: 32% 1% 65%

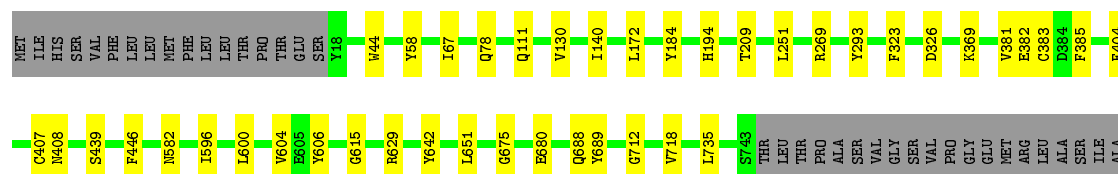
WORLDWIDE
PDB
PROTEIN DATA BANK

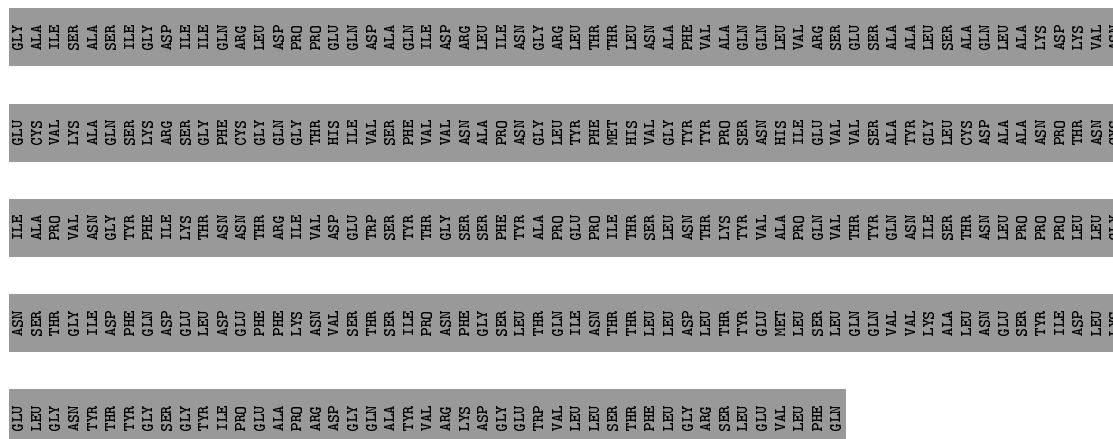
 **EMDDataBank**
Unified Data Resource for 3DEM

Chain B: 51% 1% 45%

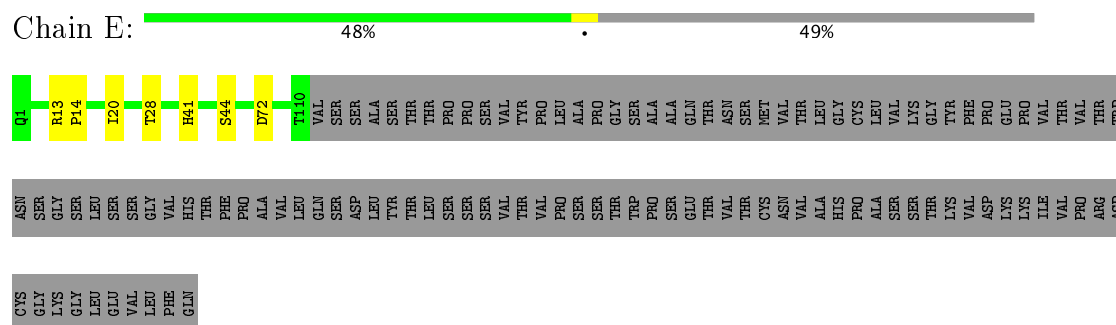


Chain C: 51% • 45%

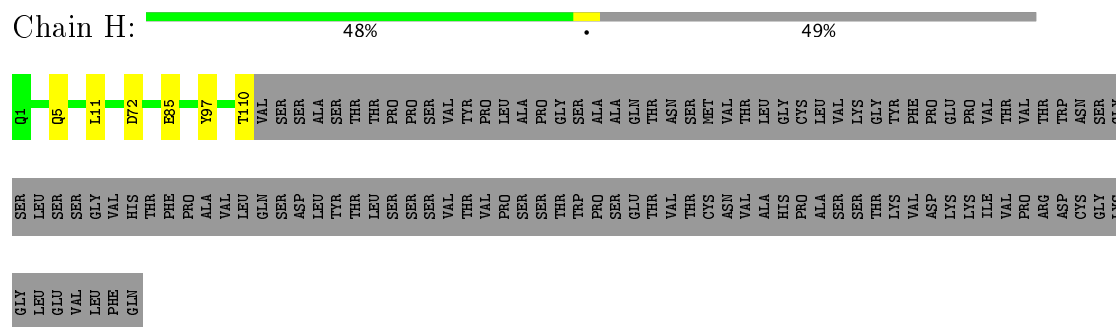




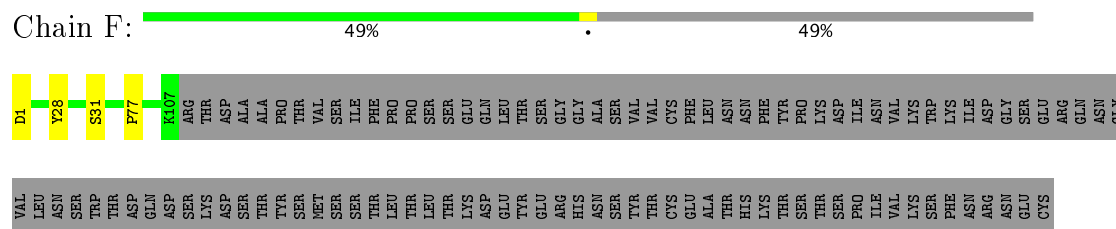
- Molecule 2: G4 VH



- Molecule 2: G4 VH



- Molecule 3: G4 VL



- Molecule 3: G4 VL



D1	12	F36	P77	Y86	K92	K107	ARG	THR	ASP	ALA	ALA	PRO	THR	VAL	SER	SER	PHE	PRO	PRO	SER	SER	GLU	GLN	LEU	THR	SER	GLY	GLY	ALA	SER	VAL	VAL	CYS	PHE	LEU	ASN	ASN	PHE	TYR	PRO	LYS	ASP	ILE	ASN	VAL	LYS	LYS	TRP	ILE	ASP	GLY	SER	GLU	ARG						
GLN	ASN	GLY	VAL	LEU	ASN	SER	TRP	THR	ASP	GLN	ASP	SER	LYS	ASP	SER	THR	TYR	SER	MET	SER	SER	THR	LEU	THR	LEU	THR	LYS	ASP	GLU	TYR	GLU	ARG	HIS	ASN	SER	TYR	THR	CYS	GLU	ALA	ALA	THR	HIS	LYS	THR	SER	THR	SER	PRO	ILE	ASN	VAL	LYS	SER	PHE	ASN	ARG	ASN	GLU	CYS

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	8496	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 ($e^-/\text{\AA}^2$)	1.89	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	29000	Depositor
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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.77	0/3560	0.75	2/4840 (0.0%)
1	B	0.72	0/5803	0.88	7/7901 (0.1%)
1	C	0.73	0/5803	0.91	6/7901 (0.1%)
1	D	0.76	0/3618	0.75	3/4921 (0.1%)
1	G	0.76	0/3618	0.75	2/4921 (0.0%)
1	J	0.73	0/5803	0.93	13/7901 (0.2%)
2	E	0.75	0/972	0.79	0/1317
2	H	0.72	0/972	0.81	1/1317 (0.1%)
3	F	0.79	0/852	0.78	0/1153
3	I	0.77	0/852	0.76	0/1153
All	All	0.74	0/31853	0.84	34/43325 (0.1%)

There are no bond length outliers.

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	642	TYR	CB-CG-CD2	-8.50	115.90	121.00
1	J	323	PHE	CB-CG-CD1	7.65	126.16	120.80
1	G	932	TYR	CB-CG-CD1	-7.46	116.53	121.00
1	J	323	PHE	CB-CG-CD2	-7.20	115.76	120.80
1	C	184	TYR	CB-CG-CD1	-7.14	116.71	121.00
1	J	399	PHE	CB-CG-CD1	-7.11	115.82	120.80
1	C	323	PHE	CB-CG-CD2	-6.99	115.91	120.80
1	J	437	CYS	O-C-N	-6.92	111.63	122.70
1	C	323	PHE	CB-CG-CD1	6.90	125.63	120.80
1	C	58	TYR	CB-CG-CD2	-6.57	117.06	121.00
1	J	691	ARG	NE-CZ-NH2	-6.52	117.04	120.30
2	H	97	TYR	CB-CG-CD2	-5.85	117.49	121.00
1	B	241	TYR	CB-CG-CD2	-5.82	117.51	121.00
1	B	316	TYR	CB-CG-CD1	-5.80	117.52	121.00
1	J	190	ARG	NE-CZ-NH1	5.61	123.11	120.30
1	J	652	ARG	NE-CZ-NH2	-5.59	117.50	120.30
1	B	323	PHE	CB-CG-CD1	5.46	124.62	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	313	PHE	CB-CG-CD2	-5.42	117.01	120.80
1	C	293	TYR	CB-CG-CD2	-5.40	117.76	121.00
1	D	887	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	B	366	PHE	CB-CG-CD1	5.38	124.56	120.80
1	J	641	TYR	CB-CG-CD2	-5.31	117.81	121.00
1	G	868	ASP	CB-CG-OD2	5.25	123.03	118.30
1	B	409	TYR	CB-CG-CD1	-5.25	117.85	121.00
1	A	932	TYR	CB-CG-CD2	-5.24	117.86	121.00
1	J	163	ARG	NE-CZ-NH2	-5.24	117.68	120.30
1	D	868	ASP	CB-CG-OD2	5.22	123.00	118.30
1	J	335	ARG	NE-CZ-NH2	-5.21	117.69	120.30
1	J	584	VAL	O-C-N	-5.20	114.38	122.70
1	A	868	ASP	CB-CG-OD2	5.16	122.94	118.30
1	B	642	TYR	CB-CG-CD1	-5.13	117.92	121.00
1	J	497	TYR	CB-CG-CD1	-5.09	117.95	121.00
1	D	758	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	J	648	TYR	CB-CG-CD2	-5.04	117.98	121.00

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	A	3488	0	3413	19	0
1	B	5658	0	5424	73	0
1	C	5658	0	5423	38	0
1	D	3545	0	3471	28	0
1	G	3545	0	3471	27	0
1	J	5658	0	5423	41	0
2	E	948	0	904	4	0
2	H	948	0	904	9	0
3	F	835	0	816	2	0
3	I	835	0	816	5	0
All	All	31118	0	30065	246	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (246) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:506:PHE:CE2	1:J:555:VAL:HG21	1.15	1.61
1:B:506:PHE:CE2	1:B:555:VAL:HG21	1.03	1.54
1:B:506:PHE:CE2	1:B:555:VAL:CG2	1.97	1.48
1:J:506:PHE:CE2	1:J:555:VAL:CG2	2.03	1.40
1:B:506:PHE:HE2	1:B:555:VAL:CG2	1.30	1.36
1:B:384:ASP:O	1:B:404:PHE:CZ	1.81	1.32
1:B:381:VAL:CG1	1:B:408:ASN:N	1.99	1.25
1:D:905:TYR:CE1	1:D:936:PRO:HB3	1.75	1.20
1:B:381:VAL:HG12	1:B:408:ASN:N	1.55	1.17
1:B:381:VAL:HB	1:B:408:ASN:CB	1.64	1.10
1:B:506:PHE:CD2	1:B:555:VAL:HG21	1.88	1.08
1:B:381:VAL:HG12	1:B:408:ASN:H	0.93	1.08
1:J:506:PHE:CD2	1:J:555:VAL:HG21	1.88	1.08
1:B:381:VAL:CG1	1:B:407:CYS:HA	1.88	1.03
1:B:381:VAL:CG1	1:B:408:ASN:H	1.65	1.03
1:B:381:VAL:HB	1:B:408:ASN:HB2	1.39	1.03
1:B:506:PHE:CD2	1:B:555:VAL:CG2	2.43	1.02
1:J:506:PHE:HE2	1:J:555:VAL:CG2	1.49	1.02
1:B:384:ASP:O	1:B:404:PHE:HZ	1.22	1.00
1:D:905:TYR:OH	1:D:936:PRO:HA	1.63	0.99
1:B:381:VAL:HG11	1:B:408:ASN:N	1.81	0.95
1:D:905:TYR:CE1	1:D:936:PRO:CB	2.50	0.95
1:J:506:PHE:CD2	1:J:555:VAL:CG2	2.46	0.93
1:B:728:LYS:O	1:B:730:PRO:CD	2.18	0.92
1:A:905:TYR:CE1	1:A:936:PRO:HB3	2.04	0.92
1:B:381:VAL:HG11	1:B:407:CYS:C	1.89	0.91
1:B:728:LYS:C	1:B:730:PRO:HD3	1.90	0.91
1:G:905:TYR:OH	1:G:935:LEU:C	2.09	0.91
1:D:905:TYR:OH	1:D:936:PRO:CA	2.19	0.91
1:B:381:VAL:CG1	1:B:407:CYS:CA	2.49	0.90
1:B:384:ASP:O	1:B:404:PHE:CE2	2.28	0.87
1:D:905:TYR:HE1	1:D:936:PRO:CB	1.88	0.87
1:B:381:VAL:CG1	1:B:407:CYS:C	2.43	0.86
1:C:383:CYS:HB2	1:C:385:PHE:CE1	2.09	0.86
1:D:905:TYR:HE1	1:D:936:PRO:HB3	1.39	0.85
1:B:728:LYS:O	1:B:730:PRO:HD2	1.78	0.83
1:C:381:VAL:O	1:C:407:CYS:HB2	1.80	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:381:VAL:HG13	1:B:407:CYS:HA	1.64	0.79
1:B:728:LYS:O	1:B:730:PRO:HD3	1.80	0.79
1:J:691:ARG:HA	1:J:691:ARG:NE	2.00	0.77
1:B:506:PHE:CD2	1:B:555:VAL:HG23	2.19	0.77
1:C:680:GLU:OE1	1:C:680:GLU:N	2.17	0.77
1:B:381:VAL:CB	1:B:408:ASN:CB	2.57	0.75
1:B:728:LYS:C	1:B:730:PRO:CD	2.57	0.73
1:J:506:PHE:HE2	1:J:555:VAL:HG22	1.53	0.73
1:B:621:THR:HG22	1:B:622:ALA:H	1.53	0.72
1:B:382:GLU:H	1:B:408:ASN:HB2	1.54	0.72
1:B:621:THR:HG22	1:B:622:ALA:N	2.04	0.72
1:D:905:TYR:OH	1:D:936:PRO:N	2.23	0.72
1:B:384:ASP:CB	1:B:404:PHE:HE2	2.04	0.71
1:C:369:LYS:O	1:C:369:LYS:HG2	1.89	0.70
1:C:385:PHE:CE2	1:C:404:PHE:CE1	2.80	0.69
1:D:871:LEU:O	1:D:871:LEU:HG	1.91	0.68
1:G:905:TYR:OH	1:G:936:PRO:N	2.28	0.67
1:C:381:VAL:O	1:C:407:CYS:CB	2.44	0.66
1:J:506:PHE:CD2	1:J:555:VAL:HG23	2.30	0.65
1:J:506:PHE:HE2	1:J:555:VAL:HG21	0.91	0.64
1:C:381:VAL:O	1:C:407:CYS:CA	2.46	0.63
1:J:381:VAL:O	1:J:407:CYS:HB2	1.98	0.63
1:B:382:GLU:O	1:B:407:CYS:HB2	1.98	0.63
1:B:688:GLN:HB2	1:B:689:TYR:HA	1.81	0.62
1:C:381:VAL:O	1:C:407:CYS:HA	1.98	0.62
2:H:110:THR:HG22	2:H:110:THR:O	2.00	0.62
1:G:915:GLN:HG2	1:G:915:GLN:O	1.99	0.62
1:G:905:TYR:HH	1:G:935:LEU:C	2.00	0.61
2:H:5:GLN:O	2:H:5:GLN:CD	2.39	0.61
2:H:5:GLN:O	2:H:5:GLN:OE1	2.19	0.61
1:B:256:ILE:O	1:B:256:ILE:HG23	2.01	0.60
1:C:194:HIS:O	1:C:194:HIS:ND1	2.35	0.60
1:D:905:TYR:CZ	1:D:936:PRO:HA	2.36	0.59
1:B:381:VAL:HG11	1:B:407:CYS:CA	2.24	0.59
1:D:905:TYR:HE1	1:D:936:PRO:CD	2.15	0.59
1:D:905:TYR:HE1	1:D:936:PRO:CG	2.15	0.59
1:D:905:TYR:OH	1:D:935:LEU:C	2.42	0.58
1:D:905:TYR:CZ	1:D:936:PRO:CA	2.86	0.58
2:H:85:GLU:N	2:H:85:GLU:OE1	2.34	0.58
1:B:621:THR:O	1:B:648:TYR:HD2	1.87	0.57
1:C:385:PHE:HE2	1:C:404:PHE:CE1	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:11:LEU:O	2:H:11:LEU:HD23	2.05	0.57
1:G:905:TYR:HE1	1:G:936:PRO:HD3	1.70	0.56
1:C:596:ILE:HD12	1:C:596:ILE:C	2.26	0.56
1:B:700:ARG:HA	1:B:700:ARG:NE	2.21	0.56
1:D:1173:ILE:HG13	1:D:1185:SER:OG	2.06	0.56
1:B:616:VAL:HG13	1:B:616:VAL:O	2.06	0.56
1:D:897:LYS:HE2	1:D:897:LYS:HA	1.88	0.56
1:B:382:GLU:N	1:B:408:ASN:HB2	2.21	0.55
1:J:399:PHE:N	1:J:399:PHE:CD1	2.73	0.55
1:A:756:GLU:N	1:A:756:GLU:OE1	2.36	0.54
1:B:727:CYS:HB3	1:B:738:LEU:HD23	1.89	0.54
1:B:385:PHE:CE2	1:B:404:PHE:CE1	2.97	0.53
1:B:381:VAL:HG12	1:B:407:CYS:CA	2.30	0.53
1:J:691:ARG:HE	1:J:691:ARG:HA	1.71	0.53
1:G:986:THR:HG21	1:G:1195:GLU:OE2	2.07	0.53
1:D:905:TYR:CE1	1:D:936:PRO:CA	2.91	0.53
1:J:67:ILE:O	1:J:67:ILE:HG13	2.09	0.53
1:C:385:PHE:CD2	1:C:404:PHE:CZ	2.97	0.52
2:H:11:LEU:C	2:H:11:LEU:HD23	2.29	0.52
1:B:604:VAL:HG23	1:B:604:VAL:O	2.09	0.52
1:J:395:GLN:OE1	1:J:395:GLN:HA	2.10	0.52
1:B:382:GLU:HG3	1:B:383:CYS:N	2.24	0.52
1:B:621:THR:CG2	1:B:622:ALA:H	2.21	0.52
1:B:621:THR:CG2	1:B:622:ALA:N	2.73	0.52
1:J:724:VAL:HG11	1:J:727:CYS:SG	2.50	0.52
1:B:506:PHE:HD2	1:B:555:VAL:HG23	1.70	0.52
1:B:382:GLU:HG3	1:B:383:CYS:H	1.75	0.51
3:I:92:LYS:O	3:I:92:LYS:HD3	2.10	0.51
1:J:369:LYS:O	1:J:369:LYS:HG2	2.10	0.51
1:J:620:CYS:O	1:J:621:THR:C	2.49	0.51
1:C:439:SER:HA	1:C:582:ASN:HA	1.94	0.50
1:C:67:ILE:O	1:C:67:ILE:HG23	2.11	0.50
1:J:172:LEU:HD23	1:J:172:LEU:N	2.27	0.50
2:E:20:ILE:HD12	2:E:20:ILE:C	2.32	0.50
1:B:381:VAL:H	1:B:408:ASN:HD22	1.60	0.50
1:B:382:GLU:C	1:B:408:ASN:O	2.50	0.50
1:C:735:LEU:N	1:C:735:LEU:HD12	2.27	0.50
1:C:383:CYS:CB	1:C:385:PHE:CE1	2.89	0.50
1:D:875:GLU:HB3	1:D:886:ALA:HB3	1.94	0.50
1:B:382:GLU:CA	1:B:408:ASN:O	2.60	0.50
1:G:905:TYR:CE1	1:G:936:PRO:HB3	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1219:PRO:HG2	1:D:1220:PRO:HD3	1.93	0.49
3:I:2:ILE:HD12	3:I:2:ILE:H	1.77	0.49
1:J:439:SER:HA	1:J:582:ASN:HA	1.93	0.49
1:J:172:LEU:O	1:J:172:LEU:HG	2.12	0.49
2:H:11:LEU:O	2:H:11:LEU:CD2	2.61	0.48
1:B:395:GLN:HA	1:B:395:GLN:OE1	2.13	0.48
1:A:905:TYR:CE1	1:A:936:PRO:CB	2.89	0.48
1:A:1060:PRO:HA	1:A:1063:GLN:HB3	1.96	0.48
1:A:905:TYR:HE1	1:A:936:PRO:HB3	1.72	0.48
1:B:251:LEU:C	1:B:251:LEU:HD23	2.33	0.48
1:G:1120:GLY:O	1:G:1121:THR:OG1	2.22	0.48
1:B:111:GLN:N	1:B:111:GLN:OE1	2.39	0.48
1:B:381:VAL:HG12	1:B:407:CYS:C	2.19	0.48
1:J:383:CYS:HB2	1:J:385:PHE:CZ	2.50	0.47
1:G:905:TYR:CE1	1:G:936:PRO:HD3	2.49	0.47
1:B:382:GLU:HA	1:B:408:ASN:O	2.15	0.47
1:G:1156:CYS:SG	1:G:1211:TYR:HB2	2.54	0.47
1:J:172:LEU:HD23	1:J:172:LEU:H	1.78	0.47
1:J:409:TYR:C	1:J:409:TYR:CD1	2.89	0.47
1:A:944:GLU:OE1	1:A:944:GLU:HA	2.13	0.46
1:G:1160:ASN:OD1	1:G:1160:ASN:C	2.53	0.46
1:A:956:ALA:N	1:A:957:GLY:CA	2.79	0.46
1:C:78:GLN:NE2	1:C:78:GLN:O	2.48	0.46
1:B:384:ASP:CA	1:B:404:PHE:HE2	2.29	0.46
1:G:927:GLN:HB2	1:G:932:TYR:HB2	1.98	0.46
1:J:111:GLN:N	1:J:111:GLN:OE1	2.44	0.46
1:J:425:CYS:HA	1:J:478:CYS:HA	1.97	0.46
1:B:602:ASN:O	1:B:616:VAL:HB	2.16	0.46
1:C:604:VAL:O	1:C:604:VAL:HG13	2.16	0.46
1:G:1102:LYS:O	1:G:1106:CYS:N	2.49	0.46
1:J:130:VAL:HG12	1:J:130:VAL:O	2.16	0.46
1:D:964:LEU:O	1:D:965:SER:CB	2.65	0.46
1:G:873:LEU:C	1:G:873:LEU:HD12	2.37	0.46
1:A:1124:VAL:O	1:A:1124:VAL:HG13	2.16	0.45
1:C:385:PHE:CE2	1:C:404:PHE:CZ	3.04	0.45
2:E:72:ASP:OD1	2:E:72:ASP:C	2.54	0.45
3:F:28:TYR:CD1	3:F:28:TYR:N	2.84	0.45
1:G:756:GLU:H	1:G:756:GLU:CD	2.17	0.45
1:B:256:ILE:O	1:B:256:ILE:CG2	2.65	0.45
3:F:1:ASP:OD1	3:F:1:ASP:C	2.55	0.45
1:G:936:PRO:HA	1:G:937:PRO:HD3	1.83	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:593:ASP:N	1:J:594:THR:HA	2.31	0.45
1:A:935:LEU:N	1:A:935:LEU:HD12	2.31	0.45
1:J:648:TYR:CD2	1:J:648:TYR:C	2.90	0.45
1:J:240:MET:SD	1:J:240:MET:C	2.96	0.44
1:B:384:ASP:HB3	1:B:404:PHE:HE2	1.76	0.44
1:C:251:LEU:HD23	1:C:251:LEU:C	2.37	0.44
1:A:1219:PRO:HG2	1:A:1220:PRO:HD3	2.00	0.44
1:B:130:VAL:HG12	1:B:130:VAL:O	2.18	0.44
1:C:172:LEU:N	1:C:172:LEU:HD23	2.33	0.44
1:B:228:PHE:CD2	1:B:228:PHE:C	2.90	0.44
1:C:446:PHE:N	1:C:446:PHE:CD2	2.85	0.44
1:G:1113:ARG:HA	1:G:1113:ARG:NE	2.32	0.44
1:A:1160:ASN:OD1	1:A:1160:ASN:C	2.56	0.44
1:A:977:PHE:CD1	1:A:977:PHE:N	2.86	0.44
1:J:383:CYS:O	1:J:385:PHE:CD1	2.71	0.44
1:J:709:THR:HB	1:J:710:PRO:HD2	1.99	0.44
1:C:600:LEU:HD12	1:C:600:LEU:H	1.83	0.43
1:G:1173:ILE:HG13	1:G:1185:SER:OG	2.18	0.43
1:J:396:VAL:HA	1:J:399:PHE:CE1	2.54	0.43
1:B:384:ASP:HB3	1:B:404:PHE:CE2	2.53	0.43
1:C:600:LEU:HD12	1:C:600:LEU:N	2.32	0.43
1:B:409:TYR:O	1:B:586:PRO:HA	2.18	0.43
2:E:41:HIS:HB3	2:E:44:SER:HB3	2.00	0.43
1:G:1155:LEU:HD22	1:G:1214:ILE:HD11	2.01	0.43
1:B:443:LEU:C	1:B:443:LEU:HD23	2.39	0.43
1:J:381:VAL:O	1:J:407:CYS:HA	2.19	0.43
1:C:130:VAL:HG12	1:C:130:VAL:O	2.18	0.43
1:C:172:LEU:O	1:C:172:LEU:HG	2.19	0.43
1:D:1005:LEU:C	1:D:1005:LEU:HD23	2.39	0.43
1:J:728:LYS:O	1:J:729:LEU:HG	2.19	0.43
1:B:664:ASP:OD1	1:B:664:ASP:C	2.57	0.42
3:I:2:ILE:HD12	3:I:2:ILE:N	2.33	0.42
1:B:665:LYS:HE3	1:B:665:LYS:HB3	1.84	0.42
1:C:606:TYR:CD1	1:C:606:TYR:C	2.92	0.42
1:G:1001:PHE:CD2	1:G:1001:PHE:C	2.93	0.42
1:D:775:SER:OG	1:D:776:SER:N	2.45	0.42
1:G:1060:PRO:HB2	1:G:1061:PRO:HD3	2.00	0.42
1:G:1202:THR:OG1	1:G:1203:LYS:N	2.52	0.42
1:B:626:ARG:O	1:B:627:GLN:HB2	2.19	0.42
2:H:110:THR:O	2:H:110:THR:CG2	2.66	0.42
1:B:49:ASP:C	1:B:49:ASP:OD1	2.56	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:92:LYS:C	3:I:92:LYS:HD3	2.40	0.42
1:J:378:ALA:HB1	1:J:379:GLU:HA	2.02	0.42
1:D:806:CYS:SG	1:D:806:CYS:O	2.77	0.42
1:D:905:TYR:OH	1:D:935:LEU:O	2.37	0.42
1:G:806:CYS:SG	1:G:806:CYS:O	2.78	0.42
1:J:381:VAL:O	1:J:407:CYS:CB	2.65	0.42
1:D:875:GLU:CD	1:D:875:GLU:H	2.19	0.42
1:J:49:ASP:OD1	1:J:49:ASP:C	2.57	0.42
1:A:827:PHE:N	1:A:827:PHE:CD1	2.87	0.42
1:A:875:GLU:N	1:A:875:GLU:OE1	2.39	0.41
1:D:1120:GLY:O	1:D:1121:THR:OG1	2.28	0.41
1:G:961:THR:O	1:G:961:THR:HG22	2.20	0.41
3:I:36:PHE:O	3:I:86:TYR:HA	2.20	0.41
1:J:240:MET:O	1:J:240:MET:SD	2.78	0.41
1:A:977:PHE:N	1:A:977:PHE:HD1	2.18	0.41
1:C:209:THR:O	1:C:209:THR:HG22	2.19	0.41
1:C:382:GLU:HA	1:C:408:ASN:O	2.19	0.41
1:A:1008:MET:O	1:A:1008:MET:HG3	2.19	0.41
1:A:871:LEU:HD12	1:A:871:LEU:N	2.36	0.41
1:C:675:GLY:HA2	1:C:712:GLY:HA3	2.03	0.41
1:C:67:ILE:O	1:C:67:ILE:CG2	2.68	0.41
1:C:688:GLN:HB2	1:C:689:TYR:HA	2.02	0.41
2:E:13:ARG:HA	2:E:14:PRO:HD3	1.95	0.41
2:H:72:ASP:C	2:H:72:ASP:OD1	2.59	0.41
1:C:172:LEU:H	1:C:172:LEU:HD23	1.85	0.41
1:D:905:TYR:CE1	1:D:936:PRO:CD	3.00	0.41
1:C:326:ASP:C	1:C:326:ASP:OD1	2.59	0.41
1:D:1102:LYS:O	1:D:1106:CYS:N	2.53	0.41
1:G:777:TYR:N	1:G:777:TYR:CD2	2.89	0.41
1:C:111:GLN:OE1	1:C:111:GLN:N	2.45	0.41
1:J:689:TYR:N	1:J:689:TYR:CD2	2.88	0.41
1:C:140:ILE:HD13	1:C:140:ILE:HG21	1.80	0.40
1:A:1183:GLU:N	1:A:1183:GLU:OE1	2.55	0.40
1:B:688:GLN:CB	1:B:689:TYR:HA	2.49	0.40
1:D:756:GLU:OE1	1:D:756:GLU:N	2.42	0.40
1:G:904:GLY:O	1:G:905:TYR:HB2	2.20	0.40
1:G:905:TYR:OH	1:G:934:VAL:O	2.38	0.40
1:B:381:VAL:CB	1:B:408:ASN:HB2	2.29	0.40
1:C:269:ARG:O	1:C:269:ARG:HD2	2.20	0.40
1:A:1017:GLU:CD	1:A:1017:GLU:H	2.21	0.40
1:B:719:ASN:C	1:B:719:ASN:OD1	2.60	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:727:CYS:O	1:B:729:LEU:N	2.45	0.40
1:C:615:GLY:HA3	1:C:651:LEU:HD11	2.03	0.40
1:J:615:GLY:HA2	1:J:654:CYS:SG	2.61	0.40
1:J:132:ILE:HD12	1:J:132:ILE:HA	1.89	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	A	450/1329 (34%)	422 (94%)	25 (6%)	3 (1%)	25	68
1	B	724/1329 (54%)	688 (95%)	28 (4%)	8 (1%)	17	60
1	C	724/1329 (54%)	686 (95%)	35 (5%)	3 (0%)	38	77
1	D	459/1329 (34%)	433 (94%)	19 (4%)	7 (2%)	12	53
1	G	459/1329 (34%)	431 (94%)	25 (5%)	3 (1%)	25	68
1	J	724/1329 (54%)	691 (95%)	27 (4%)	6 (1%)	22	66
2	E	117/233 (50%)	113 (97%)	3 (3%)	1 (1%)	20	63
2	H	117/233 (50%)	111 (95%)	6 (5%)	0	100	100
3	F	109/218 (50%)	102 (94%)	5 (5%)	2 (2%)	10	50
3	I	109/218 (50%)	102 (94%)	6 (6%)	1 (1%)	20	63
All	All	3992/8876 (45%)	3779 (95%)	179 (4%)	34 (1%)	25	63

All (34) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	961	THR
1	G	962	ALA
1	B	729	LEU

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Mol	Chain	Res	Type
1	J	378	ALA
1	A	940	ASP
1	D	961	THR
1	D	965	SER
1	B	718	VAL
1	C	718	VAL
1	J	602	ASN
1	J	718	VAL
1	D	1220	PRO
2	E	28	THR
3	F	31	SER
3	F	77	PRO
3	I	77	PRO
1	B	384	ASP
1	A	1220	PRO
1	D	956	ALA
1	D	1219	PRO
1	B	368	ALA
1	B	621	THR
1	C	629	ARG
1	J	596	ILE
1	J	598	SER
1	J	629	ARG
1	D	905	TYR
1	G	956	ALA
1	B	382	GLU
1	G	1220	PRO
1	B	678	ALA
1	B	596	ILE
1	C	44	TRP
1	D	1161	PRO

5.3.2 Protein sidechains ⓘ

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

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	381/1148 (33%)	381 (100%)	0	100	100
1	B	635/1148 (55%)	633 (100%)	2 (0%)	94	96
1	C	635/1148 (55%)	635 (100%)	0	100	100
1	D	388/1148 (34%)	388 (100%)	0	100	100
1	G	388/1148 (34%)	388 (100%)	0	100	100
1	J	635/1148 (55%)	635 (100%)	0	100	100
2	E	102/202 (50%)	102 (100%)	0	100	100
2	H	102/202 (50%)	102 (100%)	0	100	100
3	F	93/192 (48%)	93 (100%)	0	100	100
3	I	93/192 (48%)	93 (100%)	0	100	100
All	All	3452/7676 (45%)	3450 (100%)	2 (0%)	95	97

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	384	ASP
1	B	727	CYS

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.