



## wwPDB EM Validation Summary Report ⓘ

Mar 22, 2025 – 06:28 PM EDT

PDB ID : 6U5U  
EMDB ID : EMD-20656  
Title : Electron cryomicroscopy Structure of *S. cerevisiae* FAS in the KS-stalled state  
Authors : Lou, J.W.; Mazhab-Jafari, M.T.  
Deposited on : 2019-08-28  
Resolution : 2.80 Å(reported)  
Based on initial model : 2UV8

This is a wwPDB EM Validation Summary 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.dev117  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.41.4

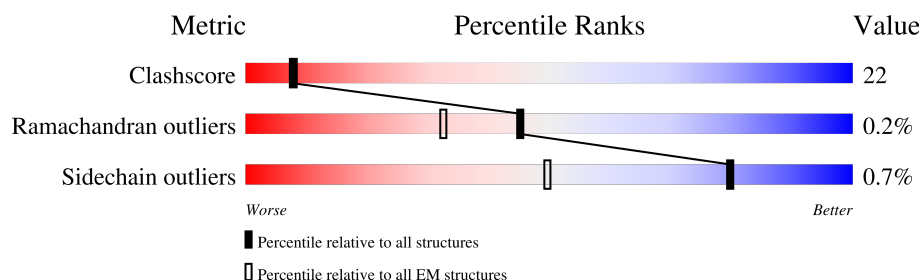
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.80 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\leq 5\%$ . 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	A	1887	<div> <div>25%</div> <div>54%</div> <div>30%</div> <div>15%</div> </div>
2	G	2073	<div> <div>47%</div> <div>52%</div> <div>45%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAP	G	2102	-	-	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 28298 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 Fatty acid synthase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1611	Total	C	N	O	S	0	0
			12171	7684	2081	2362	44		

- Molecule 2 is a protein called Fatty acid synthase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	2033	Total	C	N	O	S	0	0
			15995	10253	2660	3026	56		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	2052	ASP	-	expression tag	UNP P07149
G	2053	TYR	-	expression tag	UNP P07149
G	2054	LYS	-	expression tag	UNP P07149
G	2055	ASP	-	expression tag	UNP P07149
G	2056	HIS	-	expression tag	UNP P07149
G	2057	ASP	-	expression tag	UNP P07149
G	2058	GLY	-	expression tag	UNP P07149
G	2059	ASP	-	expression tag	UNP P07149
G	2060	TYR	-	expression tag	UNP P07149
G	2061	LYS	-	expression tag	UNP P07149
G	2062	ASP	-	expression tag	UNP P07149
G	2063	HIS	-	expression tag	UNP P07149
G	2064	ASP	-	expression tag	UNP P07149
G	2065	ILE	-	expression tag	UNP P07149
G	2066	ASP	-	expression tag	UNP P07149
G	2067	TYR	-	expression tag	UNP P07149
G	2068	LYS	-	expression tag	UNP P07149
G	2069	ASP	-	expression tag	UNP P07149
G	2070	ASP	-	expression tag	UNP P07149
G	2071	ASP	-	expression tag	UNP P07149
G	2072	ASP	-	expression tag	UNP P07149

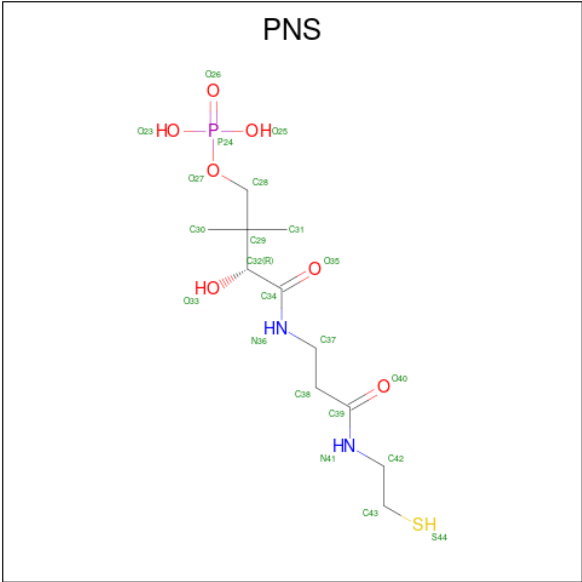
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Chain	Residue	Modelled	Actual	Comment	Reference
G	2073	LYS	-	expression tag	UNP P07149

- # NAP

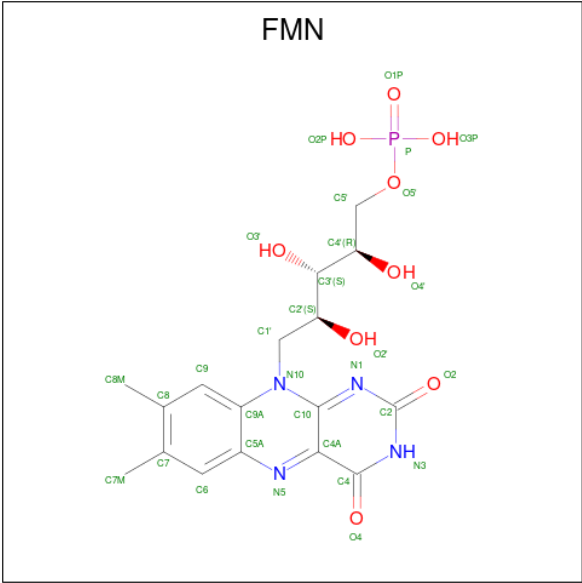
Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total 48	C 21	N 7	O 17	P 3	0
3	G	1	Total 48	C 21	N 7	O 17	P 3	0

- WORLDWIDE  
**PDB**  
PROTEIN DATA BANK



Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	O	P	0
			5	1	3	1	

- Molecule 5 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C<sub>17</sub>H<sub>21</sub>N<sub>4</sub>O<sub>9</sub>P) (labeled as "Ligand of Interest" by depositor).

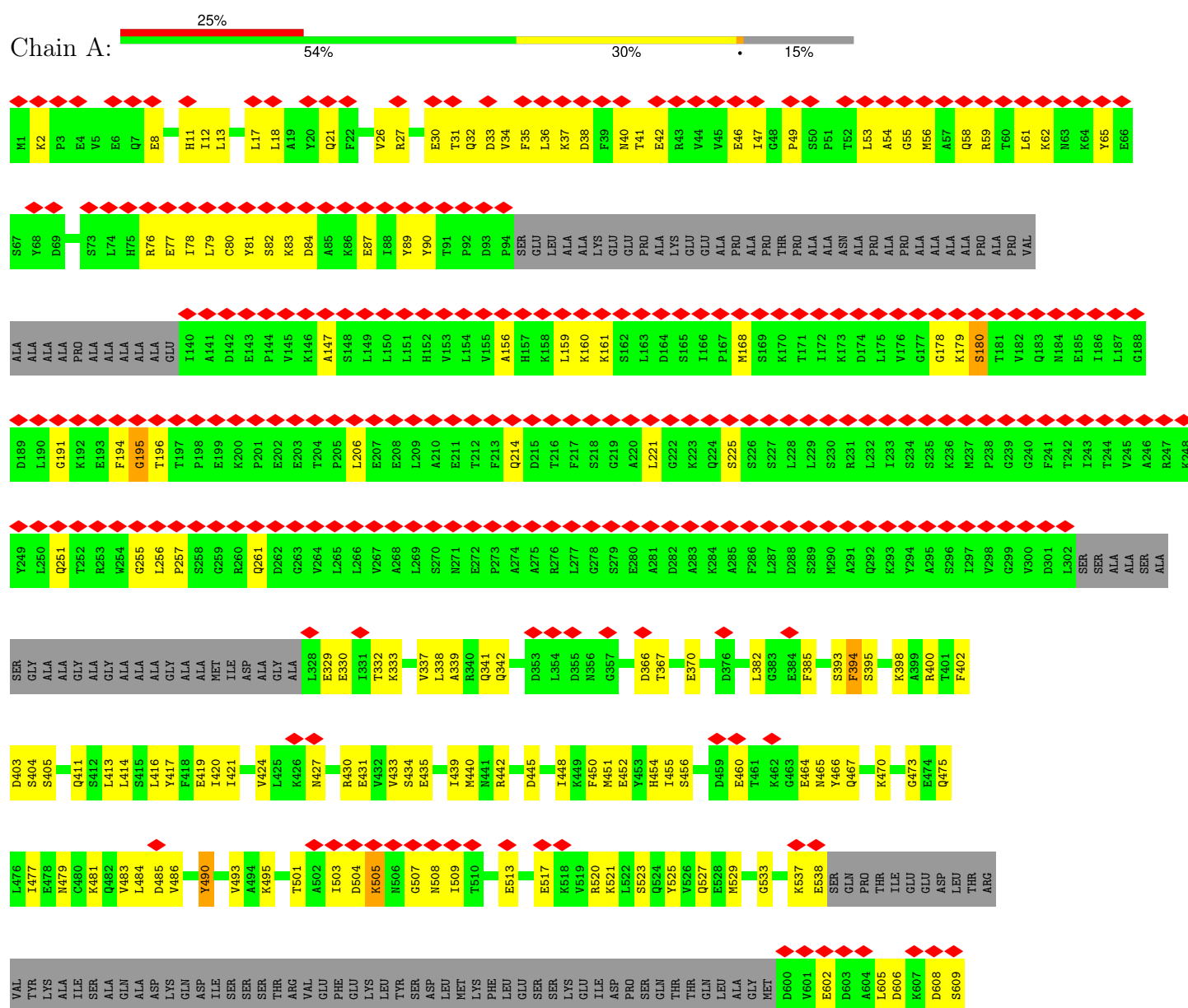


Mol	Chain	Residues	Atoms					AltConf
5	G	1	Total	C	N	O	P	0
			31	17	4	9	1	

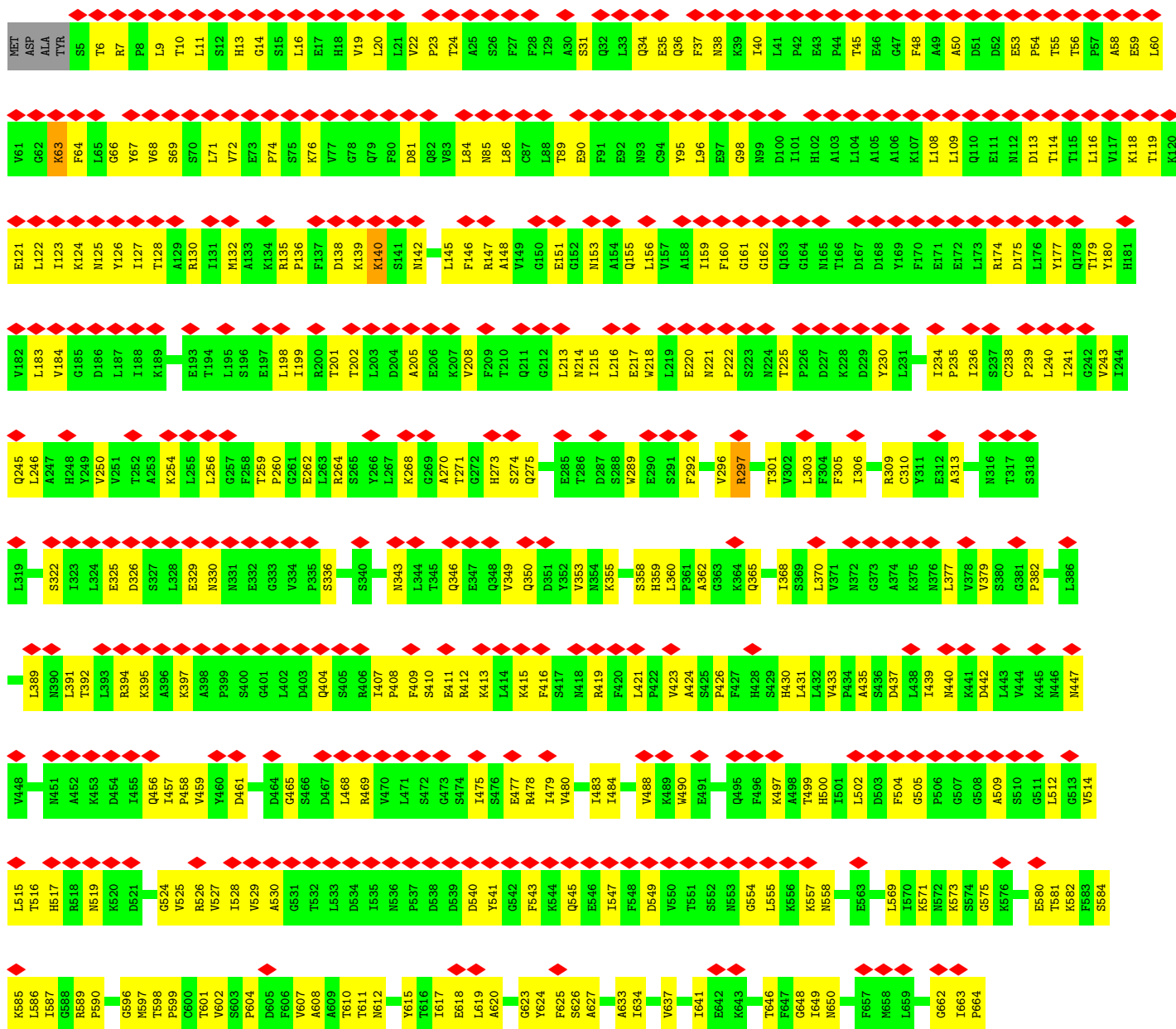
### 3 Residue-property plots

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: Fatty acid synthase subunit alpha



G1607	N1608	R1609	N1610	D1611	D1612	N1613	K1629	T1630	L1631	K1632	T1641	G1647	G1651	Y1660	L1661	A1664	D1668	Y1674	A1675	K1676	V1677	S1678	A1679	R1680	T1707	D1708	E1709	L1710	E1711	E1712	L1716	D1717	P1718	L1719	K1724	D1725	K1726	K1727	S1728	G1729	S1730	L1731	N1734	S1735	K1736	N1737	L1738







E2036	I1972	M1912	Y1852	K1793	R1730	V1661	Y1601
P2037	S1973	V1913	G1853	K1794	E1731	T1662	S1602
I2038	V1974	L1914	M1854	S1795	N1732	T1663	S1603
K2039	P1975	M1915	I1855	G1796	Y1733	F1664	R1604
E2040	F1976	F1916	A1856	G1797	A1735	V1665	V1605
I2041	H1977	I1917	I1857	L1798	M1736	F1666	G1607
I2042	S1978	K1918	N1858	P1799	L1737	T1667	Y1608
D2043	T1979	L1919	P1859	A1800	F1738	G1668	P1609
N2044		Q1920	G1860	D1801	E1739	Q1669	G1610
W2045	M1982	K1921	R1861	A1802	T1740	G1670	Q1611
E2046	N1983	I1922	V1862	T1803	L1741	S1671	F1612
K2047	G1984	D1923	A1863	F1804	V1742	Q1672	V1613
Y2048	V1985	I1924	A1864	A1805	D1743	E1673	M1615
E2049	K1986	T1925	S1865	G1806	G1744	Q1674	V1616
Q2050	P1987	I1926	F1866	H1807	K1745	L1675	L1617
SER	F1988	E1926	S1867	S1808	L1746	M1676	P1618
ASP	K1989	L1927	Q1868	L1809	K1747	G1677	M1619
TYR	S1990	Q1928	E1869	G1810	T1748	M1678	T1620
LYS	F1991	K1929	A1870	E1811	E1749	A1621	A1621
ASP	L1992	S1930	L1871	Y1812	D1679	D1679	L1622
HIS	K1993	L1931	Q1872	A1813	K1750	L1680	K1623
ASP	K1994	S1932	Y1873	A1814	L1751	Y1681	T1624
GLY	N1995	L1933	G1874	L1815	F1752	K1682	S1625
ASP	I1996	E1934	V1875	A1816	K1753	T1683	I1626
LYS	I1997	E1935	E1876	S1817	I1755	K1685	Q1627
ASP	K1998	V1936	E1877	L1818	M1756	H1628	H1628
HIS	E1999	E1937	R1877	A1819	E1757	A1686	V1629
ILE	N2000	L1938	V1878	D1820	H1758	G1688	G1630
ASP	V2001	H1939	G1879	Y1821	H1759	M1631	M1631
TYR	K2002	L1940	K1880	M1822	V1689	D1689	I1632
LYS	Y2003	F1941	R1881	S1823	Y1762	V1690	G1634
ASP	K2005	I1942	T1882	L1824	T1763	W1691	M1633
ASP	G2006	I1943	G1883	E1825	F1764	D1695	G1635
ASP	K2009	T1944	W1884	S1826	R1765	D1698	K1636
LYS	Y2010	D1945	L1885	V1828	S1766	F1698	L1637
		E1946	V1886	E1829	E1767	T1701	I1638
		A1947	E1887	V1830	K1768		K1639
		S1948	I1888	F1831	G1769	F1704	F1640
		K1949	V1889	Y1833	L1770	S1705	E1641
		K1950	Y1891	F1832	L1771	I1706	T1642
N2013		S1951	N1892	G1835	S1772	L1707	A1643
L2014		I1952	E1894	M1836	A1773	D1708	M1644
T2015		V1953	N1895	T1837	T1774	I1709	E1645
A2016		K1954	K1896	Q1839	Q1775	V1710	D1646
K2017		P1955	K1897	V1840	F1776	I1711	D1647
P2018		R1956	P1898	A1841	T1777	N1713	V1648
F2019		P1957	Y1898	V1842	Q1778	P1714	V1649
Q2020		L1958	V1899	R1843	P1779	V1715	V1650
V2021		K1959	A1900	P1844	A1780	L1716	L1651
T2022		L1960	A1901	D1845	L1781	L1717	T1652
K2023		F1961	G1902	E1846	T1782	T1718	G1653
D2024		P1962	D1903	L1847	M1783	I1719	E1654
E2025		G1963	L1904	G1848	L1784	F1720	A1655
T2026		F1964	R1905	K1849	M1785	F1721	E1656
Q2027		A1965	A1906	S1850	K1786	G1722	I1657
D2028		G1966	L1907	N1851	A1787		E1658
V2029		T1967	D1908		A1788	G1726	Q1659
D2030		P1968	T1909		F1789		P1660
Y2031		L1969	V1910		E1790		
Z2032		L1970	T1911				
L2033		G1971					

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D3	Depositor
Number of particles used	594818	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTFFIND4 within cryoSPARC2	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	43	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.727	Depositor
Minimum map value	-1.412	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.144	Depositor
Recommended contour level	0.706	Depositor
Map size ( $\text{\AA}$ )	373.12, 373.12, 373.12	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.06, 1.06, 1.06	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMN, PNS, NAP

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	A	0.61	3/12392 (0.0%)	0.60	3/16775 (0.0%)
2	G	0.44	0/16360	0.51	0/22198
All	All	0.52	3/28752 (0.0%)	0.55	3/38973 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1174	TYR	CD1-CE1	-6.37	1.29	1.39
1	A	1174	TYR	CE1-CZ	-6.33	1.30	1.38
1	A	490	TYR	CD1-CE1	-5.27	1.31	1.39

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1173	LEU	CA-CB-CG	5.66	128.33	115.30
1	A	1719	LEU	CA-CB-CG	-5.06	103.67	115.30
1	A	1174	TYR	CB-CG-CD2	5.05	124.03	121.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1132	GLU	Peptide
1	A	1173	LEU	Peptide
1	A	1584	PRO	Peptide
1	A	1716	LEU	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	12171	0	11679	490	0
2	G	15995	0	15978	772	0
3	A	48	0	22	19	0
3	G	48	0	25	27	0
4	A	5	0	0	0	0
5	G	31	0	19	3	0
All	All	28298	0	27723	1241	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 22.

The worst 5 of 1241 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:G:740:HIS:HB2	3:G:2102:NAP:C7N	1.22	1.59
1:A:147:ALA:CB	1:A:214:GLN:HA	1.50	1.41
2:G:740:HIS:HD2	3:G:2102:NAP:C2N	1.33	1.39
2:G:740:HIS:HD2	3:G:2102:NAP:C3N	1.40	1.34
2:G:740:HIS:CB	3:G:2102:NAP:C7N	2.06	1.32

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	A	1601/1887 (85%)	1433 (90%)	161 (10%)	7 (0%)	30	61
2	G	2029/2073 (98%)	1883 (93%)	146 (7%)	0	100	100
All	All	3630/3960 (92%)	3316 (91%)	307 (8%)	7 (0%)	45	73

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	160	LYS
1	A	179	LYS
1	A	195	GLY
1	A	1609	ARG
1	A	180	SER

### 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	A	1230/1566 (78%)	1223 (99%)	7 (1%)	84	95
2	G	1772/1810 (98%)	1757 (99%)	15 (1%)	79	93
All	All	3002/3376 (89%)	2980 (99%)	22 (1%)	80	94

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	809	LYS
2	G	1315	PRO
2	G	1023	ARG
2	G	1439	LYS
1	A	1307	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63

such sidechains are listed below:

Mol	Chain	Res	Type
2	G	428	HIS
2	G	1716	ASN
2	G	741	HIS
2	G	1674	GLN
2	G	1897	GLN

### 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](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
5	FMN	G	2101	-	33,33,33	1.23	5 (15%)	48,50,50	1.28	8 (16%)
3	NAP	A	1901	-	46,52,52	2.56	25 (54%)	61,80,80	2.33	16 (26%)
4	PNS	A	1902	1	1,4,21	0.65	0	0,4,29	-	-
3	NAP	G	2102	-	46,52,52	0.84	1 (2%)	61,80,80	1.10	3 (4%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.  
'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	FMN	G	2101	-	-	3/18/18/18	0/3/3/3
3	NAP	A	1901	-	-	6/31/67/67	0/5/5/5
4	PNS	A	1902	1	-	0/0/2/27	-
3	NAP	G	2102	-	-	6/31/67/67	0/5/5/5

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1901	NAP	C3N-C7N	-5.46	1.42	1.50
3	A	1901	NAP	PN-O3	-4.93	1.54	1.59
3	A	1901	NAP	O4D-C4D	-4.91	1.34	1.45
3	A	1901	NAP	C2N-N1N	-4.21	1.30	1.35
3	A	1901	NAP	C4A-N3A	-4.18	1.30	1.35

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1901	NAP	C4D-O4D-C1D	-9.30	101.40	109.92
3	A	1901	NAP	O3D-C3D-C4D	-5.30	95.86	111.08
3	A	1901	NAP	C6N-N1N-C2N	-5.22	117.44	121.88
3	A	1901	NAP	O4B-C1B-N9A	-4.76	102.43	108.75
3	A	1901	NAP	P2B-O2B-C2B	-4.64	111.04	123.43

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1901	NAP	C5B-O5B-PA-O1A
3	A	1901	NAP	C5D-O5D-PN-O3
3	A	1901	NAP	C5D-O5D-PN-O2N
3	A	1901	NAP	C4D-C5D-O5D-PN
3	G	2102	NAP	C5D-O5D-PN-O1N

There are no ring outliers.

3 monomers are involved in 49 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	G	2101	FMN	3	0
3	A	1901	NAP	19	0

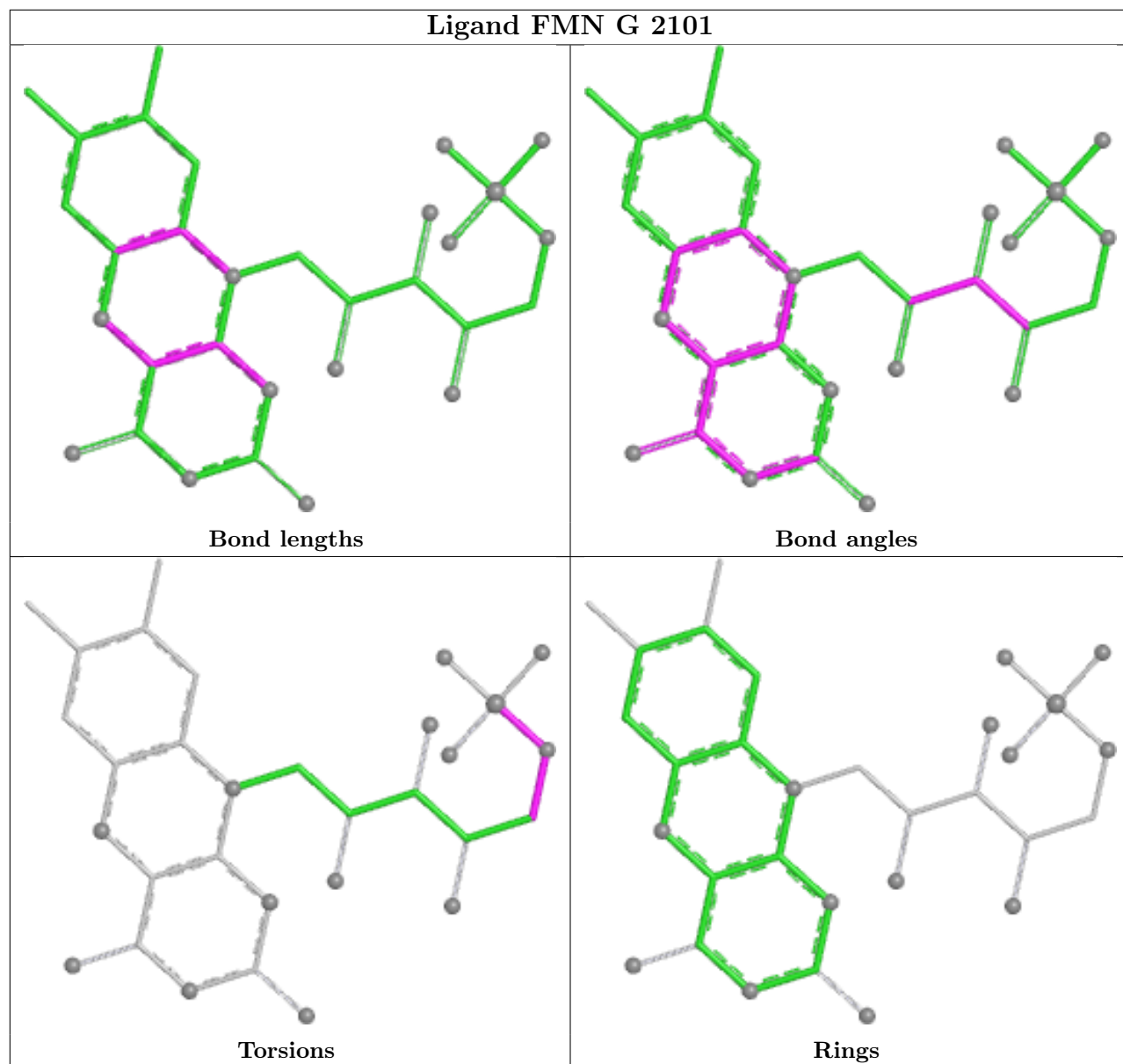
*Continued on next page...*

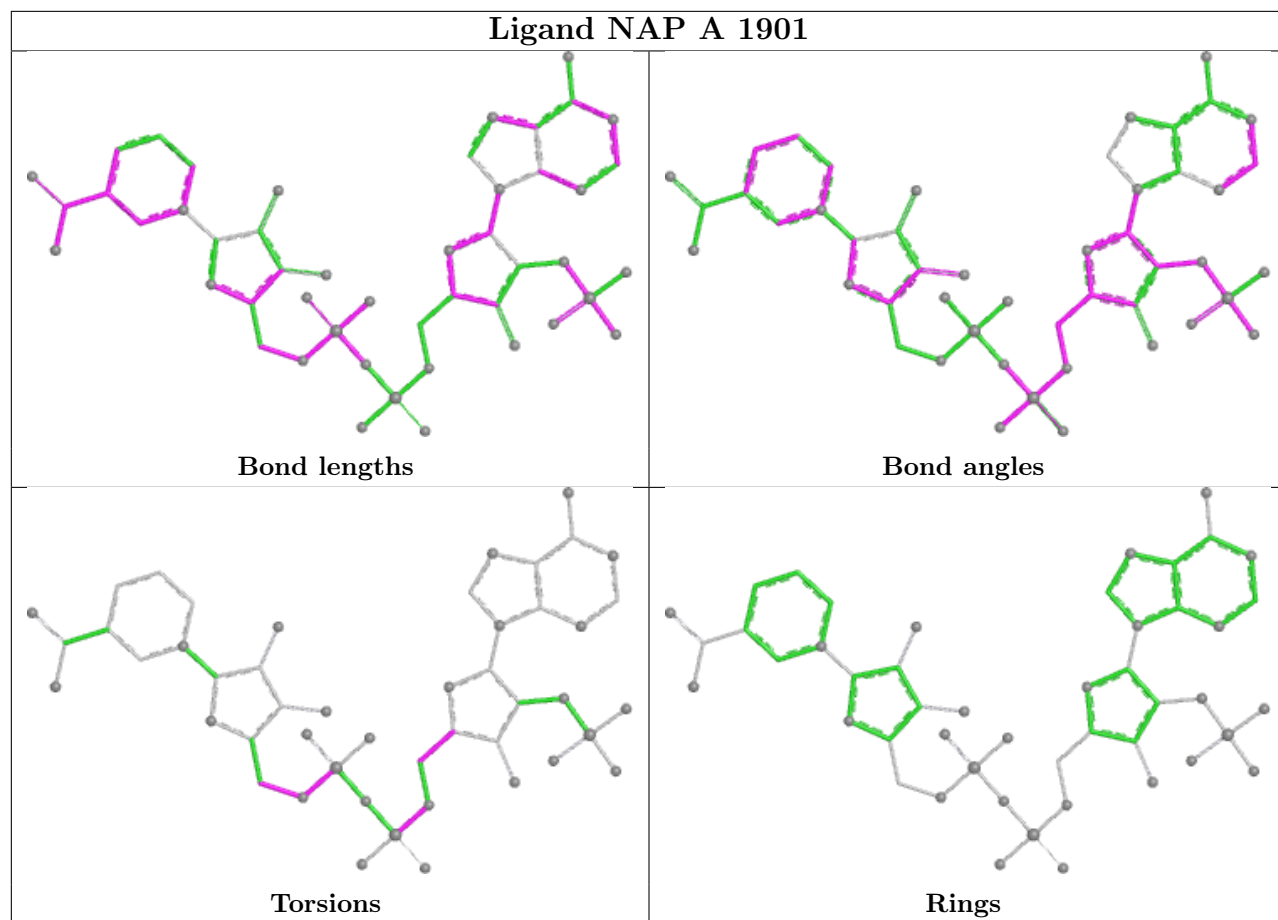


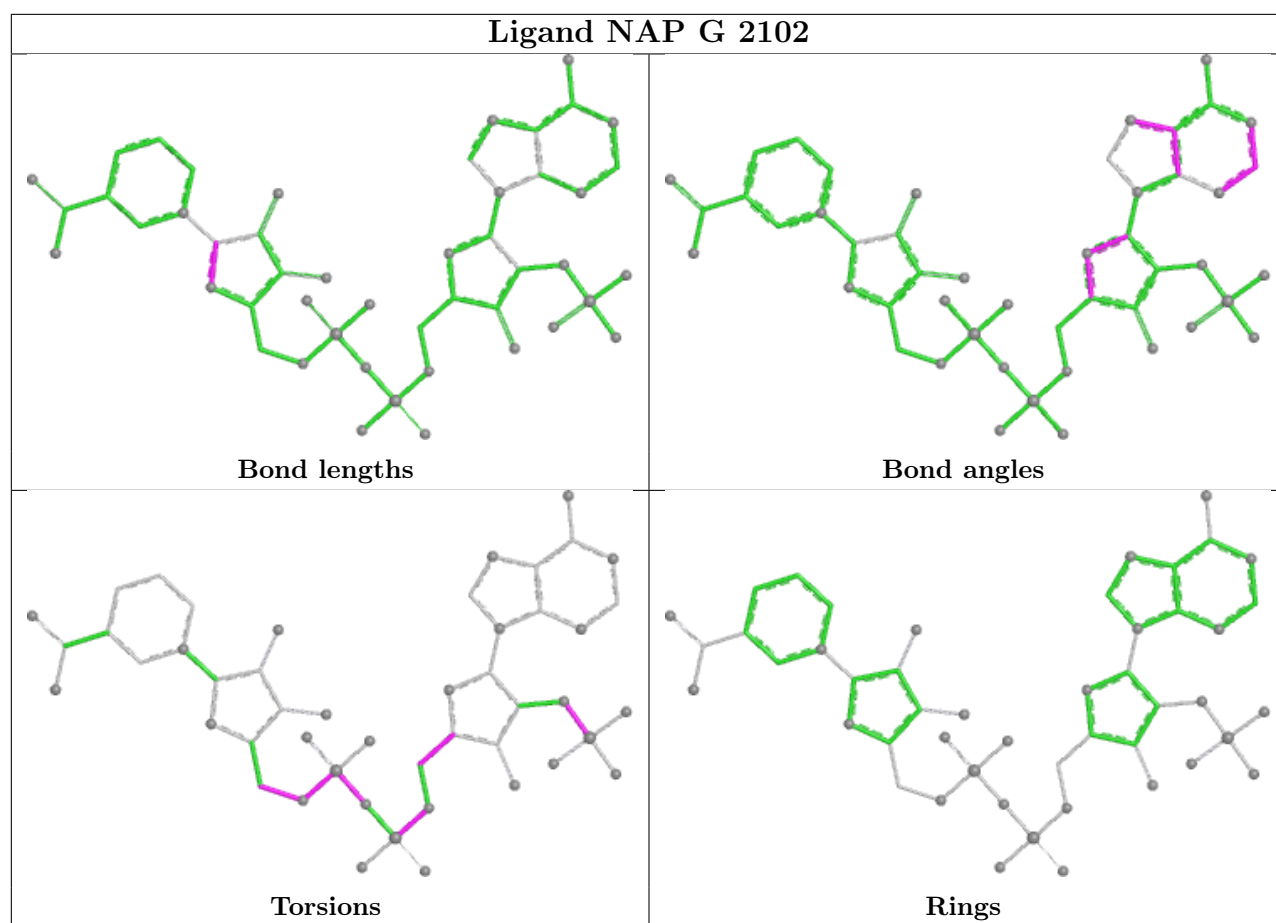
*Continued from previous page...*

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	2102	NAP	27	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







## 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.

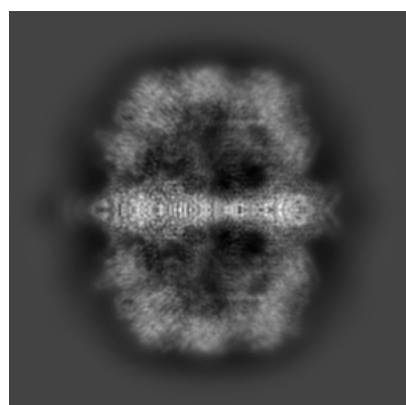
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20656. These allow visual inspection of the internal detail of the map and identification of artifacts.

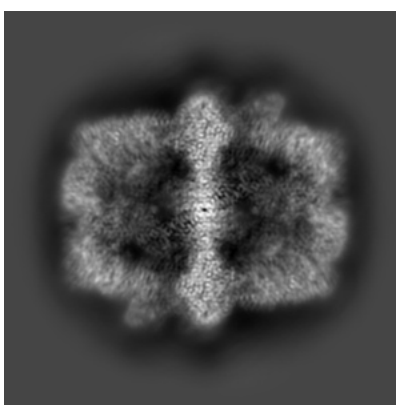
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

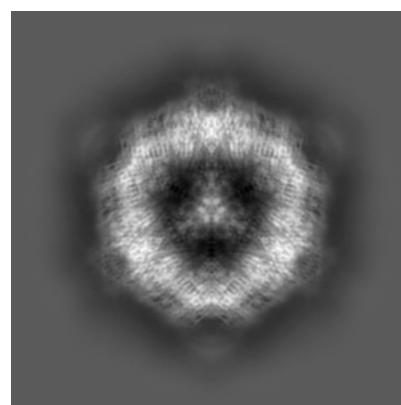
#### 6.1.1 Primary map



X



Y

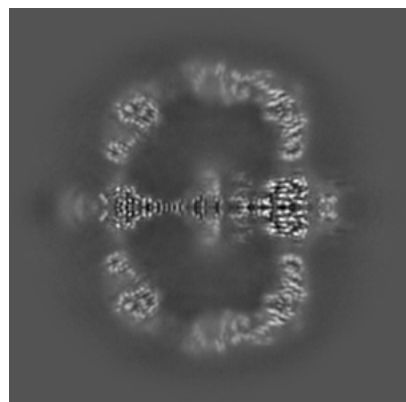


Z

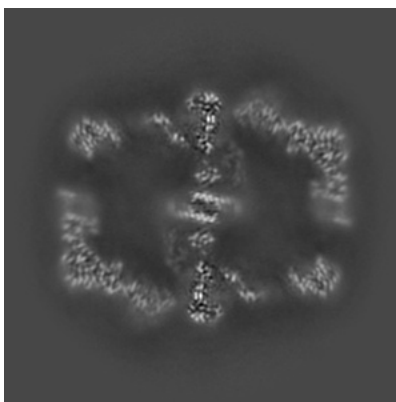
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

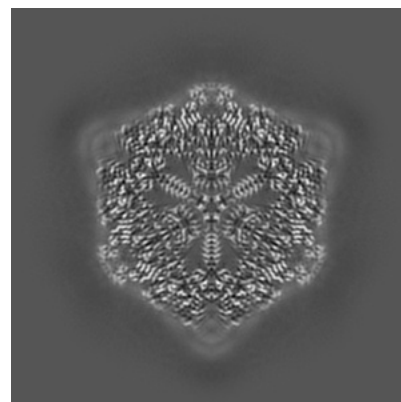
#### 6.2.1 Primary map



X Index: 176



Y Index: 176

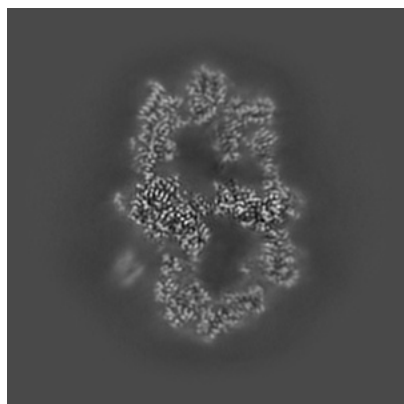


Z Index: 176

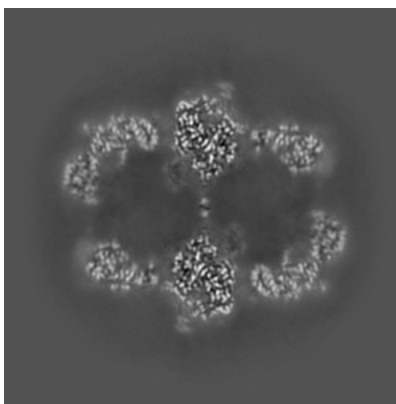
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

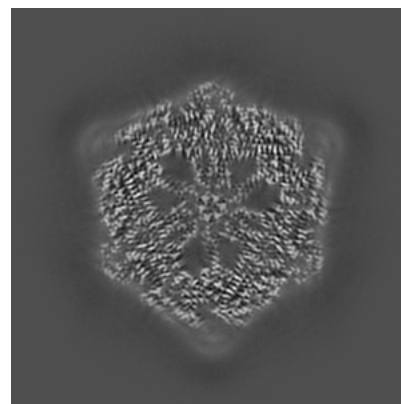
### 6.3.1 Primary map



X Index: 237



Y Index: 140

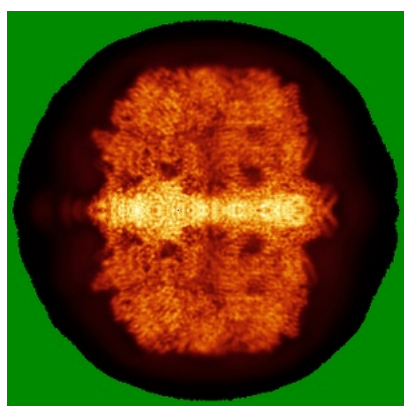


Z Index: 172

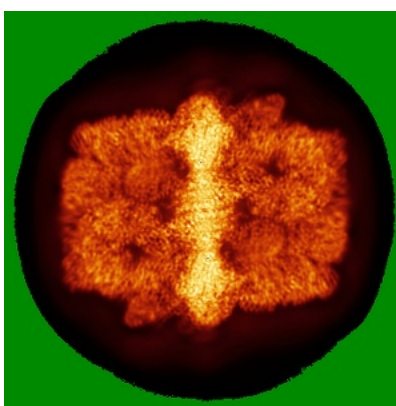
The images above show the largest variance slices of the map in three orthogonal directions.

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

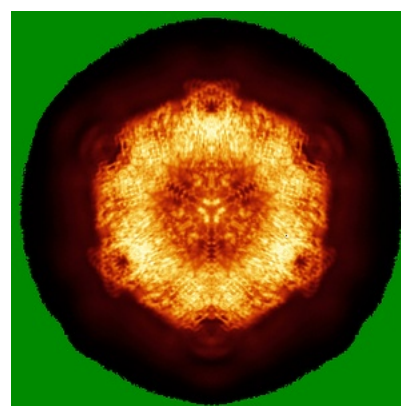
### 6.4.1 Primary map



X



Y

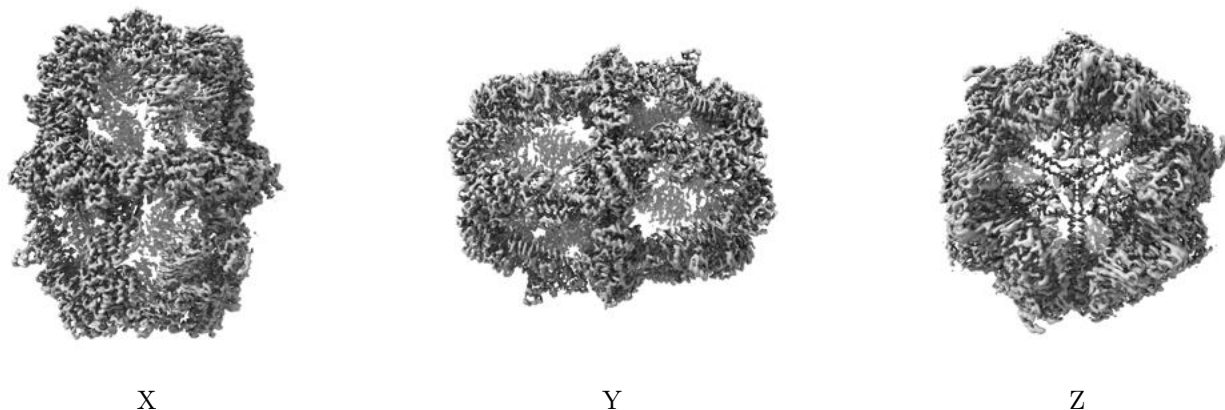


Z

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 0.706. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

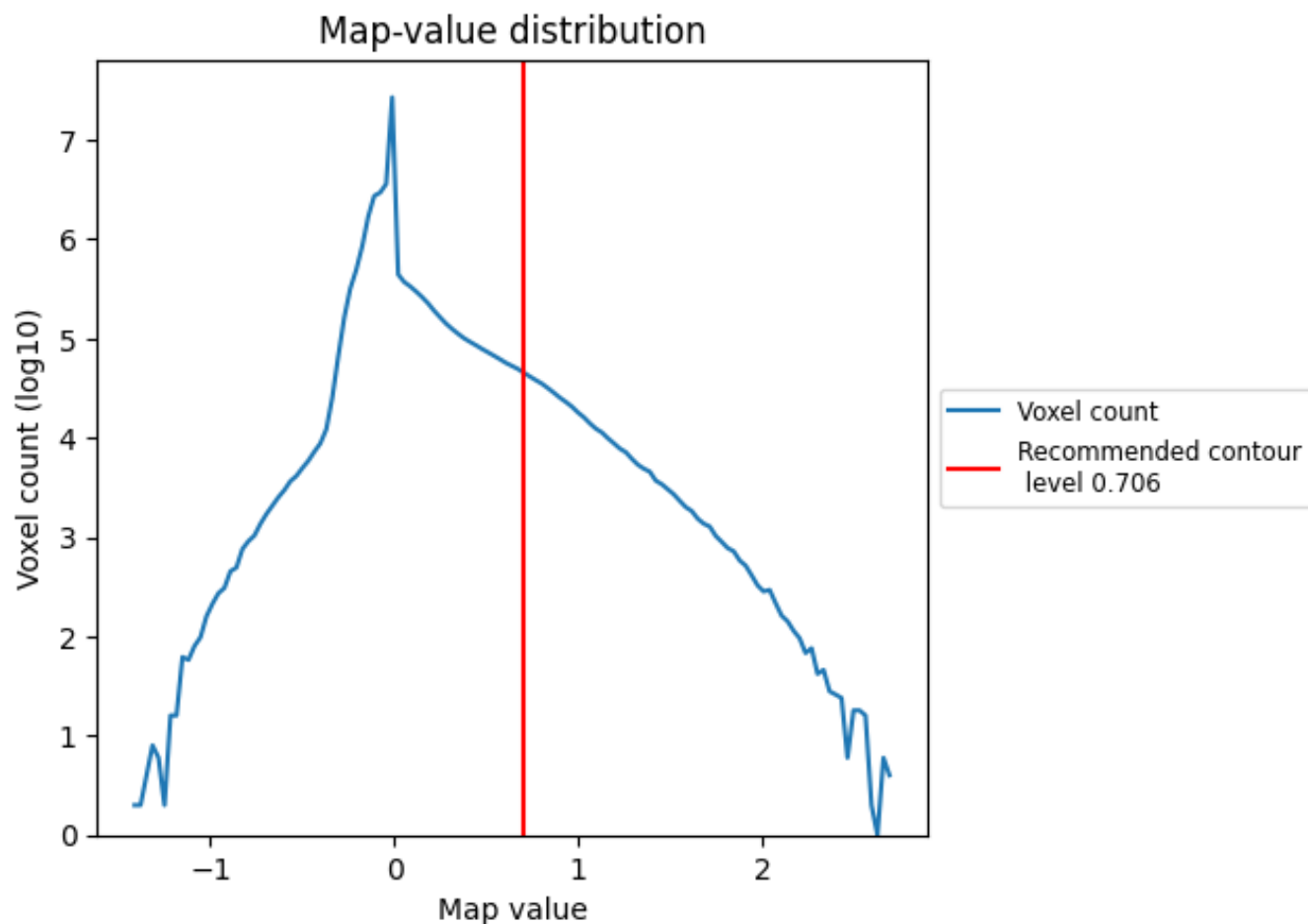
## 6.6 Mask visualisation [i](#)

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.

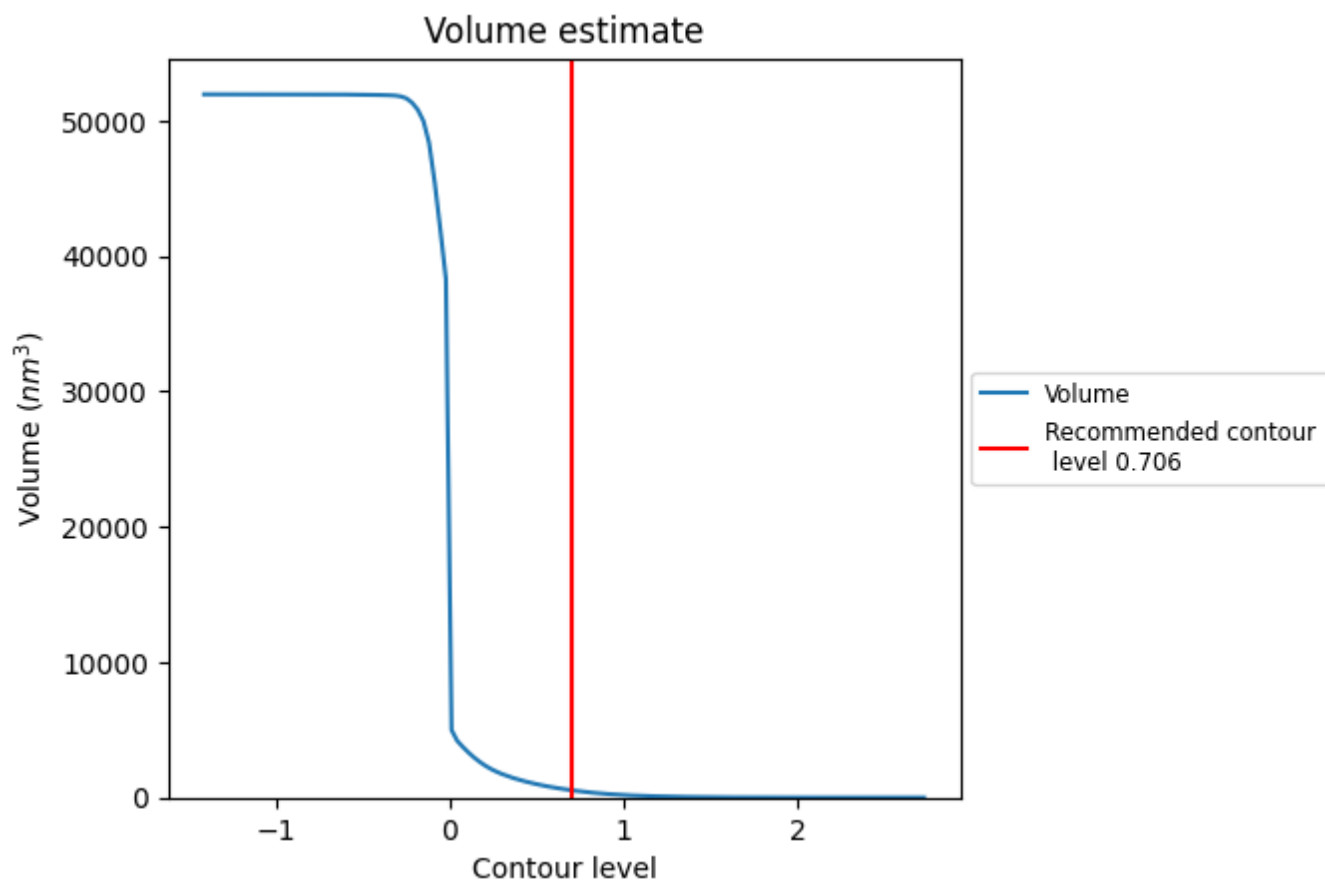
### 7.1 Map-value distribution [i](#)



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.



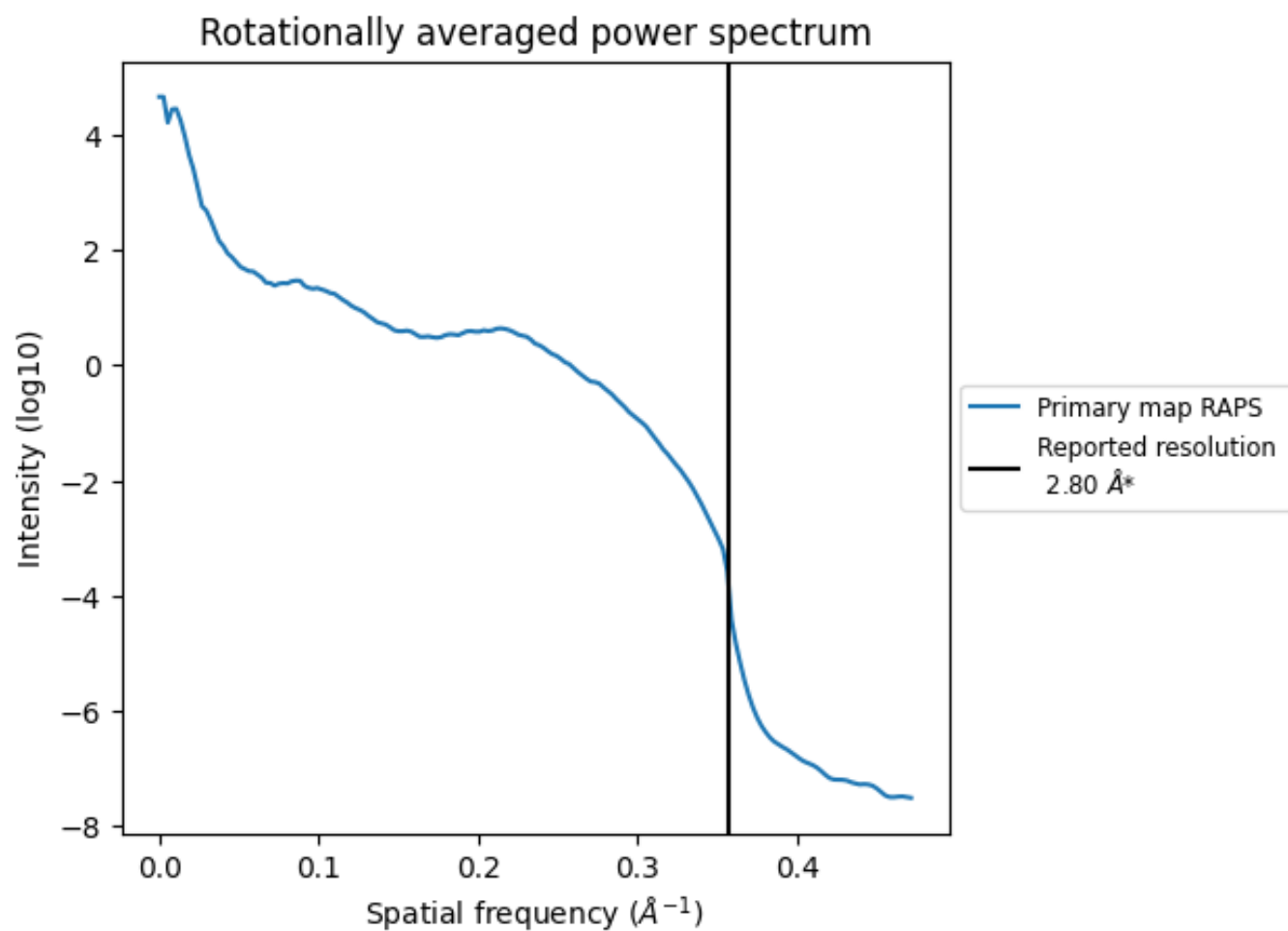
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 531 nm<sup>3</sup>; this corresponds to an approximate mass of 480 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 0.357 Å<sup>-1</sup>

## 8 Fourier-Shell correlation ⓘ

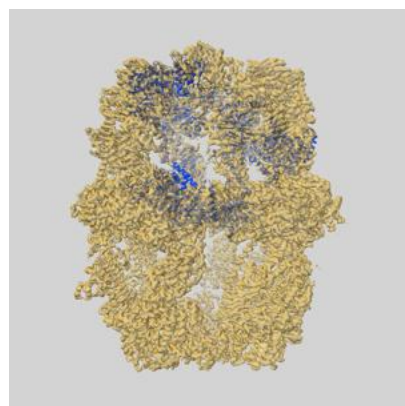
This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit [i](#)

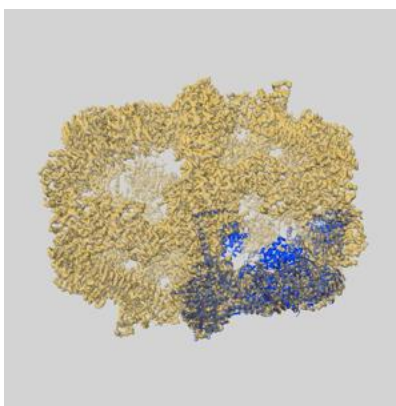
This section contains information regarding the fit between EMDB map EMD-20656 and PDB model 6U5U. Per-residue inclusion information can be found in section 3 on page 6.

### 9.1 Map-model overlays

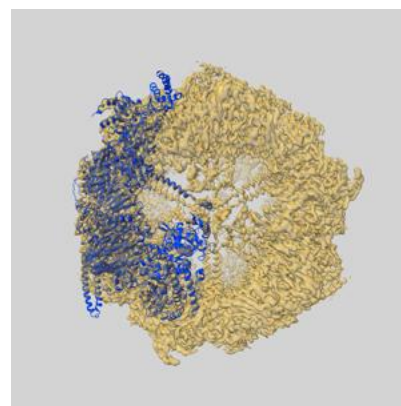
#### 9.1.1 Map-model overlay [i](#)



X

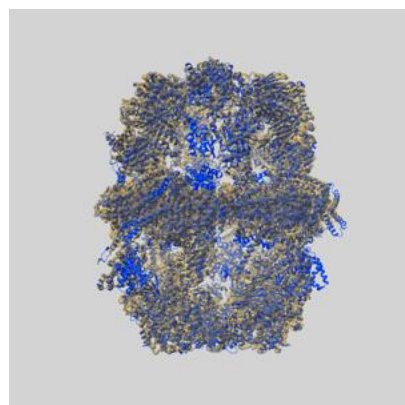


Y

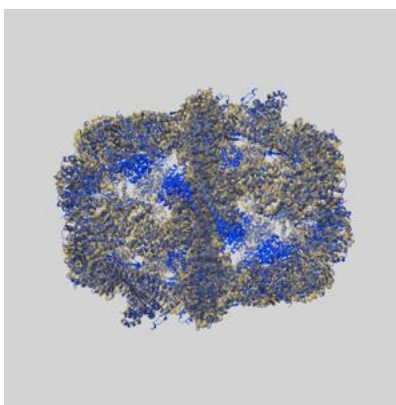


Z

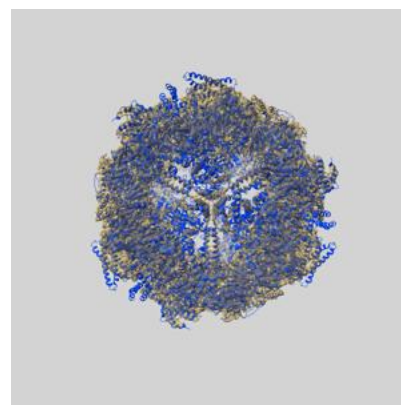
#### 9.1.2 Map-model assembly overlay [i](#)



X



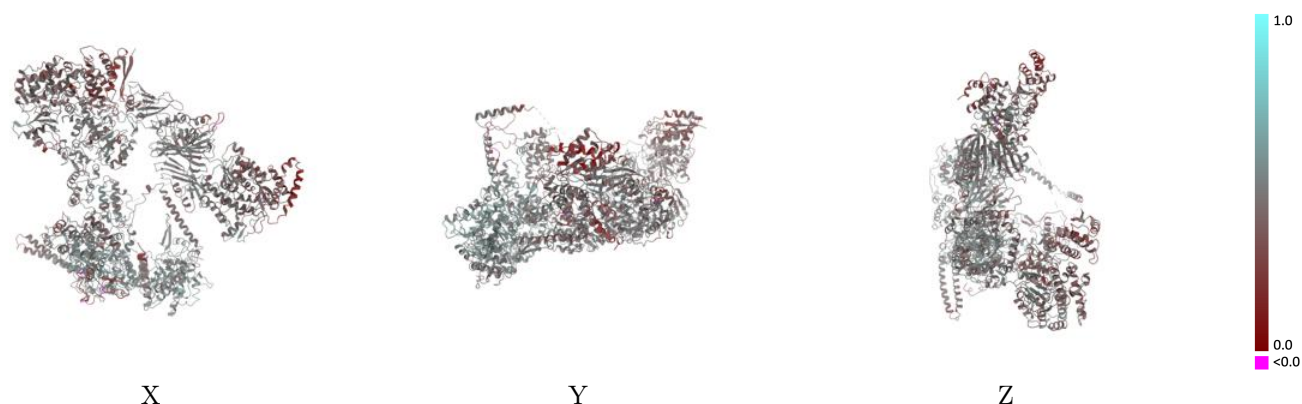
Y



Z

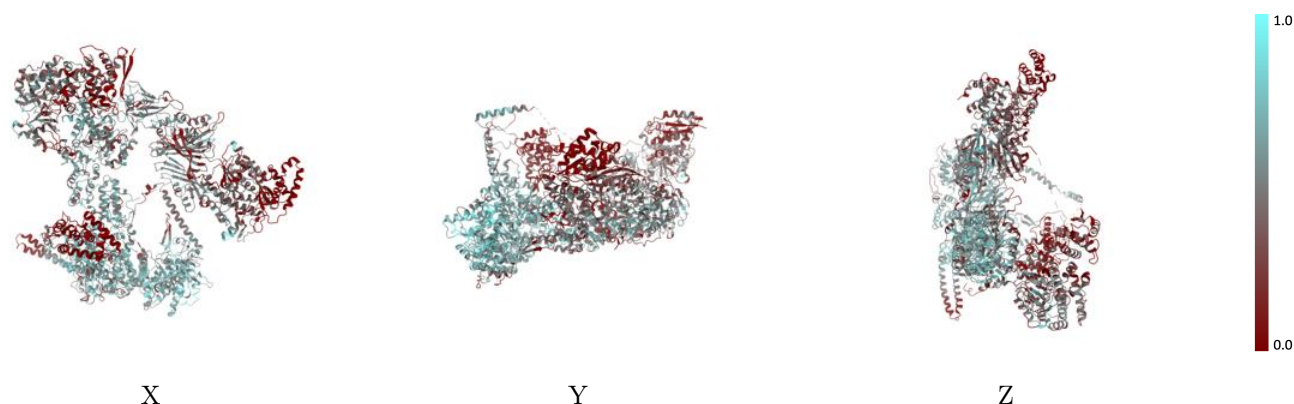
The images above show the 3D surface view of the map at the recommended contour level 0.706 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



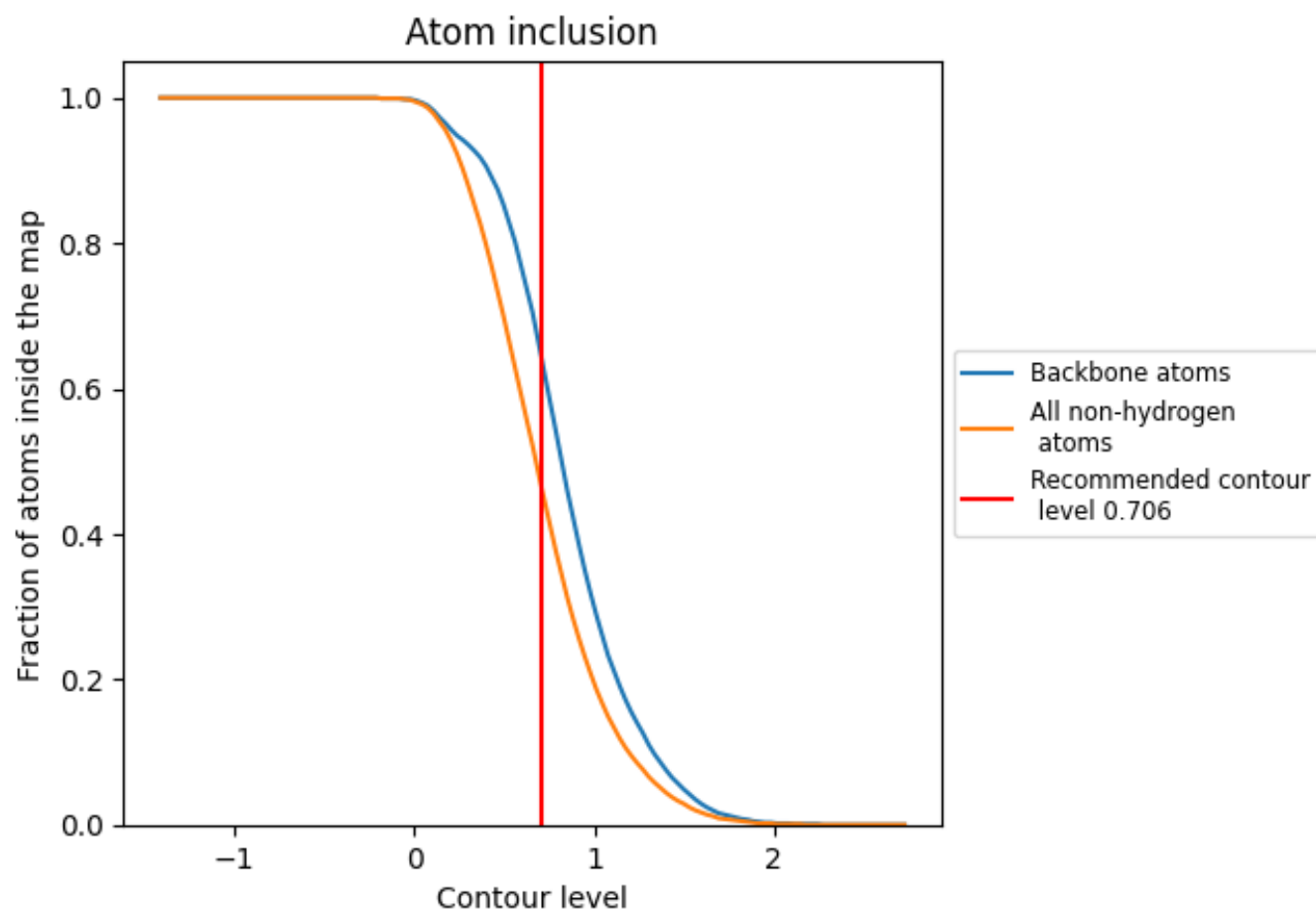
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.706).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 46% 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 (0.706) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.4650	<div></div> 0.4490
A	<div></div> 0.5460	<div></div> 0.4800
G	<div></div> 0.4030	<div></div> 0.4260

