



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 02:20 AM UTC

PDB ID : 6GK9 / pdb_00006gk9
Title : Inhibited structure of IMPDH from Pseudomonas aeruginosa
Authors : Labesse, G.; Alexandre, T.; Haouz, A.; Munier-Lehmann, H.
Deposited on : 2018-05-18
Resolution : 2.54 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

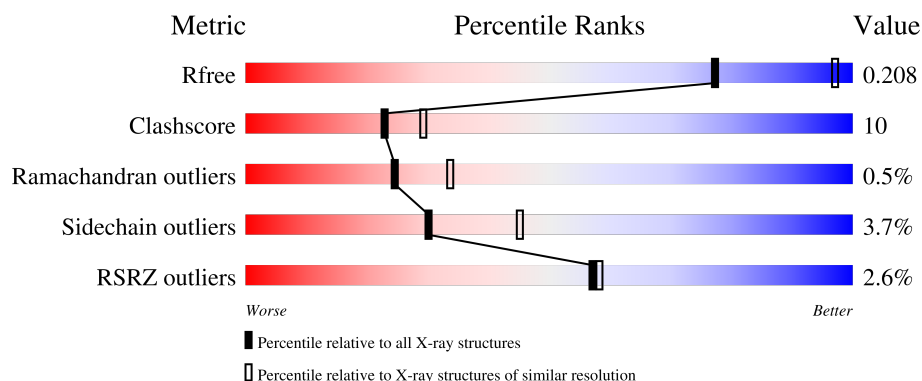
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.54 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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

Mol	Chain	Length	Quality of chain
1	A	509	 2% 66% 16% 17%
1	B	509	 2% 69% 13% 17%
1	C	509	 4% 60% 13% 25%
1	D	509	 % 63% 18% 17%
1	E	509	 2% 69% 14% 17%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	509	% 54% 7% 38%
1	G	509	2% 49% 14% 35%
1	H	509	3% 60% 20% 18%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 24276 atoms, of which 18 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Inosine-5'-monophosphate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	3	0	0
			3136	1978	550	591	17			
1	B	424	Total	C	N	O	S	6	0	0
			3145	1985	551	592	17			
1	C	381	Total	C	N	O	S	2	0	0
			2816	1775	493	531	17			
1	D	424	Total	C	N	O	S	5	1	0
			3161	1992	555	597	17			
1	E	424	Total	C	N	O	S	6	1	0
			3158	1991	555	595	17			
1	F	317	Total	C	N	O	S	3	0	0
			2314	1451	413	437	13			
1	G	329	Total	C	N	O	S	4	0	0
			2390	1499	425	453	13			
1	H	419	Total	C	N	O	S	2	0	0
			3107	1958	547	585	17			

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q9HXM5
A	-18	GLY	-	expression tag	UNP Q9HXM5
A	-17	SER	-	expression tag	UNP Q9HXM5
A	-16	SER	-	expression tag	UNP Q9HXM5
A	-15	HIS	-	expression tag	UNP Q9HXM5
A	-14	HIS	-	expression tag	UNP Q9HXM5
A	-13	HIS	-	expression tag	UNP Q9HXM5
A	-12	HIS	-	expression tag	UNP Q9HXM5
A	-11	HIS	-	expression tag	UNP Q9HXM5
A	-10	HIS	-	expression tag	UNP Q9HXM5
A	-9	SER	-	expression tag	UNP Q9HXM5
A	-8	SER	-	expression tag	UNP Q9HXM5
A	-7	GLY	-	expression tag	UNP Q9HXM5

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	expression tag	UNP Q9HXM5
A	-5	VAL	-	expression tag	UNP Q9HXM5
A	-4	PRO	-	expression tag	UNP Q9HXM5
A	-3	ARG	-	expression tag	UNP Q9HXM5
A	-2	GLY	-	expression tag	UNP Q9HXM5
A	-1	SER	-	expression tag	UNP Q9HXM5
A	0	HIS	-	expression tag	UNP Q9HXM5
B	-19	MET	-	initiating methionine	UNP Q9HXM5
B	-18	GLY	-	expression tag	UNP Q9HXM5
B	-17	SER	-	expression tag	UNP Q9HXM5
B	-16	SER	-	expression tag	UNP Q9HXM5
B	-15	HIS	-	expression tag	UNP Q9HXM5
B	-14	HIS	-	expression tag	UNP Q9HXM5
B	-13	HIS	-	expression tag	UNP Q9HXM5
B	-12	HIS	-	expression tag	UNP Q9HXM5
B	-11	HIS	-	expression tag	UNP Q9HXM5
B	-10	HIS	-	expression tag	UNP Q9HXM5
B	-9	SER	-	expression tag	UNP Q9HXM5
B	-8	SER	-	expression tag	UNP Q9HXM5
B	-7	GLY	-	expression tag	UNP Q9HXM5
B	-6	LEU	-	expression tag	UNP Q9HXM5
B	-5	VAL	-	expression tag	UNP Q9HXM5
B	-4	PRO	-	expression tag	UNP Q9HXM5
B	-3	ARG	-	expression tag	UNP Q9HXM5
B	-2	GLY	-	expression tag	UNP Q9HXM5
B	-1	SER	-	expression tag	UNP Q9HXM5
B	0	HIS	-	expression tag	UNP Q9HXM5
C	-19	MET	-	initiating methionine	UNP Q9HXM5
C	-18	GLY	-	expression tag	UNP Q9HXM5
C	-17	SER	-	expression tag	UNP Q9HXM5
C	-16	SER	-	expression tag	UNP Q9HXM5
C	-15	HIS	-	expression tag	UNP Q9HXM5
C	-14	HIS	-	expression tag	UNP Q9HXM5
C	-13	HIS	-	expression tag	UNP Q9HXM5
C	-12	HIS	-	expression tag	UNP Q9HXM5
C	-11	HIS	-	expression tag	UNP Q9HXM5
C	-10	HIS	-	expression tag	UNP Q9HXM5
C	-9	SER	-	expression tag	UNP Q9HXM5
C	-8	SER	-	expression tag	UNP Q9HXM5
C	-7	GLY	-	expression tag	UNP Q9HXM5
C	-6	LEU	-	expression tag	UNP Q9HXM5
C	-5	VAL	-	expression tag	UNP Q9HXM5

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	PRO	-	expression tag	UNP Q9HXM5
C	-3	ARG	-	expression tag	UNP Q9HXM5
C	-2	GLY	-	expression tag	UNP Q9HXM5
C	-1	SER	-	expression tag	UNP Q9HXM5
C	0	HIS	-	expression tag	UNP Q9HXM5
D	-19	MET	-	initiating methionine	UNP Q9HXM5
D	-18	GLY	-	expression tag	UNP Q9HXM5
D	-17	SER	-	expression tag	UNP Q9HXM5
D	-16	SER	-	expression tag	UNP Q9HXM5
D	-15	HIS	-	expression tag	UNP Q9HXM5
D	-14	HIS	-	expression tag	UNP Q9HXM5
D	-13	HIS	-	expression tag	UNP Q9HXM5
D	-12	HIS	-	expression tag	UNP Q9HXM5
D	-11	HIS	-	expression tag	UNP Q9HXM5
D	-10	HIS	-	expression tag	UNP Q9HXM5
D	-9	SER	-	expression tag	UNP Q9HXM5
D	-8	SER	-	expression tag	UNP Q9HXM5
D	-7	GLY	-	expression tag	UNP Q9HXM5
D	-6	LEU	-	expression tag	UNP Q9HXM5
D	-5	VAL	-	expression tag	UNP Q9HXM5
D	-4	PRO	-	expression tag	UNP Q9HXM5
D	-3	ARG	-	expression tag	UNP Q9HXM5
D	-2	GLY	-	expression tag	UNP Q9HXM5
D	-1	SER	-	expression tag	UNP Q9HXM5
D	0	HIS	-	expression tag	UNP Q9HXM5
E	-19	MET	-	initiating methionine	UNP Q9HXM5
E	-18	GLY	-	expression tag	UNP Q9HXM5
E	-17	SER	-	expression tag	UNP Q9HXM5
E	-16	SER	-	expression tag	UNP Q9HXM5
E	-15	HIS	-	expression tag	UNP Q9HXM5
E	-14	HIS	-	expression tag	UNP Q9HXM5
E	-13	HIS	-	expression tag	UNP Q9HXM5
E	-12	HIS	-	expression tag	UNP Q9HXM5
E	-11	HIS	-	expression tag	UNP Q9HXM5
E	-10	HIS	-	expression tag	UNP Q9HXM5
E	-9	SER	-	expression tag	UNP Q9HXM5
E	-8	SER	-	expression tag	UNP Q9HXM5
E	-7	GLY	-	expression tag	UNP Q9HXM5
E	-6	LEU	-	expression tag	UNP Q9HXM5
E	-5	VAL	-	expression tag	UNP Q9HXM5
E	-4	PRO	-	expression tag	UNP Q9HXM5
E	-3	ARG	-	expression tag	UNP Q9HXM5

Continued on next page...

Continued from previous page...

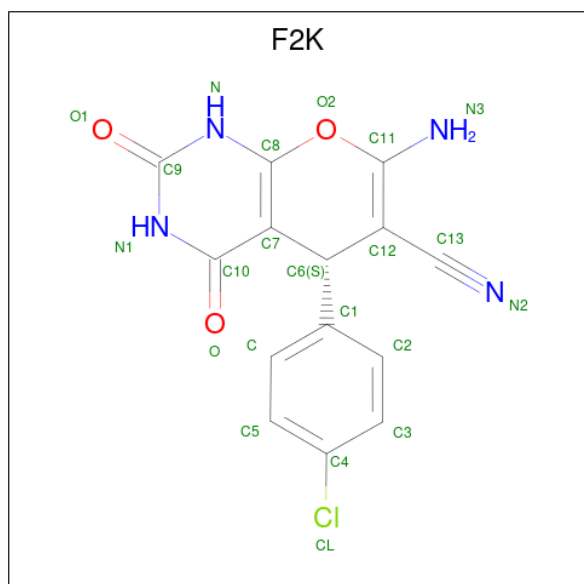
Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	GLY	-	expression tag	UNP Q9HXM5
E	-1	SER	-	expression tag	UNP Q9HXM5
E	0	HIS	-	expression tag	UNP Q9HXM5
F	-19	MET	-	initiating methionine	UNP Q9HXM5
F	-18	GLY	-	expression tag	UNP Q9HXM5
F	-17	SER	-	expression tag	UNP Q9HXM5
F	-16	SER	-	expression tag	UNP Q9HXM5
F	-15	HIS	-	expression tag	UNP Q9HXM5
F	-14	HIS	-	expression tag	UNP Q9HXM5
F	-13	HIS	-	expression tag	UNP Q9HXM5
F	-12	HIS	-	expression tag	UNP Q9HXM5
F	-11	HIS	-	expression tag	UNP Q9HXM5
F	-10	HIS	-	expression tag	UNP Q9HXM5
F	-9	SER	-	expression tag	UNP Q9HXM5
F	-8	SER	-	expression tag	UNP Q9HXM5
F	-7	GLY	-	expression tag	UNP Q9HXM5
F	-6	LEU	-	expression tag	UNP Q9HXM5
F	-5	VAL	-	expression tag	UNP Q9HXM5
F	-4	PRO	-	expression tag	UNP Q9HXM5
F	-3	ARG	-	expression tag	UNP Q9HXM5
F	-2	GLY	-	expression tag	UNP Q9HXM5
F	-1	SER	-	expression tag	UNP Q9HXM5
F	0	HIS	-	expression tag	UNP Q9HXM5
G	-19	MET	-	initiating methionine	UNP Q9HXM5
G	-18	GLY	-	expression tag	UNP Q9HXM5
G	-17	SER	-	expression tag	UNP Q9HXM5
G	-16	SER	-	expression tag	UNP Q9HXM5
G	-15	HIS	-	expression tag	UNP Q9HXM5
G	-14	HIS	-	expression tag	UNP Q9HXM5
G	-13	HIS	-	expression tag	UNP Q9HXM5
G	-12	HIS	-	expression tag	UNP Q9HXM5
G	-11	HIS	-	expression tag	UNP Q9HXM5
G	-10	HIS	-	expression tag	UNP Q9HXM5
G	-9	SER	-	expression tag	UNP Q9HXM5
G	-8	SER	-	expression tag	UNP Q9HXM5
G	-7	GLY	-	expression tag	UNP Q9HXM5
G	-6	LEU	-	expression tag	UNP Q9HXM5
G	-5	VAL	-	expression tag	UNP Q9HXM5
G	-4	PRO	-	expression tag	UNP Q9HXM5
G	-3	ARG	-	expression tag	UNP Q9HXM5
G	-2	GLY	-	expression tag	UNP Q9HXM5
G	-1	SER	-	expression tag	UNP Q9HXM5

Continued on next page...

Continued from previous page...

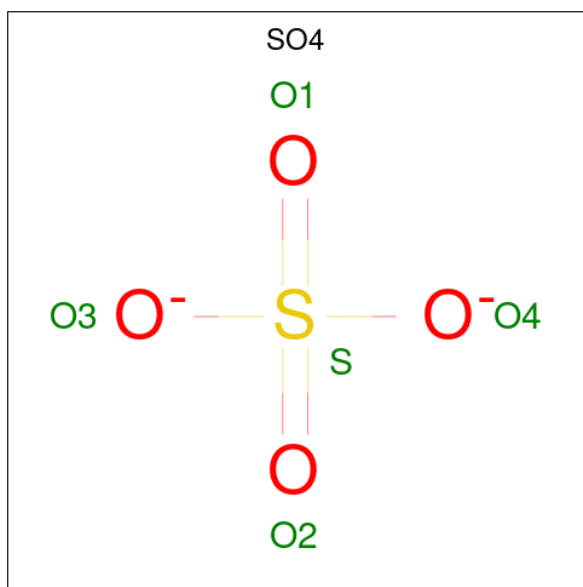
Chain	Residue	Modelled	Actual	Comment	Reference
G	0	HIS	-	expression tag	UNP Q9HXM5
H	-19	MET	-	initiating methionine	UNP Q9HXM5
H	-18	GLY	-	expression tag	UNP Q9HXM5
H	-17	SER	-	expression tag	UNP Q9HXM5
H	-16	SER	-	expression tag	UNP Q9HXM5
H	-15	HIS	-	expression tag	UNP Q9HXM5
H	-14	HIS	-	expression tag	UNP Q9HXM5
H	-13	HIS	-	expression tag	UNP Q9HXM5
H	-12	HIS	-	expression tag	UNP Q9HXM5
H	-11	HIS	-	expression tag	UNP Q9HXM5
H	-10	HIS	-	expression tag	UNP Q9HXM5
H	-9	SER	-	expression tag	UNP Q9HXM5
H	-8	SER	-	expression tag	UNP Q9HXM5
H	-7	GLY	-	expression tag	UNP Q9HXM5
H	-6	LEU	-	expression tag	UNP Q9HXM5
H	-5	VAL	-	expression tag	UNP Q9HXM5
H	-4	PRO	-	expression tag	UNP Q9HXM5
H	-3	ARG	-	expression tag	UNP Q9HXM5
H	-2	GLY	-	expression tag	UNP Q9HXM5
H	-1	SER	-	expression tag	UNP Q9HXM5
H	0	HIS	-	expression tag	UNP Q9HXM5

- Molecule 2 is (5 {S})-7-azanyl-5-(4-chlorophenyl)-2,4-bis(oxidanylidene)-1,5-dihydropyrano[2,3-d]pyrimidine-6-carbonitrile (CCD ID: F2K) (formula: C₁₄H₉ClN₄O₃).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 31	C 14	Cl 1	H 9	N 4	O 3	0	0
2	D	1	Total 31	C 14	Cl 1	H 9	N 4	O 3	0	0

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	1	Total	O S	0	0
			5	4 1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	155	Total	O	0	0
			155	155		
4	B	164	Total	O	0	0
			164	164		
4	C	154	Total	O	0	0
			154	154		
4	D	123	Total	O	0	0
			123	123		
4	E	123	Total	O	0	0
			123	123		
4	F	133	Total	O	0	0
			133	133		
4	G	72	Total	O	0	0
			72	72		

Continued on next page...

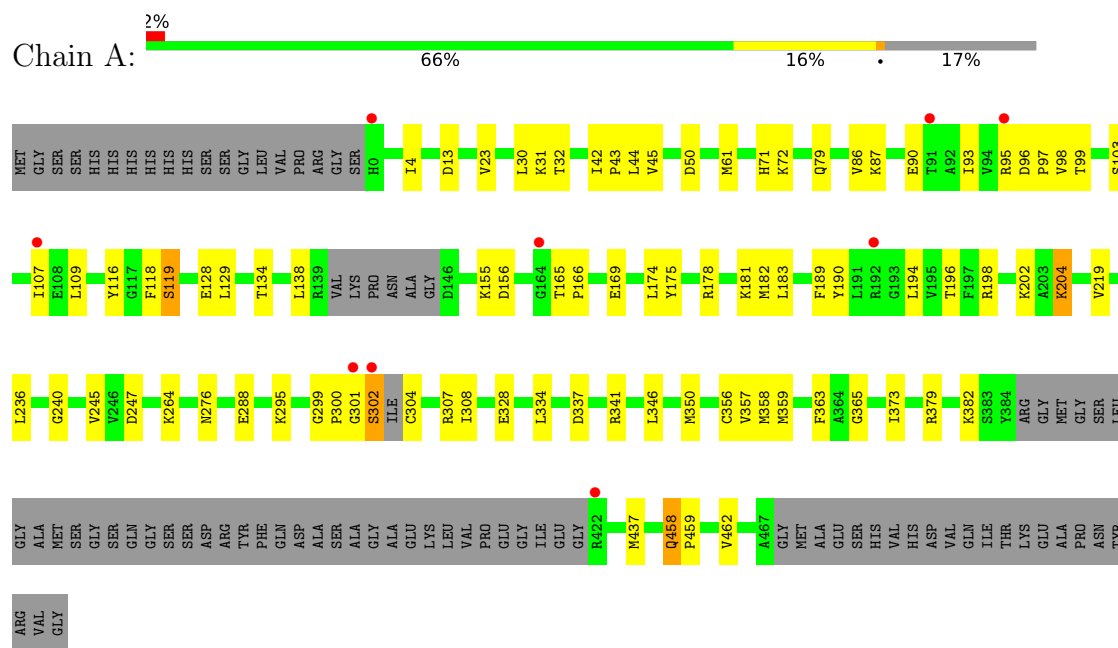
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	58	Total	O	0	0
			58	58		

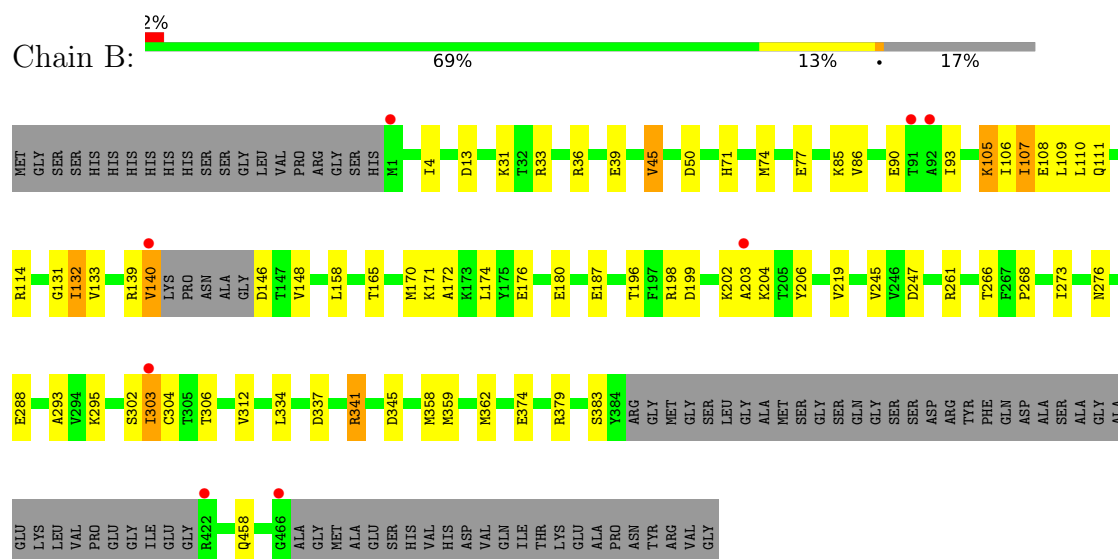
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: Inosine-5'-monophosphate dehydrogenase



• Molecule 1: Inosine-5'-monophosphate dehydrogenase

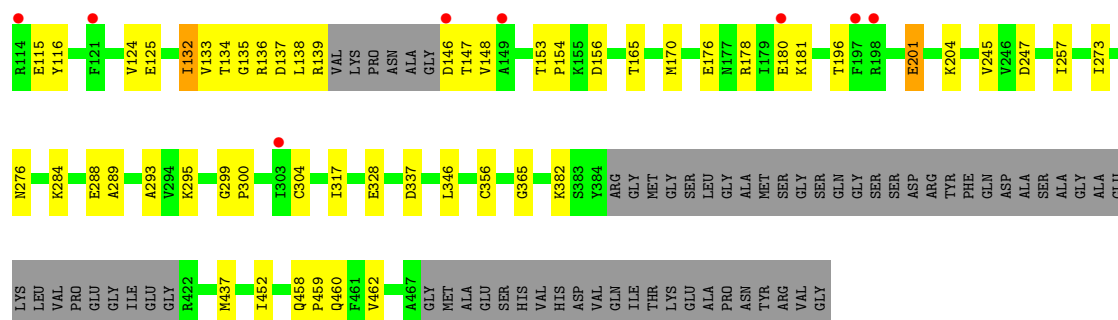


[illegible][illegible]

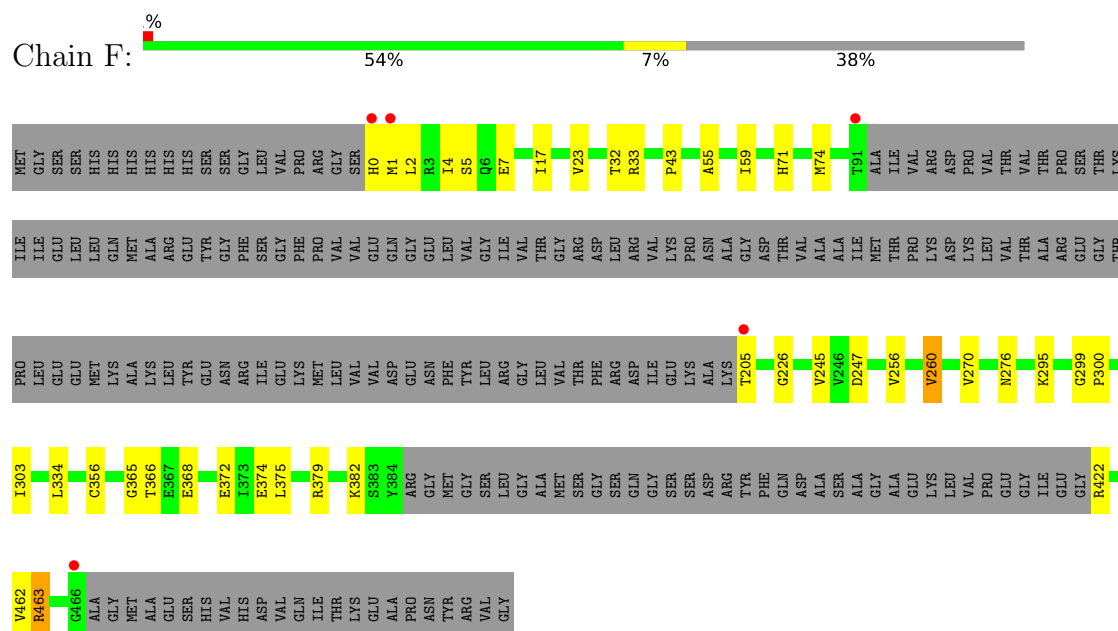
Chain E:

Sequence logo for Chain E. The y-axis represents information content in bits (0.00 to 0.10). The x-axis lists amino acid positions. A color scale at the top indicates conservation levels: 2% (red), 69% (green), 14% (yellow), and 17% (grey).

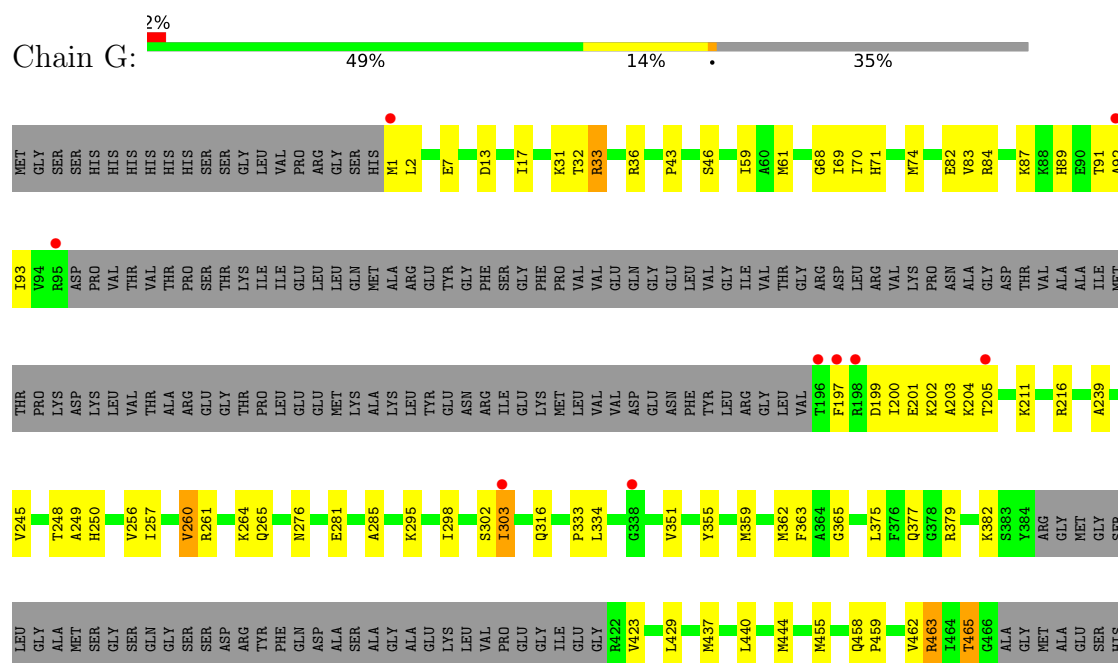
Position	Amino Acid	Conservation Level (%)
1	Met	2%
2	Gly	69%
3	Ser	69%
4	Ser	69%
5	His	69%
6	His	69%
7	His	69%
8	His	69%
9	His	69%
10	His	69%
11	Ser	69%
12	Ser	69%
13	Gly	69%
14	Leu	69%
15	Val	69%
16	Pro	69%
17	Arg	69%
18	Gly	69%
19	Gly	69%
20	Ser	69%
21	His	69%
22	Met	2%
23	Lys	69%
24	Lys	69%
25	Lys	69%
26	Lys	69%
27	Lys	69%
28	Lys	69%
29	Lys	69%
30	Lys	69%
31	Lys	69%
32	Lys	69%
33	Lys	69%
34	Lys	69%
35	Lys	69%
36	Lys	69%
37	Lys	69%
38	Lys	69%
39	Lys	69%
40	Lys	69%
41	Lys	69%
42	Lys	69%
43	Lys	69%
44	Lys	69%
45	Lys	69%
46	Lys	69%
47	Lys	69%
48	Lys	69%
49	Lys	69%
50	Lys	69%
51	Lys	69%
52	Lys	69%
53	Lys	69%
54	Lys	69%
55	Lys	69%
56	Lys	69%
57	Lys	69%
58	Lys	69%
59	Lys	69%
60	Lys	69%
61	Lys	69%
62	Lys	69%
63	Lys	69%
64	Lys	69%
65	Lys	69%
66	Lys	69%
67	Lys	69%
68	Lys	69%
69	Lys	69%
70	Lys	69%
71	Lys	69%
72	Lys	69%
73	Lys	69%
74	Lys	69%
75	Lys	69%
76	Lys	69%
77	Lys	69%
78	Lys	69%
79	Lys	69%
80	Lys	69%
81	Lys	69%
82	Lys	69%
83	Lys	69%
84	Lys	69%
85	Lys	69%
86	Lys	69%
87	Lys	69%
88	Lys	69%
89	Lys	69%
90	Lys	69%
91	Lys	69%
92	Lys	69%
93	Lys	69%
94	Lys	69%
95	Lys	69%
96	Lys	69%
97	Lys	69%
98	Lys	69%
99	Lys	69%
100	Lys	69%
101	Lys	69%
102	Lys	69%
103	Lys	69%
104	Lys	69%
105	Lys	69%
106	Lys	69%
107	Lys	69%
108	Lys	69%
109	Lys	69%
110	Lys	69%
111	Lys	69%
112	Lys	69%
113	Lys	69%
114	Lys	69%
115	Lys	69%
116	Lys	69%
117	Lys	69%
118	Lys	69%
119	Lys	69%
120	Lys	69%
121	Lys	69%
122	Lys	69%
123	Lys	69%
124	Lys	69%
125	Lys	69%
126	Lys	69%
127	Lys	69%



• Molecule 1: Inosine-5'-monophosphate dehydrogenase

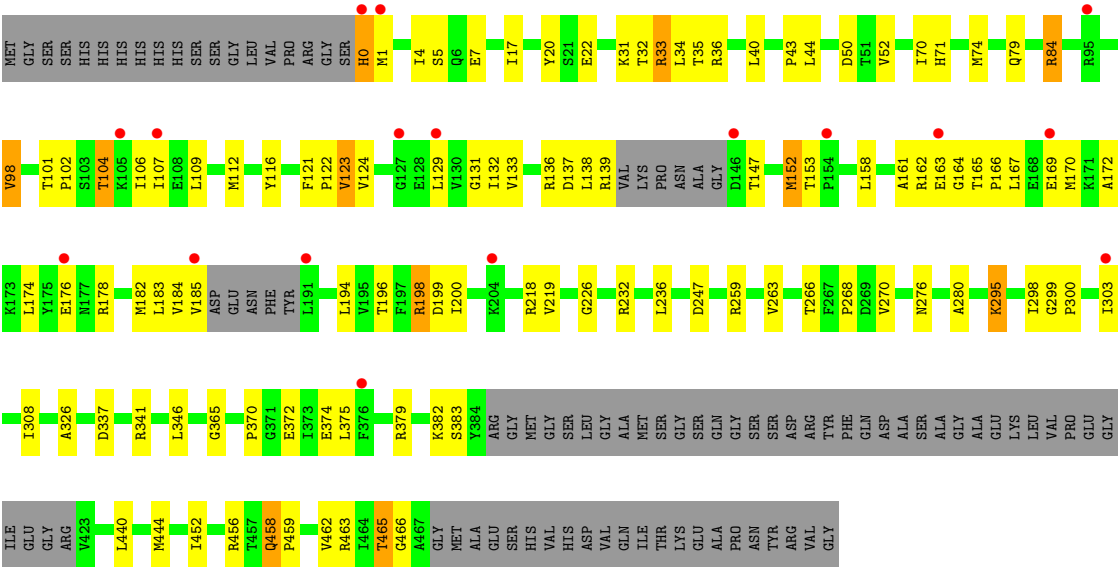


• Molecule 1: Inosine-5'-monophosphate dehydrogenase



VAL
HIS
ASP
VAL
GLN
ILE
THR
LYS
GLU
ALA
PRO
ASN
TYR
ARG
VAL
GLY

● Molecule 1: Inosine-5'-monophosphate dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	115.64Å 196.96Å 123.63Å 90.00° 113.99° 90.00°	Depositor
Resolution (Å)	48.99 – 2.54 48.99 – 2.54	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.99-2.54) 100.0 (48.99-2.54)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 2.54Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.159 , 0.205 0.165 , 0.208	Depositor DCC
R_{free} test set	8272 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	43.4	Xtriage
Anisotropy	0.125	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 64.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	24276	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, F2K

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	0.36	0/3176	0.56	0/4294
1	B	0.34	0/3185	0.54	0/4306
1	C	0.34	0/2847	0.53	0/3839
1	D	0.35	0/3204	0.57	0/4329
1	E	0.34	0/3202	0.54	0/4327
1	F	0.36	0/2341	0.54	0/3164
1	G	0.29	0/2416	0.50	0/3265
1	H	0.28	0/3145	0.49	0/4249
All	All	0.33	0/23516	0.53	0/31773

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3136	0	3227	73	1
1	B	3145	0	3246	52	0
1	C	2816	0	2903	70	0
1	D	3161	0	3265	82	1
1	E	3158	0	3261	60	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2314	0	2375	23	0
1	G	2390	0	2446	54	0
1	H	3107	0	3218	95	0
2	A	22	9	0	0	0
2	D	22	9	0	1	0
3	E	5	0	0	0	0
4	A	155	0	0	3	0
4	B	164	0	0	3	0
4	C	154	0	0	1	0
4	D	123	0	0	0	0
4	E	123	0	0	1	0
4	F	133	0	0	2	0
4	G	72	0	0	4	0
4	H	58	0	0	1	0
All	All	24258	18	23941	490	1

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 10.

The worst 5 of 490 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:A:30:LEU:HD13	1:A:437:MET:HE3	1.15	1.14
1:A:43:PRO:HD2	1:A:437:MET:HE1	1.21	1.13
1:D:196:THR:HG22	1:D:199:ASP:H	1.23	1.01
1:B:13:ASP:OD1	1:G:465:THR:HG21	1.62	0.98
1:G:13:ASP:OD1	1:H:465:THR:HG21	1.62	0.97

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:TYR:OH	1:D:108:GLU:OE2[1_656]	1.92	0.28

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 X-ray entries followed by that with respect to entries of similar resolution.

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	418/509 (82%)	400 (96%)	15 (4%)	3 (1%)	18	25
1	B	418/509 (82%)	402 (96%)	13 (3%)	3 (1%)	18	25
1	C	367/509 (72%)	353 (96%)	13 (4%)	1 (0%)	36	45
1	D	419/509 (82%)	401 (96%)	17 (4%)	1 (0%)	43	56
1	E	419/509 (82%)	403 (96%)	15 (4%)	1 (0%)	43	56
1	F	311/509 (61%)	299 (96%)	11 (4%)	1 (0%)	36	45
1	G	323/509 (64%)	308 (95%)	13 (4%)	2 (1%)	21	29
1	H	411/509 (81%)	389 (95%)	19 (5%)	3 (1%)	18	25
All	All	3086/4072 (76%)	2955 (96%)	116 (4%)	15 (0%)	24	34

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	2	LEU
1	G	377	GLN
1	H	152	MET
1	B	303	ILE
1	C	158	LEU

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 X-ray entries followed by that with respect to entries of similar resolution.

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	321/390 (82%)	309 (96%)	12 (4%)	30	45

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	324/390 (83%)	312 (96%)	12 (4%)	30	45
1	C	288/390 (74%)	275 (96%)	13 (4%)	24	38
1	D	327/390 (84%)	313 (96%)	14 (4%)	26	39
1	E	326/390 (84%)	322 (99%)	4 (1%)	63	78
1	F	233/390 (60%)	224 (96%)	9 (4%)	28	43
1	G	238/390 (61%)	229 (96%)	9 (4%)	29	44
1	H	321/390 (82%)	306 (95%)	15 (5%)	23	36
All	All	2378/3120 (76%)	2290 (96%)	88 (4%)	30	45

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	33	ARG
1	G	463	ARG
1	F	260	VAL
1	G	33	ARG
1	H	31	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	460	GLN
1	H	111	GLN
1	D	111	GLN
1	C	111	GLN
1	E	271	GLN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
2	F2K	D	501	-	24,24,24	0.54	1 (4%)	31,35,35	0.84	2 (6%)
2	F2K	A	501	-	24,24,24	0.55	1 (4%)	31,35,35	0.84	2 (6%)
3	SO4	E	501	-	4,4,4	0.34	0	6,6,6	0.41	0

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
2	F2K	D	501	-	-	2/4/22/22	0/3/3/3
2	F2K	A	501	-	-	2/4/22/22	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	F2K	C8-N	2.53	1.41	1.37
2	D	501	F2K	C8-N	2.43	1.41	1.37

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	F2K	O2-C8-C7	3.08	126.09	122.71
2	D	501	F2K	O2-C8-C7	3.06	126.07	122.71
2	D	501	F2K	C6-C7-C10	2.32	122.42	119.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	F2K	C6-C7-C10	2.29	122.38	119.52

There are no chirality outliers.

All (4) torsion outliers are listed below:

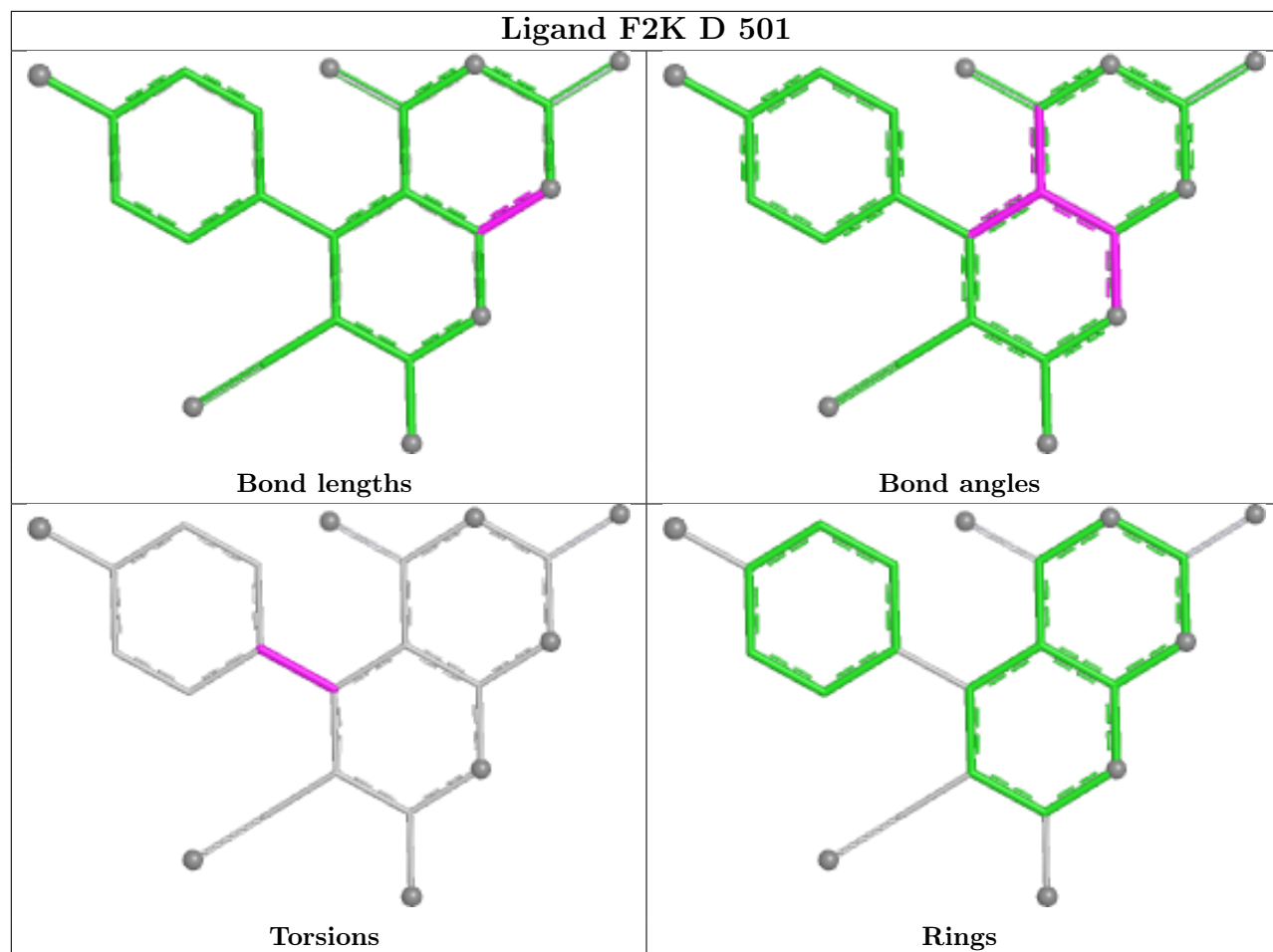
Mol	Chain	Res	Type	Atoms
2	A	501	F2K	C-C1-C6-C7
2	A	501	F2K	C2-C1-C6-C7
2	D	501	F2K	C-C1-C6-C7
2	D	501	F2K	C2-C1-C6-C7

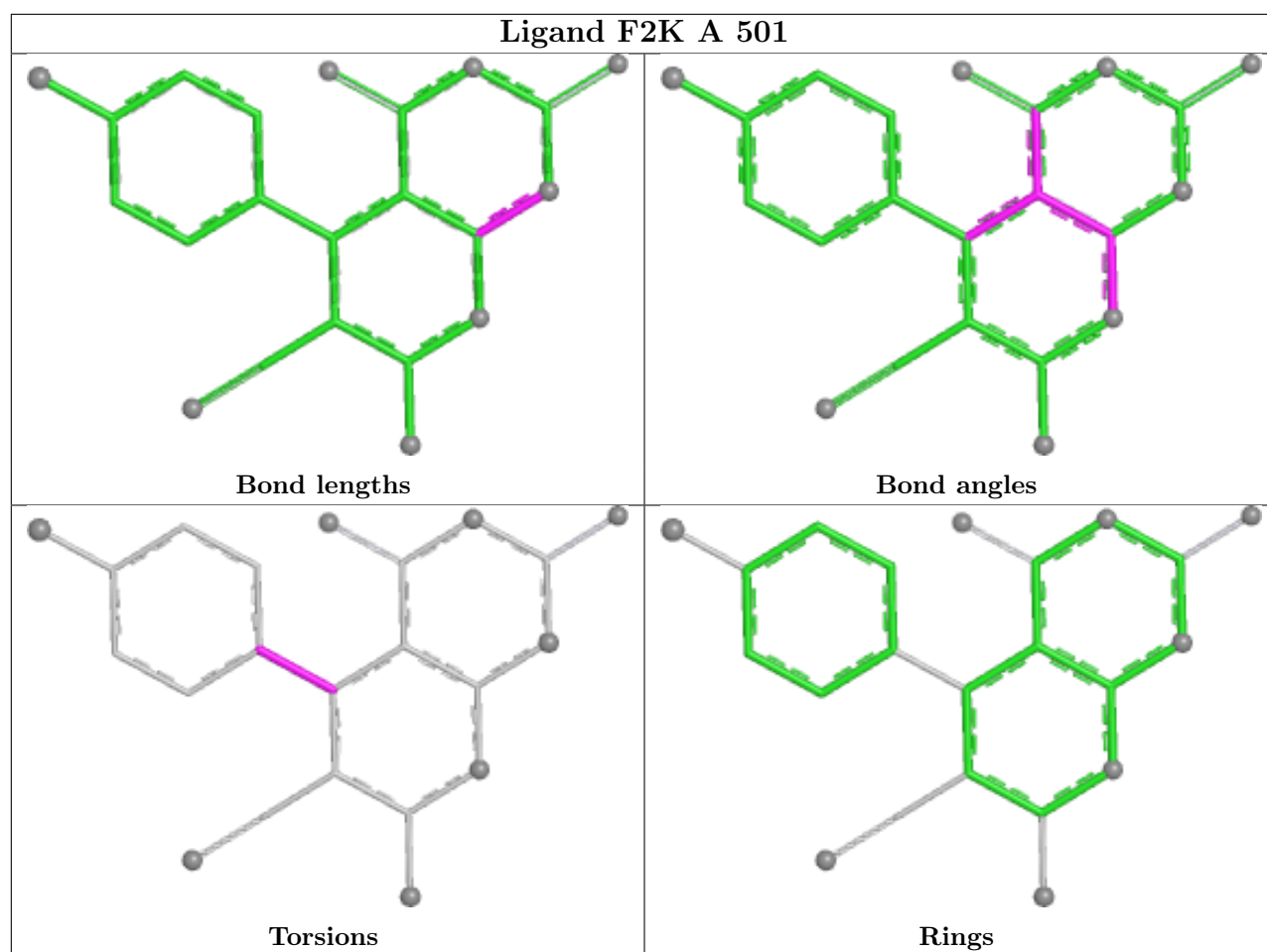
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	501	F2K	1	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 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å ²)	Q < 0.9
1	A	424/509 (83%)	-0.44	9 (2%) 63 64	24, 39, 82, 121	23 (5%)
1	B	424/509 (83%)	-0.46	8 (1%) 66 66	26, 39, 82, 99	24 (5%)
1	C	381/509 (74%)	-0.29	19 (4%) 34 33	24, 39, 122, 158	22 (5%)
1	D	424/509 (83%)	-0.39	6 (1%) 73 74	26, 45, 89, 108	24 (5%)
1	E	424/509 (83%)	-0.32	10 (2%) 59 61	23, 39, 110, 138	27 (6%)
1	F	317/509 (62%)	-0.56	5 (1%) 70 71	21, 41, 76, 109	15 (4%)
1	G	329/509 (64%)	-0.26	9 (2%) 56 57	34, 50, 97, 132	17 (5%)
1	H	419/509 (82%)	-0.03	17 (4%) 41 42	34, 54, 112, 159	22 (5%)
All	All	3142/4072 (77%)	-0.34	83 (2%) 57 58	21, 44, 100, 159	174 (5%)

The worst 5 of 83 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	140	VAL	9.8
1	G	1	MET	4.8
1	E	1	MET	4.6
1	B	91	THR	4.4
1	A	0	HIS	4.2

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

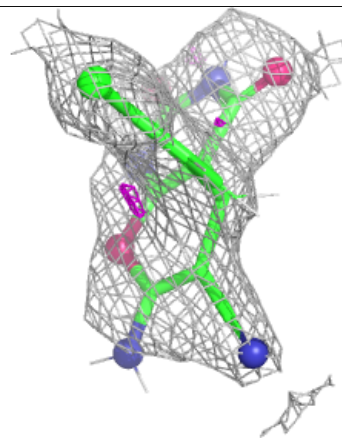
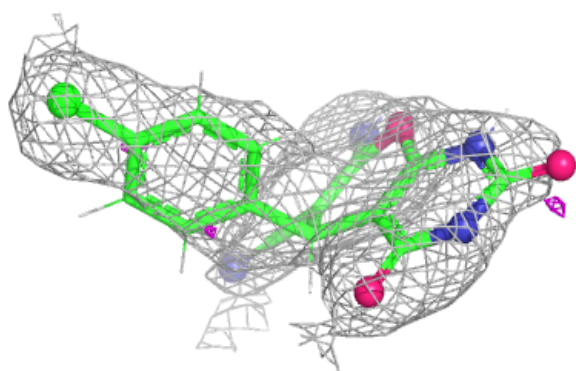
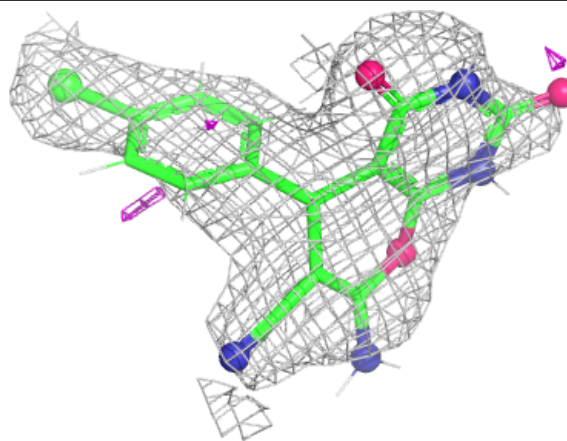
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	E	501	5/5	0.86	0.17	40,48,52,59	5
2	F2K	D	501	22/22	0.87	0.17	73,86,99,114	31
2	F2K	A	501	22/22	0.87	0.15	73,101,122,128	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

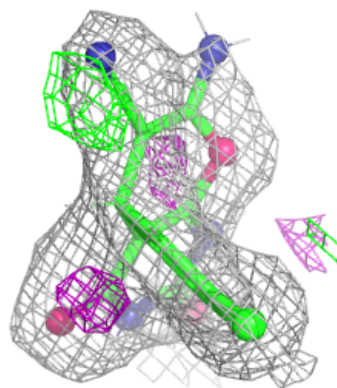
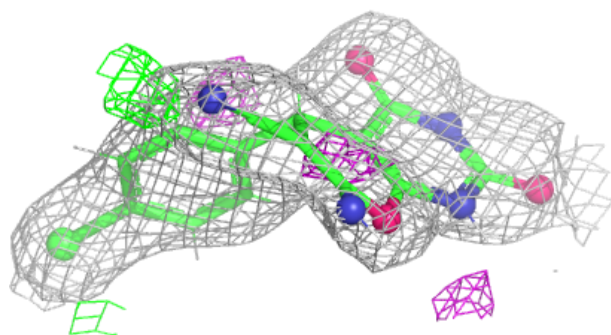
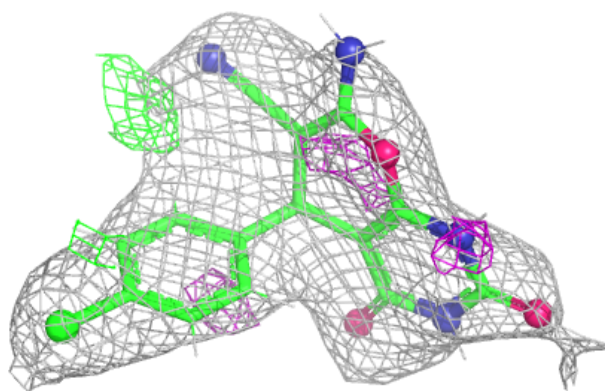
Electron density around F2K D 501:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around F2K A 501:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.