



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 11:35 PM GMT

PDB ID : 4JBI
Title : 2.35Å resolution structure of NADPH bound thermostable alcohol dehydrogenase from *Pyrobaculum aerophilum*
Authors : Lovell, S.; Battaile, K.P.; Vitale, A.; Throne, N.; Hu, X.; Shen, M.; D'Auria, S.; Auld, D.S.
Deposited on : 2013-02-19
Resolution : 2.35 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

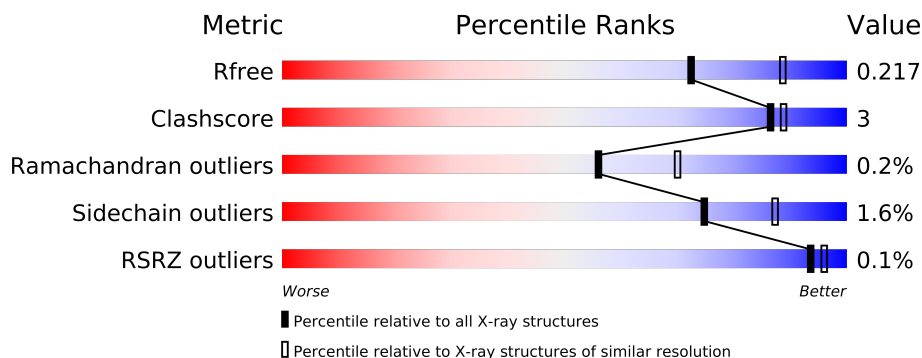
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.35 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}	66092	3327 (2.40-2.32)
Clashscore	79885	1064 (2.38-2.34)
Ramachandran outliers	78287	1048 (2.38-2.34)
Sidechain outliers	78261	1049 (2.38-2.34)
RSRZ outliers	66119	3330 (2.40-2.32)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	B	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	C	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	D	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	E	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	F	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	G	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	H	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	I	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	J	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	K	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	L	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	M	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	N	370	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>

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Mol	Chain	Length	Quality of chain
1	O	370	
1	P	370	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 40799 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Alcohol dehydrogenase (Zinc).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	333	Total	C	N	O	S	0	1	0
			2444	1554	428	453	9			
1	B	333	Total	C	N	O	S	0	1	0
			2436	1550	424	453	9			
1	C	333	Total	C	N	O	S	0	1	0
			2452	1556	434	453	9			
1	D	333	Total	C	N	O	S	0	1	0
			2425	1544	421	451	9			
1	E	333	Total	C	N	O	S	0	1	0
			2446	1553	431	453	9			
1	F	333	Total	C	N	O	S	0	1	0
			2448	1553	433	453	9			
1	G	333	Total	C	N	O	S	0	1	0
			2437	1548	427	453	9			
1	H	333	Total	C	N	O	S	0	1	0
			2427	1545	420	453	9			
1	I	333	Total	C	N	O	S	0	1	0
			2430	1545	423	453	9			
1	J	333	Total	C	N	O	S	0	0	0
			2424	1542	420	453	9			
1	K	333	Total	C	N	O	S	0	1	0
			2422	1541	423	449	9			
1	L	333	Total	C	N	O	S	0	1	0
			2432	1546	424	453	9			
1	M	333	Total	C	N	O	S	0	1	0
			2431	1547	424	451	9			
1	N	333	Total	C	N	O	S	0	1	0
			2433	1548	423	453	9			
1	O	333	Total	C	N	O	S	0	1	0
			2406	1532	414	451	9			
1	P	333	Total	C	N	O	S	0	0	0
			2415	1536	417	453	9			

There are 624 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
A	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
A	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
A	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
A	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
A	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
A	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
A	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
A	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
A	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
A	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
A	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
A	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
A	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
A	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
A	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
A	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
A	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
A	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
A	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
A	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
A	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
A	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
A	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
A	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
A	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
A	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
A	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
A	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
A	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
A	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
A	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
A	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
A	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
A	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
A	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
A	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
A	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
A	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
B	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
B	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
B	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
B	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
B	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
B	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
B	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
B	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
B	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
B	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
B	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
B	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
B	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
B	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
B	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
B	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
B	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
B	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
B	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
B	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
B	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
B	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
B	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
B	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
B	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
B	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
B	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
B	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
B	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
B	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
B	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
B	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
B	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
B	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
B	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
B	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
B	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
B	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
C	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
C	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
C	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
C	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
C	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
C	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
C	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
C	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
C	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
C	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
C	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
C	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
C	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
C	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
C	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
C	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
C	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
C	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
C	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
C	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
C	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
C	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
C	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
C	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
C	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
C	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
C	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
C	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
C	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
C	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
C	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
C	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
C	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
C	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
C	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
C	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
C	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
C	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
D	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
D	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
D	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
D	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
D	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
D	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
D	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
D	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
D	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
D	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
D	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
D	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
D	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
D	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
D	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
D	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
D	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
D	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
D	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
D	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
D	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
D	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
D	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
D	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
D	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
D	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
D	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
D	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
D	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
D	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
D	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
D	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
D	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
D	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
D	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
D	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
D	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
D	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
E	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
E	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
E	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
E	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
E	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
E	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
E	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
E	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
E	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
E	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
E	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
E	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
E	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
E	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
E	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
E	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
E	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
E	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
E	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
E	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
E	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
E	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
E	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
E	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
E	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
E	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
E	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
E	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
E	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
E	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
E	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
E	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
E	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
E	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
E	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
E	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
E	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
E	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
F	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
F	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
F	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
F	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
F	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
F	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
F	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
F	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
F	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
F	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
F	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
F	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
F	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
F	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
F	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
F	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
F	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
F	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
F	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
F	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
F	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
F	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
F	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
F	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
F	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
F	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
F	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
F	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
F	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
F	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
F	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
F	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
F	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
F	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
F	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
F	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
F	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
F	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
G	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
G	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
G	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
G	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
G	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
G	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
G	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
G	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
G	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
G	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
G	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
G	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
G	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
G	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
G	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
G	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
G	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
G	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
G	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
G	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
G	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
G	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
G	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
G	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
G	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
G	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
G	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
G	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
G	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
G	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
G	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
G	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
G	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
G	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
G	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
G	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
G	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
G	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
H	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
H	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
H	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
H	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
H	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
H	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
H	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
H	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
H	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
H	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
H	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
H	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
H	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
H	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
H	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
H	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
H	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
H	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
H	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
H	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
H	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
H	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
H	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
H	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
H	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
H	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
H	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
H	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
H	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
H	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
H	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
H	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
H	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
H	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
H	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
H	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
H	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
H	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
I	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
I	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
I	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
I	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
I	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
I	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
I	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
I	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
I	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
I	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
I	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
I	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
I	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
I	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
I	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
I	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
I	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
I	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
I	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
I	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
I	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
I	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
I	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
I	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
I	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
I	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
I	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
I	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
I	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
I	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
I	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
I	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
I	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
I	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
I	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
I	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
I	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
I	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
J	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
J	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
J	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
J	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
J	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
J	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
J	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
J	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
J	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
J	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
J	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
J	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
J	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
J	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
J	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
J	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
J	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
J	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
J	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
J	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
J	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
J	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
J	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
J	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
J	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
J	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
J	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
J	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
J	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
J	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
J	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
J	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
J	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
J	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
J	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
J	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
J	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
J	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
K	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
K	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
K	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
K	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
K	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
K	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
K	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
K	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
K	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
K	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
K	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
K	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
K	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
K	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
K	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
K	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
K	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
K	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
K	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
K	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
K	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
K	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
K	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
K	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
K	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
K	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
K	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
K	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
K	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
K	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
K	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
K	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
K	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
K	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
K	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
K	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
K	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
K	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
L	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
L	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
L	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
L	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
L	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
L	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
L	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
L	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
L	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
L	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
L	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
L	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
L	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
L	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
L	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
L	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
L	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
L	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
L	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
L	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
L	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
L	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
L	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
L	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
L	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
L	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
L	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
L	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
L	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
L	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
L	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
L	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
L	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0

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Chain	Residue	Modelled	Actual	Comment	Reference
L	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
L	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
L	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
L	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
L	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
L	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
M	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
M	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
M	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
M	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
M	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
M	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
M	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
M	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
M	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
M	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
M	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
M	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
M	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
M	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
M	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
M	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
M	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
M	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
M	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
M	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
M	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
M	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
M	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
M	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
M	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
M	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
M	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
M	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
M	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
M	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
M	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
M	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
M	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
M	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
M	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
M	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0

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Chain	Residue	Modelled	Actual	Comment	Reference
M	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
M	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
M	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
N	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
N	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
N	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
N	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
N	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
N	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
N	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
N	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
N	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
N	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
N	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
N	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
N	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
N	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
N	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
N	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
N	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
N	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
N	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
N	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
N	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
N	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
N	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
N	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
N	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
N	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
N	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
N	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
N	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
N	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
N	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
N	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
N	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
N	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
N	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
N	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
N	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
N	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
N	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0

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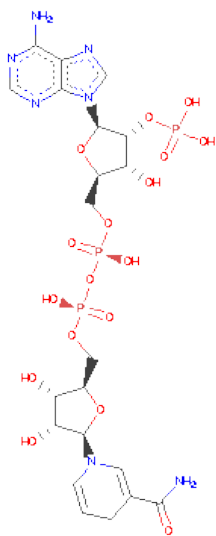
Chain	Residue	Modelled	Actual	Comment	Reference
O	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
O	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
O	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0
O	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
O	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
O	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
O	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
O	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
O	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
O	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
O	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
O	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
O	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
O	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
O	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
O	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
O	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
O	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
O	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
O	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
O	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
O	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
O	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
O	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
O	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
O	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
O	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
O	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
O	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
O	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
O	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
O	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
O	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
O	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
O	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
O	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
O	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
O	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
O	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0
P	-38	MET	-	EXPRESSION TAG	UNP Q8ZUP0
P	-37	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
P	-36	SER	-	EXPRESSION TAG	UNP Q8ZUP0

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Chain	Residue	Modelled	Actual	Comment	Reference
P	-35	SER	-	EXPRESSION TAG	UNP Q8ZUP0
P	-34	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
P	-33	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
P	-32	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
P	-31	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
P	-30	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
P	-29	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
P	-28	SER	-	EXPRESSION TAG	UNP Q8ZUP0
P	-27	SER	-	EXPRESSION TAG	UNP Q8ZUP0
P	-26	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
P	-25	LEU	-	EXPRESSION TAG	UNP Q8ZUP0
P	-24	VAL	-	EXPRESSION TAG	UNP Q8ZUP0
P	-23	PRO	-	EXPRESSION TAG	UNP Q8ZUP0
P	-22	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
P	-21	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
P	-20	SER	-	EXPRESSION TAG	UNP Q8ZUP0
P	-19	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
P	-18	MET	-	EXPRESSION TAG	UNP Q8ZUP0
P	-17	ALA	-	EXPRESSION TAG	UNP Q8ZUP0
P	-16	SER	-	EXPRESSION TAG	UNP Q8ZUP0
P	-15	MET	-	EXPRESSION TAG	UNP Q8ZUP0
P	-14	THR	-	EXPRESSION TAG	UNP Q8ZUP0
P	-13	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
P	-12	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
P	-11	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
P	-10	GLN	-	EXPRESSION TAG	UNP Q8ZUP0
P	-9	MET	-	EXPRESSION TAG	UNP Q8ZUP0
P	-8	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
P	-7	ARG	-	EXPRESSION TAG	UNP Q8ZUP0
P	-6	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
P	-5	SER	-	EXPRESSION TAG	UNP Q8ZUP0
P	-4	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
P	-3	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
P	-2	GLY	-	EXPRESSION TAG	UNP Q8ZUP0
P	-1	HIS	-	EXPRESSION TAG	UNP Q8ZUP0
P	0	GLU	-	EXPRESSION TAG	UNP Q8ZUP0

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDEPHOSPHATE (three-letter code: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	E	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	F	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	G	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	H	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	I	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	J	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	K	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	L	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	M	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	N	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	P	1	Total	Zn	0	0
			1	1		
3	G	1	Total	Zn	0	0
			1	1		
3	J	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		
3	K	1	Total	Zn	0	0
			1	1		
3	E	1	Total	Zn	0	0
			1	1		
3	H	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		
3	I	1	Total	Zn	0	0
			1	1		
3	C	1	Total	Zn	0	0
			1	1		
3	A	1	Total	Zn	0	0
			1	1		
3	N	1	Total	Zn	0	0
			1	1		
3	O	1	Total	Zn	0	0
			1	1		
3	L	1	Total	Zn	0	0
			1	1		
3	F	1	Total	Zn	0	0
			1	1		
3	M	1	Total	Zn	0	0
			1	1		

- Molecule 4 is water.

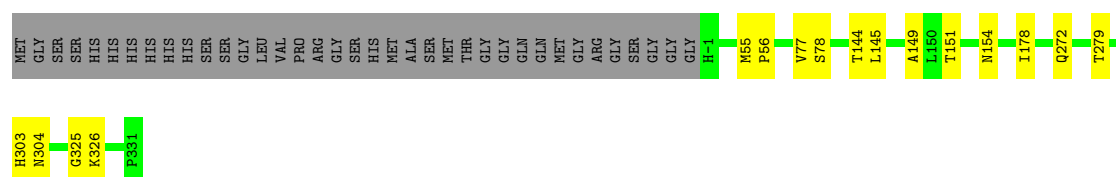
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	101	Total 101	O 101	0	0
4	B	91	Total 91	O 91	0	0
4	C	89	Total 89	O 89	0	0
4	D	81	Total 81	O 81	0	0
4	E	84	Total 84	O 84	0	0
4	F	91	Total 91	O 91	0	0
4	G	67	Total 67	O 67	0	0
4	H	83	Total 83	O 83	0	0
4	I	64	Total 64	O 64	0	0
4	J	68	Total 68	O 68	0	0
4	K	51	Total 51	O 51	0	0
4	L	53	Total 53	O 53	0	0
4	M	44	Total 44	O 44	0	0
4	N	54	Total 54	O 54	0	0
4	O	44	Total 44	O 44	0	0
4	P	42	Total 42	O 42	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

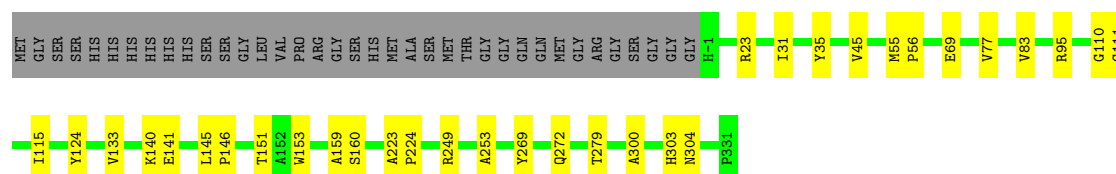
- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain A: 



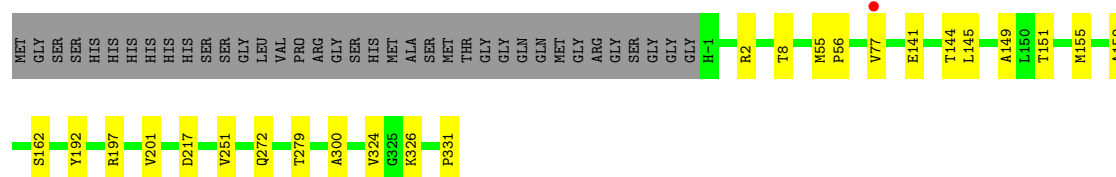
- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain B: 



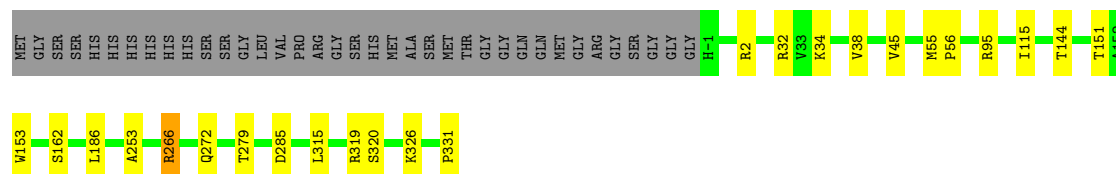
- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain C: 

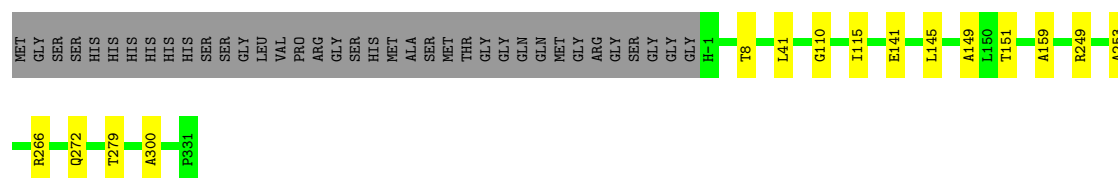


- Molecule 1: Alcohol dehydrogenase (Zinc)

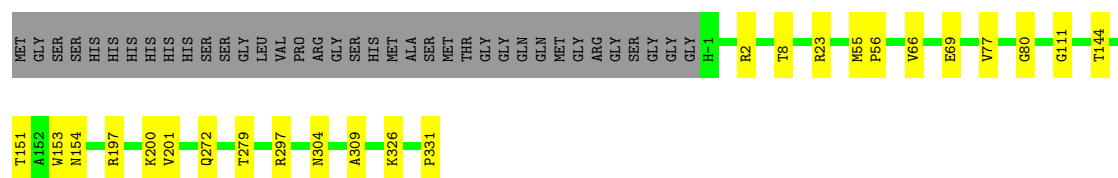
Chain D: 



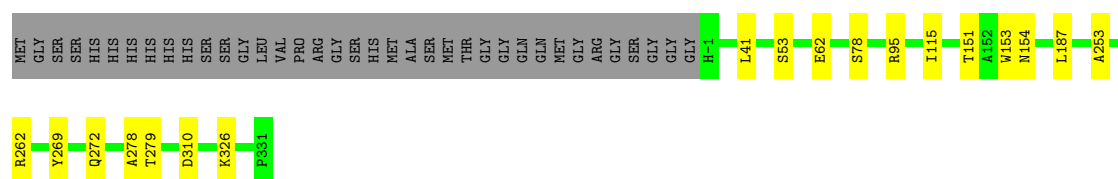
- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain E: 

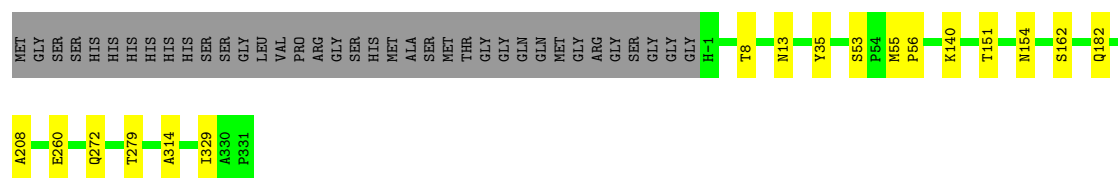
- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain F: 

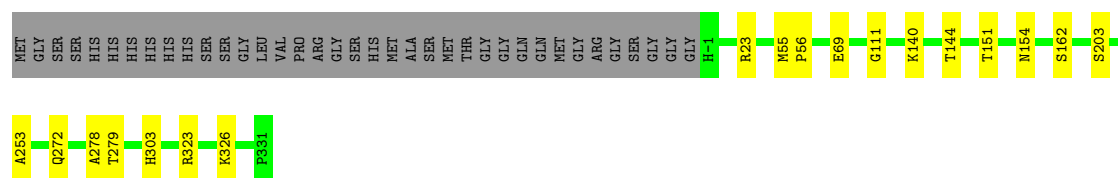
- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain G: 

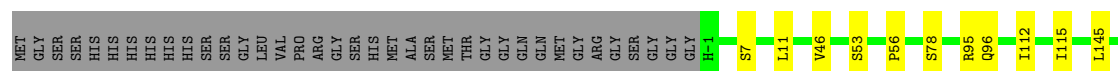
- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain H: 

- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain I: 

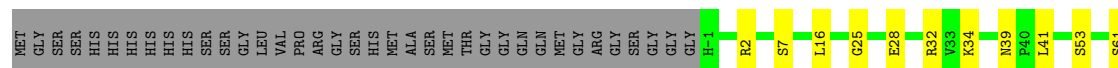
- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain J: 



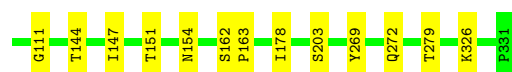
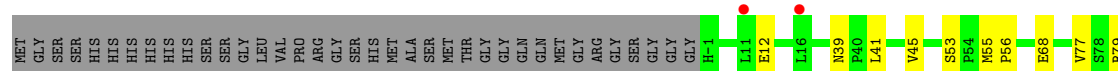
- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain K:



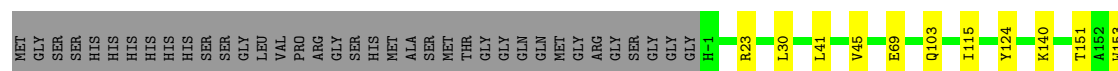
- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain L:



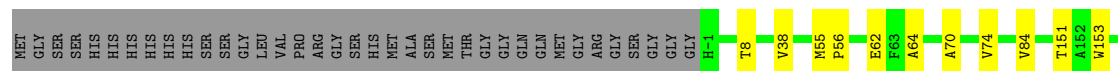
- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain M:



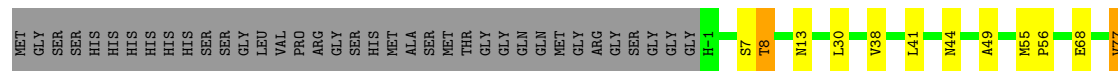
- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain N:



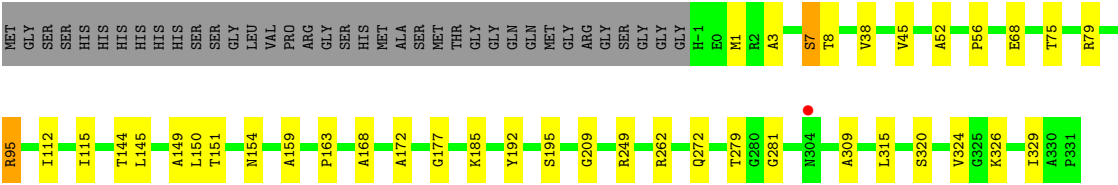
- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain O:



- Molecule 1: Alcohol dehydrogenase (Zinc)

Chain P: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	138.13Å 169.26Å 149.15Å 90.00° 116.25° 90.00°	Depositor
Resolution (Å)	44.59 – 2.35 49.51 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.9 (44.59-2.35) 99.9 (49.51-2.35)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 2.34Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1241)	Depositor
R, R_{free}	0.161 , 0.213 0.168 , 0.217	Depositor DCC
R_{free} test set	12808 reflections (5.03%)	DCC
Wilson B-factor (Å ²)	32.9	Xtriage
Anisotropy	0.222	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 26.5	EDS
Estimated twinning fraction	0.088 for h,-k,-h-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 254690 reflections (0.000%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	40799	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.03% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0/2494	0.72	0/3393
1	B	0.58	0/2486	0.73	0/3384
1	C	0.59	0/2502	0.73	0/3403
1	D	0.58	1/2475 (0.0%)	0.73	2/3371 (0.1%)
1	E	0.58	0/2496	0.69	0/3396
1	F	0.58	0/2498	0.72	0/3399
1	G	0.57	0/2487	0.69	0/3386
1	H	0.56	0/2477	0.68	0/3373
1	I	0.55	0/2480	0.69	0/3378
1	J	0.57	0/2470	0.69	0/3363
1	K	0.55	0/2472	0.69	0/3368
1	L	0.53	0/2482	0.68	0/3380
1	M	0.56	0/2481	0.67	0/3378
1	N	0.54	0/2483	0.69	0/3381
1	O	0.55	0/2456	0.67	0/3350
1	P	0.54	0/2460	0.66	1/3352 (0.0%)
All	All	0.56	1/39699 (0.0%)	0.70	3/54055 (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	O	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	319	ARG	C-N	7.23	1.50	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	285	ASP	CB-CG-OD2	-5.78	113.10	118.30
1	P	95	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	D	266	ARG	NE-CZ-NH1	5.33	122.97	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	O	323	ARG	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2444	0	2477	12	0
1	B	2436	0	2459	18	0
1	C	2452	0	2491	13	0
1	D	2425	0	2442	14	0
1	E	2446	0	2477	10	0
1	F	2448	0	2480	16	0
1	G	2437	0	2460	11	0
1	H	2427	0	2446	11	0
1	I	2430	0	2444	10	0
1	J	2424	0	2446	12	0
1	K	2422	0	2436	17	0
1	L	2432	0	2451	12	0
1	M	2431	0	2453	12	0
1	N	2433	0	2450	15	0
1	O	2406	0	2403	27	0
1	P	2415	0	2421	26	0
2	A	48	0	26	1	0
2	B	48	0	26	4	0
2	C	48	0	26	1	0
2	D	48	0	26	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	48	0	26	2	0
2	F	48	0	26	1	0
2	G	48	0	26	1	0
2	H	48	0	26	1	0
2	I	48	0	26	1	0
2	J	48	0	26	0	0
2	K	48	0	26	2	0
2	L	48	0	26	3	0
2	M	48	0	26	1	0
2	N	48	0	26	2	0
2	O	48	0	26	1	0
2	P	48	0	26	4	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
3	K	1	0	0	0	0
3	L	1	0	0	0	0
3	M	1	0	0	0	0
3	N	1	0	0	0	0
3	O	1	0	0	0	0
3	P	1	0	0	0	0
4	A	101	0	0	1	0
4	B	91	0	0	2	0
4	C	89	0	0	0	0
4	D	81	0	0	3	0
4	E	84	0	0	2	0
4	F	91	0	0	2	0
4	G	67	0	0	0	0
4	H	83	0	0	0	0
4	I	64	0	0	0	0
4	J	68	0	0	1	0
4	K	51	0	0	2	0
4	L	53	0	0	0	0
4	M	44	0	0	0	0
4	N	54	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	O	44	0	0	1	0
4	P	42	0	0	1	0
All	All	40799	0	39652	207	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (207) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:32:ARG:NH2	4:D:566:HOH:O	2.27	0.68
1:F:23:ARG:NH1	1:F:69:GLU:OE1	2.28	0.67
1:O:151:THR:OG1	2:O:401:NDP:H41N	1.95	0.67
1:L:68:GLU:OE2	1:L:79:ARG:NH2	2.29	0.66
1:P:151:THR:OG1	2:P:401:NDP:H41N	1.97	0.65
1:A:279:THR:H	1:F:272:GLN:HE21	1.45	0.65
1:A:272:GLN:HE21	1:F:279:THR:H	1.44	0.63
1:L:151:THR:OG1	2:L:401:NDP:H41N	1.99	0.63
1:I:151:THR:OG1	2:I:401:NDP:H41N	2.00	0.62
1:B:279:THR:H	1:L:272:GLN:HE21	1.47	0.60
1:M:23:ARG:NH1	1:M:69:GLU:OE1	2.35	0.59
1:H:272:GLN:HE21	1:P:279:THR:H	1.52	0.58
1:K:2:ARG:NH2	1:K:331:PRO:O	2.36	0.58
1:E:279:THR:H	1:K:272:GLN:HE21	1.51	0.58
1:D:2:ARG:NH2	1:D:331:PRO:O	2.35	0.58
1:K:39:ASN:OD1	1:K:326:LYS:NZ	2.37	0.57
1:I:272:GLN:HE21	1:O:279:THR:H	1.53	0.57
1:N:62:GLU:OE1	1:N:326:LYS:NZ	2.34	0.57
1:G:272:GLN:HE21	1:N:279:THR:H	1.53	0.56
1:I:154:ASN:HD21	1:O:272:GLN:HE22	1.53	0.56
1:A:154:ASN:HD21	1:F:272:GLN:NE2	2.04	0.56
1:P:38:VAL:HG13	1:P:315:LEU:HD23	1.88	0.56
1:G:151:THR:OG1	2:G:401:NDP:H41N	2.05	0.56
1:G:279:THR:H	1:N:272:GLN:HE21	1.54	0.55
1:P:151:THR:HG21	2:P:401:NDP:H41N	1.86	0.55
1:J:272:GLN:HE21	1:M:279:THR:H	1.55	0.55
1:C:279:THR:H	1:D:272:GLN:HE21	1.55	0.55
1:I:279:THR:H	1:O:272:GLN:HE21	1.53	0.54
1:J:223:ALA:HB1	1:J:224:PRO:HA	1.90	0.54
1:B:141:GLU:HG2	1:B:300:ALA:HB3	1.90	0.54
2:B:401:NDP:H3B	2:B:401:NDP:H8A	1.88	0.54
1:H:151:THR:OG1	2:H:401:NDP:H41N	2.07	0.54
1:O:320:SER:O	1:O:322:GLU:N	2.41	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:145:LEU:HA	1:E:149:ALA:HB3	1.89	0.53
1:N:317:GLU:HG2	1:N:327:VAL:HG21	1.90	0.53
1:C:141:GLU:HG2	1:C:300:ALA:HB3	1.90	0.53
1:D:151:THR:OG1	2:D:401:NDP:H41N	2.08	0.53
1:A:154:ASN:HD21	1:F:272:GLN:HE22	1.55	0.53
1:B:272:GLN:HE21	1:L:279:THR:H	1.55	0.53
1:C:272:GLN:HE21	1:D:279:THR:H	1.57	0.53
1:L:39:ASN:OD1	1:L:326:LYS:NZ	2.42	0.53
1:E:151:THR:OG1	2:E:401:NDP:H41N	2.10	0.52
1:E:253:ALA:O	2:E:401:NDP:H2N	2.10	0.51
1:D:38:VAL:HG13	1:D:315:LEU:HD23	1.93	0.50
1:D:253:ALA:O	2:D:401:NDP:H2N	2.11	0.50
1:K:151:THR:OG1	2:K:401:NDP:H41N	2.11	0.50
1:L:147:ILE:CG2	2:L:401:NDP:H5N	2.42	0.50
1:H:182:GLN:HG2	1:H:208:ALA:O	2.11	0.49
1:B:23:ARG:HD2	4:B:537:HOH:O	2.12	0.49
1:A:144:THR:HG22	1:A:326:LYS:HG2	1.95	0.49
1:O:8:THR:HG23	1:O:13:ASN:ND2	2.28	0.49
1:D:144:THR:HG22	1:D:326:LYS:HG2	1.95	0.49
1:E:41:LEU:HD21	1:E:115:ILE:HD11	1.94	0.48
1:H:55:MET:HA	1:H:56:PRO:C	2.34	0.48
1:F:66:VAL:CG1	1:F:80:GLY:HA2	2.43	0.48
1:N:38:VAL:CG2	1:N:329:ILE:HD13	2.43	0.48
2:K:401:NDP:H3B	2:K:401:NDP:H8A	1.94	0.48
1:P:7:SER:HA	1:P:56:PRO:HB3	1.95	0.48
1:E:110:GLY:HA2	4:E:516:HOH:O	2.12	0.48
1:H:272:GLN:HE22	1:P:154:ASN:HD21	1.62	0.48
1:C:159:ALA:HB2	1:C:251:VAL:HG21	1.96	0.48
1:E:141:GLU:HG2	1:E:300:ALA:HB3	1.95	0.48
1:D:326:LYS:HE2	4:D:525:HOH:O	2.13	0.48
1:P:68:GLU:OE2	1:P:79:ARG:NH2	2.46	0.48
1:B:272:GLN:HE22	1:L:154:ASN:HD21	1.62	0.48
1:P:144:THR:HG22	1:P:326:LYS:HG2	1.95	0.48
1:I:23:ARG:NH1	1:I:69:GLU:OE1	2.40	0.48
1:M:151:THR:OG1	2:M:401:NDP:H41N	2.14	0.48
1:K:32:ARG:HG3	1:K:34:LYS:HE2	1.96	0.48
1:I:154:ASN:HD21	1:O:272:GLN:NE2	2.12	0.47
1:O:55:MET:HA	1:O:56:PRO:C	2.35	0.47
1:C:144:THR:HG22	1:C:326:LYS:HG2	1.95	0.47
1:N:151:THR:HG21	2:N:401:NDP:H41N	1.94	0.47
1:J:323:ARG:HD2	1:J:327:VAL:HG23	1.96	0.47
1:K:110:GLY:HA2	4:K:510:HOH:O	2.15	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:J:159:ALA:O	1:J:249:ARG:HD2	2.15	0.47
1:P:1:MET:HE3	1:P:3:ALA:HB2	1.97	0.47
1:P:150:LEU:HG	1:P:281:GLY:HA3	1.97	0.47
1:O:320:SER:C	1:O:322:GLU:H	2.18	0.46
1:B:253:ALA:O	2:B:401:NDP:H2N	2.16	0.46
1:M:45:VAL:HG21	1:M:115:ILE:HG12	1.98	0.46
1:O:145:LEU:HA	1:O:149:ALA:HB3	1.98	0.46
1:A:272:GLN:HE22	1:F:154:ASN:HD21	1.63	0.46
1:F:144:THR:HG22	1:F:326:LYS:HG2	1.98	0.46
1:A:325:GLY:N	4:A:600:HOH:O	2.37	0.46
1:O:314:ALA:CB	1:O:329:ILE:HD11	2.46	0.46
1:A:151:THR:OG1	2:A:401:NDP:H41N	2.15	0.46
1:C:192:TYR:CD1	1:C:192:TYR:N	2.83	0.46
1:B:223:ALA:HB1	1:B:224:PRO:HA	1.97	0.46
1:M:30:LEU:HD11	1:M:124:TYR:HB3	1.98	0.46
1:O:153:TRP:CD1	1:O:153:TRP:C	2.89	0.46
1:J:278:ALA:O	1:M:269:TYR:HB2	2.16	0.46
1:C:145:LEU:HA	1:C:149:ALA:HB3	1.97	0.46
1:P:262:ARG:NE	1:P:262:ARG:NH1	2.64	0.45
1:K:25:GLY:N	1:K:28:GLU:OE1	2.43	0.45
1:O:148:GLY:HA3	4:O:518:HOH:O	2.16	0.45
1:K:144:THR:HG22	1:K:326:LYS:HG2	1.98	0.45
1:N:64:ALA:HB2	1:N:84:VAL:HG23	1.99	0.45
1:I:303:HIS:CE1	1:I:323:ARG:HA	2.52	0.45
1:O:30:LEU:HD11	1:O:124:TYR:HB3	1.98	0.45
1:D:55:MET:HA	1:D:56:PRO:C	2.37	0.45
1:B:303:HIS:CD2	1:B:304:ASN:HB2	2.52	0.45
1:D:186:LEU:HD23	1:L:163:PRO:HB3	1.98	0.45
1:E:266:ARG:NH2	4:E:584:HOH:O	2.48	0.45
1:P:112:ILE:HB	1:P:115:ILE:HD12	1.99	0.45
1:E:272:GLN:NE2	1:K:154:ASN:HD21	2.15	0.44
1:N:223:ALA:HB1	1:N:224:PRO:HA	1.98	0.44
1:A:303:HIS:CD2	1:A:304:ASN:HB2	2.52	0.44
1:K:62:GLU:HG3	1:K:146:PRO:HB2	2.00	0.44
1:O:198:LYS:HG3	1:O:213:VAL:HG12	1.99	0.44
1:G:187:LEU:HD23	1:P:163:PRO:HG3	2.00	0.44
1:B:45:VAL:HG21	1:B:115:ILE:HG12	1.99	0.44
1:O:159:ALA:HB2	1:O:251:VAL:HG21	1.99	0.44
1:P:151:THR:CG2	2:P:401:NDP:H41N	2.47	0.44
1:L:144:THR:HG22	1:L:326:LYS:HG2	2.00	0.43
1:P:309:ALA:O	4:P:538:HOH:O	2.21	0.43
1:K:201:VAL:HG12	1:K:324:VAL:HG21	1.99	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:151:THR:OG1	2:B:401:NDP:H41N	2.18	0.43
1:B:159:ALA:O	1:B:249:ARG:HD2	2.18	0.43
1:L:55:MET:HA	1:L:56:PRO:C	2.39	0.43
1:M:223:ALA:HB1	1:M:224:PRO:HA	2.00	0.43
1:I:55:MET:HA	1:I:56:PRO:C	2.37	0.43
1:G:253:ALA:HA	1:G:278:ALA:O	2.19	0.43
1:A:272:GLN:NE2	1:F:154:ASN:HD21	2.16	0.43
1:O:311:VAL:CG1	1:O:312:ARG:N	2.82	0.43
1:O:7:SER:HB3	1:O:56:PRO:HG3	2.00	0.43
1:F:153:TRP:CD1	1:F:153:TRP:C	2.92	0.43
2:B:401:NDP:H8A	2:B:401:NDP:C3B	2.49	0.42
1:C:2:ARG:NH2	1:C:331:PRO:O	2.52	0.42
1:P:159:ALA:O	1:P:249:ARG:HD2	2.19	0.42
1:P:168:ALA:HA	1:P:192:TYR:O	2.19	0.42
1:J:189:GLY:O	1:O:297:ARG:NH2	2.52	0.42
1:N:314:ALA:CB	1:N:329:ILE:HD11	2.50	0.42
1:G:187:LEU:HD21	1:P:163:PRO:HG2	1.99	0.42
1:J:145:LEU:HA	1:J:149:ALA:HB3	2.01	0.42
1:B:31:ILE:O	1:B:124:TYR:HA	2.20	0.42
1:F:197:ARG:O	1:F:201:VAL:HG22	2.20	0.42
1:K:61:SER:N	4:K:548:HOH:O	2.49	0.42
1:E:159:ALA:O	1:E:249:ARG:HD2	2.20	0.42
1:H:154:ASN:HD21	1:P:272:GLN:NE2	2.17	0.42
1:N:55:MET:HA	1:N:56:PRO:C	2.39	0.42
1:G:153:TRP:C	1:G:153:TRP:CD1	2.93	0.42
1:B:110:GLY:HA2	4:B:525:HOH:O	2.20	0.42
1:P:45:VAL:HG13	1:P:52:ALA:HB2	2.01	0.42
1:I:144:THR:HG22	1:I:326:LYS:HG2	2.00	0.42
1:L:147:ILE:HG22	2:L:401:NDP:H5N	2.01	0.42
1:O:41:LEU:HD21	1:O:115:ILE:HD11	2.01	0.42
1:O:144:THR:HG22	1:O:326:LYS:HG2	2.01	0.42
1:M:103:GLN:HG3	1:M:279:THR:O	2.19	0.42
1:G:262:ARG:HD2	1:N:260:GLU:OE1	2.20	0.42
1:H:35:TYR:CZ	1:H:140:LYS:HG3	2.55	0.42
1:A:55:MET:HA	1:A:56:PRO:C	2.40	0.42
1:H:260:GLU:OE1	1:P:262:ARG:HD2	2.19	0.41
1:F:2:ARG:NH2	1:F:331:PRO:O	2.53	0.41
1:G:62:GLU:OE1	1:G:326:LYS:NZ	2.40	0.41
1:F:151:THR:OG1	2:F:401:NDP:H41N	2.20	0.41
1:B:153:TRP:C	1:B:153:TRP:CD1	2.91	0.41
1:B:83:VAL:HA	1:B:133:VAL:O	2.20	0.41
1:P:151:THR:CB	2:P:401:NDP:H41N	2.49	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:J:7:SER:HA	1:J:56:PRO:HB3	2.02	0.41
1:O:38:VAL:HG21	1:O:327:VAL:HG12	2.03	0.41
1:C:197:ARG:O	1:C:201:VAL:HG22	2.20	0.41
1:N:151:THR:OG1	2:N:401:NDP:H41N	2.20	0.41
1:M:41:LEU:HD21	1:M:115:ILE:HD11	2.02	0.41
1:O:266:ARG:HA	1:O:269:TYR:CE2	2.56	0.41
1:K:41:LEU:HD21	1:K:115:ILE:HD11	2.02	0.41
1:C:151:THR:OG1	2:C:401:NDP:H41N	2.20	0.41
1:I:253:ALA:HA	1:I:278:ALA:O	2.21	0.41
1:N:153:TRP:CD1	1:N:153:TRP:C	2.94	0.41
1:C:55:MET:HA	1:C:56:PRO:C	2.41	0.41
1:O:44:ASN:HB3	1:O:49:ALA:HB3	2.02	0.41
1:J:193:ALA:HB1	1:J:205:LEU:HD13	2.03	0.41
1:H:314:ALA:CB	1:H:329:ILE:HD11	2.51	0.41
1:F:309:ALA:N	4:F:532:HOH:O	2.38	0.41
1:M:140:LYS:HG2	1:M:328:LEU:CD1	2.51	0.41
1:N:70:ALA:HB1	1:N:74:VAL:HB	2.03	0.41
1:D:34:LYS:NZ	4:D:566:HOH:O	2.53	0.41
1:G:154:ASN:HD21	1:N:272:GLN:HE22	1.68	0.41
1:H:279:THR:H	1:P:272:GLN:HE21	1.68	0.41
1:K:314:ALA:HB3	1:K:329:ILE:HD11	2.02	0.41
1:B:145:LEU:N	1:B:146:PRO:CD	2.83	0.41
1:K:244:LEU:HD11	1:K:250:TYR:HB2	2.02	0.41
1:F:55:MET:HA	1:F:56:PRO:C	2.41	0.41
1:M:153:TRP:C	1:M:153:TRP:CD1	2.94	0.41
1:D:45:VAL:HG21	1:D:115:ILE:HG12	2.03	0.41
1:B:35:TYR:CZ	1:B:140:LYS:HG3	2.56	0.41
1:L:41:LEU:O	1:L:45:VAL:HG23	2.21	0.41
1:H:8:THR:HG23	1:H:13:ASN:ND2	2.36	0.41
1:O:159:ALA:O	1:O:249:ARG:HD2	2.21	0.41
1:C:201:VAL:HG12	1:C:324:VAL:HG21	2.03	0.41
1:G:41:LEU:HD21	1:G:115:ILE:HD11	2.02	0.41
1:C:151:THR:O	1:C:155:MET:HG3	2.22	0.40
1:B:55:MET:HA	1:B:56:PRO:C	2.40	0.40
1:A:145:LEU:HA	1:A:149:ALA:HB3	2.02	0.40
1:K:145:LEU:N	1:K:146:PRO:CD	2.85	0.40
1:K:196:ARG:HB2	1:K:196:ARG:HE	1.77	0.40
1:O:103:GLN:HG3	1:O:279:THR:O	2.20	0.40
1:P:172:ALA:HA	1:P:177:GLY:HA3	2.03	0.40
1:P:185:LYS:NZ	1:P:209:GLY:O	2.44	0.40
1:F:297:ARG:NE	4:F:565:HOH:O	2.45	0.40
1:J:96:GLN:NE2	4:J:548:HOH:O	2.40	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:153:TRP:CD1	1:D:153:TRP:C	2.95	0.40
1:J:112:ILE:HB	1:J:115:ILE:HD12	2.03	0.40
1:O:68:GLU:HG2	1:O:124:TYR:HE2	1.87	0.40
1:P:145:LEU:HA	1:P:149:ALA:HB3	2.04	0.40
1:J:11:LEU:HD12	1:J:46:VAL:HG11	2.04	0.40
1:M:303:HIS:CE1	1:M:323:ARG:HA	2.57	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 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	332/370 (90%)	327 (98%)	5 (2%)	0	100	100
1	B	332/370 (90%)	328 (99%)	3 (1%)	1 (0%)	50	62
1	C	332/370 (90%)	327 (98%)	4 (1%)	1 (0%)	50	62
1	D	332/370 (90%)	324 (98%)	8 (2%)	0	100	100
1	E	332/370 (90%)	325 (98%)	7 (2%)	0	100	100
1	F	332/370 (90%)	325 (98%)	5 (2%)	2 (1%)	33	39
1	G	332/370 (90%)	327 (98%)	5 (2%)	0	100	100
1	H	332/370 (90%)	323 (97%)	9 (3%)	0	100	100
1	I	332/370 (90%)	324 (98%)	7 (2%)	1 (0%)	50	62
1	J	331/370 (90%)	324 (98%)	7 (2%)	0	100	100
1	K	332/370 (90%)	323 (97%)	9 (3%)	0	100	100
1	L	332/370 (90%)	320 (96%)	10 (3%)	2 (1%)	33	39
1	M	332/370 (90%)	319 (96%)	13 (4%)	0	100	100
1	N	332/370 (90%)	323 (97%)	9 (3%)	0	100	100
1	O	332/370 (90%)	315 (95%)	15 (4%)	2 (1%)	33	39
1	P	331/370 (90%)	321 (97%)	9 (3%)	1 (0%)	50	62
All	All	5310/5920 (90%)	5175 (98%)	125 (2%)	10 (0%)	56	70

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	111	GLY
1	I	111	GLY
1	B	111	GLY
1	C	77	VAL
1	L	111	GLY
1	O	77	VAL
1	O	321	PRO
1	P	324	VAL
1	F	77	VAL
1	L	77	VAL

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	244/274 (89%)	241 (99%)	3 (1%)	82	92
1	B	242/274 (88%)	237 (98%)	5 (2%)	66	82
1	C	246/274 (90%)	243 (99%)	3 (1%)	82	92
1	D	240/274 (88%)	236 (98%)	4 (2%)	73	86
1	E	244/274 (89%)	243 (100%)	1 (0%)	95	98
1	F	245/274 (89%)	242 (99%)	3 (1%)	82	92
1	G	243/274 (89%)	238 (98%)	5 (2%)	66	82
1	H	241/274 (88%)	239 (99%)	2 (1%)	89	95
1	I	241/274 (88%)	238 (99%)	3 (1%)	82	92
1	J	241/274 (88%)	236 (98%)	5 (2%)	66	82
1	K	239/274 (87%)	235 (98%)	4 (2%)	73	86
1	L	242/274 (88%)	236 (98%)	6 (2%)	60	76
1	M	241/274 (88%)	240 (100%)	1 (0%)	95	98
1	N	241/274 (88%)	235 (98%)	6 (2%)	60	76
1	O	237/274 (86%)	232 (98%)	5 (2%)	66	82
1	P	238/274 (87%)	231 (97%)	7 (3%)	55	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	3865/4384 (88%)	3802 (98%)	63 (2%)	75	87

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	77	VAL
1	A	78	SER
1	A	178	ILE
1	B	69	GLU
1	B	77	VAL
1	B	95	ARG
1	B	160	SER
1	B	269	TYR
1	C	8	THR
1	C	162	SER
1	C	217	ASP
1	D	95	ARG
1	D	162	SER
1	D	266	ARG
1	D	320	SER
1	E	8	THR
1	F	8	THR
1	F	200	LYS
1	F	304	ASN
1	G	53	SER
1	G	78	SER
1	G	95	ARG
1	G	269	TYR
1	G	310	ASP
1	H	53	SER
1	H	162	SER
1	I	140	LYS
1	I	162	SER
1	I	203	SER
1	J	53	SER
1	J	78	SER
1	J	95	ARG
1	J	221	SER
1	J	320	SER
1	K	7	SER
1	K	16	LEU
1	K	53	SER

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Mol	Chain	Res	Type
1	K	269	TYR
1	L	12	GLU
1	L	53	SER
1	L	162	SER
1	L	178	ILE
1	L	203	SER
1	L	269	TYR
1	M	217	ASP
1	N	8	THR
1	N	221	SER
1	N	252	THR
1	N	269	TYR
1	N	304	ASN
1	N	329	ILE
1	O	8	THR
1	O	77	VAL
1	O	162	SER
1	O	260	GLU
1	O	311	VAL
1	P	7	SER
1	P	8	THR
1	P	75	THR
1	P	95	ARG
1	P	195	SER
1	P	320	SER
1	P	329	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	ASN
1	A	272	GLN
1	B	96	GLN
1	B	131	ASN
1	B	272	GLN
1	C	131	ASN
1	C	272	GLN
1	D	131	ASN
1	D	272	GLN
1	E	96	GLN
1	E	131	ASN
1	E	272	GLN

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Mol	Chain	Res	Type
1	E	303	HIS
1	F	131	ASN
1	F	272	GLN
1	G	96	GLN
1	G	131	ASN
1	G	272	GLN
1	H	131	ASN
1	H	272	GLN
1	I	131	ASN
1	I	272	GLN
1	I	303	HIS
1	J	96	GLN
1	J	131	ASN
1	J	272	GLN
1	K	96	GLN
1	K	131	ASN
1	K	272	GLN
1	K	303	HIS
1	L	96	GLN
1	L	131	ASN
1	L	272	GLN
1	L	303	HIS
1	M	96	GLN
1	M	131	ASN
1	M	272	GLN
1	M	303	HIS
1	N	96	GLN
1	N	131	ASN
1	N	272	GLN
1	O	13	ASN
1	O	96	GLN
1	O	131	ASN
1	O	272	GLN
1	P	131	ASN
1	P	272	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

Of 32 ligands modelled in this entry, 16 are monoatomic - leaving 16 for Mogul analysis.

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	NDP	A	401	-	52,52,52	1.49	6 (11%)	80,80,80	1.63	10 (12%)
2	NDP	B	401	-	52,52,52	1.42	5 (9%)	80,80,80	1.57	6 (7%)
2	NDP	C	401	-	52,52,52	1.36	6 (11%)	80,80,80	1.88	11 (13%)
2	NDP	D	401	-	52,52,52	1.55	9 (17%)	80,80,80	1.81	9 (11%)
2	NDP	E	401	-	52,52,52	1.55	6 (11%)	80,80,80	1.70	5 (6%)
2	NDP	F	401	-	52,52,52	1.49	6 (11%)	80,80,80	1.71	8 (10%)
2	NDP	G	401	-	52,52,52	1.52	5 (9%)	80,80,80	1.71	6 (7%)
2	NDP	H	401	-	52,52,52	1.55	6 (11%)	80,80,80	1.90	10 (12%)
2	NDP	I	401	-	52,52,52	1.51	6 (11%)	80,80,80	1.68	13 (16%)
2	NDP	J	401	-	52,52,52	1.53	5 (9%)	80,80,80	1.50	6 (7%)
2	NDP	K	401	-	52,52,52	1.55	6 (11%)	80,80,80	1.61	8 (10%)
2	NDP	L	401	-	52,52,52	1.45	6 (11%)	80,80,80	1.65	6 (7%)
2	NDP	M	401	-	52,52,52	1.56	5 (9%)	80,80,80	1.79	9 (11%)
2	NDP	N	401	-	52,52,52	1.46	6 (11%)	80,80,80	1.87	11 (13%)
2	NDP	O	401	-	52,52,52	1.52	6 (11%)	80,80,80	1.81	10 (12%)
2	NDP	P	401	-	52,52,52	1.51	7 (13%)	80,80,80	1.74	13 (16%)

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	NDP	A	401	-	-	0/35/77/77	0/3/5/5
2	NDP	B	401	-	-	0/35/77/77	0/3/5/5
2	NDP	C	401	-	-	0/35/77/77	0/3/5/5
2	NDP	D	401	-	-	0/35/77/77	0/3/5/5
2	NDP	E	401	-	-	0/35/77/77	0/3/5/5
2	NDP	F	401	-	-	0/35/77/77	0/3/5/5
2	NDP	G	401	-	-	0/35/77/77	0/3/5/5
2	NDP	H	401	-	-	0/35/77/77	0/3/5/5
2	NDP	I	401	-	-	0/35/77/77	0/3/5/5
2	NDP	J	401	-	-	0/35/77/77	0/3/5/5
2	NDP	K	401	-	-	0/35/77/77	0/3/5/5
2	NDP	L	401	-	-	0/35/77/77	0/3/5/5
2	NDP	M	401	-	-	0/35/77/77	0/3/5/5
2	NDP	N	401	-	-	0/35/77/77	0/3/5/5
2	NDP	O	401	-	-	0/35/77/77	0/3/5/5
2	NDP	P	401	-	-	0/35/77/77	0/3/5/5

All (96) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	401	NDP	O7N-C7N	7.46	1.44	1.24
2	H	401	NDP	O7N-C7N	7.20	1.43	1.24
2	O	401	NDP	O7N-C7N	6.90	1.42	1.24
2	K	401	NDP	O7N-C7N	6.78	1.42	1.24
2	G	401	NDP	O7N-C7N	6.78	1.42	1.24
2	D	401	NDP	O7N-C7N	6.74	1.42	1.24
2	J	401	NDP	O7N-C7N	6.56	1.41	1.24
2	F	401	NDP	O7N-C7N	6.52	1.41	1.24
2	B	401	NDP	O7N-C7N	6.45	1.41	1.24
2	I	401	NDP	O7N-C7N	6.45	1.41	1.24
2	E	401	NDP	O7N-C7N	6.34	1.41	1.24
2	N	401	NDP	O7N-C7N	6.33	1.41	1.24
2	L	401	NDP	O7N-C7N	6.19	1.40	1.24
2	A	401	NDP	O7N-C7N	5.95	1.40	1.24
2	P	401	NDP	O7N-C7N	5.92	1.40	1.24
2	C	401	NDP	O7N-C7N	5.12	1.37	1.24
2	I	401	NDP	C2A-N3A	4.74	1.41	1.32
2	P	401	NDP	C2A-N3A	4.42	1.40	1.32
2	C	401	NDP	C2A-N3A	4.07	1.40	1.32
2	J	401	NDP	C2A-N3A	3.86	1.39	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	NDP	C2A-N3A	3.86	1.39	1.32
2	G	401	NDP	C2A-N3A	3.83	1.39	1.32
2	J	401	NDP	C2A-N1A	3.79	1.41	1.33
2	B	401	NDP	C2A-N3A	3.79	1.39	1.32
2	O	401	NDP	C2A-N3A	3.75	1.39	1.32
2	E	401	NDP	C6N-C5N	3.73	1.41	1.33
2	M	401	NDP	C2A-N3A	3.67	1.39	1.32
2	N	401	NDP	C2A-N3A	3.57	1.39	1.32
2	P	401	NDP	C6N-C5N	3.51	1.40	1.33
2	L	401	NDP	C2A-N3A	3.49	1.39	1.32
2	D	401	NDP	C2A-N3A	3.46	1.39	1.32
2	F	401	NDP	C2A-N1A	3.39	1.40	1.33
2	K	401	NDP	C2A-N3A	3.38	1.38	1.32
2	E	401	NDP	C2A-N3A	3.34	1.38	1.32
2	H	401	NDP	C2A-N3A	3.31	1.38	1.32
2	L	401	NDP	C6N-C5N	3.31	1.40	1.33
2	G	401	NDP	C2A-N1A	3.30	1.40	1.33
2	I	401	NDP	C2A-N1A	3.28	1.40	1.33
2	P	401	NDP	C2A-N1A	3.27	1.40	1.33
2	G	401	NDP	C6N-C5N	3.25	1.40	1.33
2	H	401	NDP	C2A-N1A	3.25	1.40	1.33
2	B	401	NDP	C2A-N1A	3.25	1.40	1.33
2	K	401	NDP	C2N-C3N	3.22	1.41	1.34
2	H	401	NDP	C2N-C3N	3.21	1.41	1.34
2	K	401	NDP	C2A-N1A	3.21	1.40	1.33
2	A	401	NDP	C2A-N1A	3.20	1.40	1.33
2	N	401	NDP	C2A-N1A	3.19	1.40	1.33
2	O	401	NDP	C6N-C5N	3.15	1.40	1.33
2	D	401	NDP	C2A-N1A	3.08	1.40	1.33
2	E	401	NDP	C2N-C3N	3.04	1.40	1.34
2	H	401	NDP	C6N-C5N	2.98	1.39	1.33
2	L	401	NDP	C2A-N1A	2.97	1.39	1.33
2	F	401	NDP	C2A-N3A	2.94	1.38	1.32
2	O	401	NDP	C2A-N1A	2.92	1.39	1.33
2	M	401	NDP	C6N-C5N	2.88	1.39	1.33
2	A	401	NDP	C2N-C3N	2.84	1.40	1.34
2	M	401	NDP	C2A-N1A	2.83	1.39	1.33
2	E	401	NDP	C2A-N1A	2.82	1.39	1.33
2	C	401	NDP	C2A-N1A	2.78	1.39	1.33
2	J	401	NDP	C6N-C5N	2.78	1.39	1.33
2	A	401	NDP	PA-O3	2.74	1.64	1.59
2	F	401	NDP	C8A-N9A	2.72	1.40	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	401	NDP	C2N-C3N	2.72	1.40	1.34
2	K	401	NDP	C6N-C5N	2.69	1.38	1.33
2	D	401	NDP	C6N-C5N	2.65	1.38	1.33
2	F	401	NDP	C6N-C5N	2.62	1.38	1.33
2	F	401	NDP	C2N-C3N	2.58	1.39	1.34
2	N	401	NDP	C6N-C5N	2.55	1.38	1.33
2	I	401	NDP	C6N-C5N	2.55	1.38	1.33
2	B	401	NDP	C6N-C5N	2.54	1.38	1.33
2	O	401	NDP	C2N-C3N	2.53	1.39	1.34
2	L	401	NDP	C2N-C3N	2.47	1.39	1.34
2	D	401	NDP	PA-O3	2.44	1.64	1.59
2	N	401	NDP	O4B-C4B	-2.40	1.39	1.45
2	P	401	NDP	C8A-N9A	2.38	1.40	1.36
2	A	401	NDP	C6N-C5N	2.37	1.38	1.33
2	N	401	NDP	C2N-C3N	2.35	1.39	1.34
2	C	401	NDP	C6N-C5N	2.35	1.38	1.33
2	I	401	NDP	C2N-C3N	2.34	1.39	1.34
2	D	401	NDP	C2N-C3N	2.33	1.39	1.34
2	J	401	NDP	C2N-C3N	2.32	1.39	1.34
2	M	401	NDP	C8A-N9A	2.28	1.40	1.36
2	D	401	NDP	PN-O2N	-2.22	1.45	1.55
2	I	401	NDP	PN-O3	2.21	1.63	1.59
2	C	401	NDP	PA-O3	2.17	1.63	1.59
2	B	401	NDP	C8A-N9A	2.16	1.39	1.36
2	L	401	NDP	C8A-N9A	2.16	1.39	1.36
2	E	401	NDP	C8A-N9A	2.15	1.39	1.36
2	O	401	NDP	O4B-C4B	-2.12	1.40	1.45
2	K	401	NDP	C4A-N9A	-2.11	1.34	1.37
2	P	401	NDP	C2N-C3N	2.09	1.38	1.34
2	C	401	NDP	C2N-C3N	2.04	1.38	1.34
2	D	401	NDP	PA-O2A	-2.03	1.46	1.55
2	H	401	NDP	PN-O3	2.02	1.63	1.59
2	D	401	NDP	C1D-N1N	2.01	1.50	1.46
2	P	401	NDP	C8A-N7A	2.00	1.38	1.34

All (141) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	401	NDP	N3A-C2A-N1A	-12.86	117.96	128.71
2	C	401	NDP	N3A-C2A-N1A	-12.59	118.18	128.71
2	O	401	NDP	N3A-C2A-N1A	-12.30	118.43	128.71
2	D	401	NDP	N3A-C2A-N1A	-12.24	118.47	128.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	401	NDP	N3A-C2A-N1A	-11.82	118.83	128.71
2	M	401	NDP	N3A-C2A-N1A	-11.43	119.15	128.71
2	F	401	NDP	N3A-C2A-N1A	-11.41	119.17	128.71
2	L	401	NDP	N3A-C2A-N1A	-11.38	119.19	128.71
2	N	401	NDP	N3A-C2A-N1A	-11.23	119.32	128.71
2	G	401	NDP	N3A-C2A-N1A	-11.16	119.38	128.71
2	A	401	NDP	N3A-C2A-N1A	-10.57	119.87	128.71
2	P	401	NDP	N3A-C2A-N1A	-10.29	120.11	128.71
2	B	401	NDP	N3A-C2A-N1A	-9.86	120.46	128.71
2	K	401	NDP	N3A-C2A-N1A	-9.75	120.56	128.71
2	I	401	NDP	N3A-C2A-N1A	-9.56	120.72	128.71
2	J	401	NDP	N3A-C2A-N1A	-9.31	120.92	128.71
2	P	401	NDP	O4B-C1B-N9A	5.45	113.51	108.44
2	N	401	NDP	O4B-C1B-N9A	4.25	112.39	108.44
2	B	401	NDP	N3A-C4A-N9A	4.12	132.87	125.43
2	I	401	NDP	N3A-C4A-N9A	3.85	132.39	125.43
2	N	401	NDP	C8A-N9A-C4A	3.75	109.77	106.90
2	C	401	NDP	N3A-C4A-N9A	3.71	132.13	125.43
2	L	401	NDP	N3A-C4A-N9A	3.65	132.02	125.43
2	I	401	NDP	O4B-C1B-N9A	3.62	111.81	108.44
2	A	401	NDP	N3A-C4A-N9A	3.58	131.89	125.43
2	O	401	NDP	N3A-C4A-N9A	3.41	131.59	125.43
2	M	401	NDP	N3A-C4A-N9A	3.35	131.48	125.43
2	O	401	NDP	PN-O3-PA	-3.34	121.88	131.68
2	M	401	NDP	PN-O3-PA	-3.34	121.89	131.68
2	D	401	NDP	PN-O3-PA	-3.33	121.91	131.68
2	N	401	NDP	N3A-C4A-N9A	3.33	131.45	125.43
2	G	401	NDP	N3A-C4A-N9A	3.33	131.44	125.43
2	G	401	NDP	O4B-C1B-N9A	3.30	111.51	108.44
2	D	401	NDP	C8A-N9A-C4A	3.28	109.40	106.90
2	K	401	NDP	N3A-C4A-N9A	3.24	131.29	125.43
2	H	401	NDP	C1B-N9A-C4A	-3.22	121.07	126.64
2	N	401	NDP	C1B-N9A-C4A	-3.22	121.08	126.64
2	H	401	NDP	O4D-C1D-N1N	3.21	114.86	108.05
2	P	401	NDP	N3A-C4A-N9A	3.17	131.16	125.43
2	L	401	NDP	PN-O3-PA	-3.17	122.38	131.68
2	I	401	NDP	O4D-C1D-N1N	3.16	114.73	108.05
2	D	401	NDP	O4B-C1B-C2B	3.15	109.89	106.95
2	A	401	NDP	C3N-C2N-N1N	-3.09	118.67	123.05
2	J	401	NDP	PN-O3-PA	-3.06	122.71	131.68
2	E	401	NDP	N3A-C4A-N9A	3.06	130.95	125.43
2	F	401	NDP	N3A-C4A-N9A	3.03	130.90	125.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	401	NDP	C1D-N1N-C2N	-3.00	115.91	121.02
2	C	401	NDP	C8A-N9A-C4A	2.99	109.18	106.90
2	D	401	NDP	N3A-C4A-N9A	2.99	130.82	125.43
2	H	401	NDP	PN-O3-PA	-2.94	123.06	131.68
2	K	401	NDP	P2B-O2B-C2B	-2.91	115.83	121.96
2	I	401	NDP	C6N-N1N-C2N	2.88	123.20	119.44
2	A	401	NDP	C4B-O4B-C1B	2.88	112.87	109.75
2	J	401	NDP	N3A-C4A-N9A	2.86	130.60	125.43
2	H	401	NDP	C8A-N9A-C4A	2.83	109.06	106.90
2	B	401	NDP	C2B-C1B-N9A	-2.82	103.04	113.74
2	F	401	NDP	C8A-N9A-C4A	2.79	109.03	106.90
2	J	401	NDP	P2B-O2B-C2B	-2.77	116.12	121.96
2	N	401	NDP	C6N-N1N-C2N	2.75	123.04	119.44
2	F	401	NDP	PN-O3-PA	-2.74	123.66	131.68
2	B	401	NDP	PN-O3-PA	-2.74	123.66	131.68
2	M	401	NDP	O4B-C1B-N9A	2.73	110.98	108.44
2	G	401	NDP	PN-O3-PA	-2.73	123.69	131.68
2	H	401	NDP	N3A-C4A-N9A	2.71	130.32	125.43
2	K	401	NDP	PN-O3-PA	-2.70	123.77	131.68
2	E	401	NDP	C8A-N9A-C4A	2.69	108.95	106.90
2	F	401	NDP	N7A-C8A-N9A	-2.69	106.75	114.36
2	E	401	NDP	PN-O3-PA	-2.69	123.80	131.68
2	C	401	NDP	C6N-N1N-C2N	2.67	122.94	119.44
2	A	401	NDP	C6N-N1N-C2N	2.67	122.93	119.44
2	M	401	NDP	P2B-O2B-C2B	-2.65	116.37	121.96
2	N	401	NDP	C1D-N1N-C6N	-2.62	114.98	120.79
2	I	401	NDP	C3N-C2N-N1N	-2.60	119.36	123.05
2	K	401	NDP	N6A-C6A-N1A	2.58	124.42	119.36
2	E	401	NDP	O4B-C1B-C2B	2.57	109.35	106.95
2	A	401	NDP	PN-O3-PA	-2.56	124.19	131.68
2	C	401	NDP	O4B-C1B-C2B	2.55	109.33	106.95
2	G	401	NDP	C8A-N9A-C4A	2.55	108.84	106.90
2	P	401	NDP	C1B-N9A-C4A	-2.54	122.25	126.64
2	P	401	NDP	C4B-O4B-C1B	2.50	112.46	109.75
2	K	401	NDP	C4B-O4B-C1B	2.47	112.43	109.75
2	L	401	NDP	O7N-C7N-C3N	-2.46	115.90	120.51
2	I	401	NDP	C8A-N9A-C4A	2.45	108.77	106.90
2	N	401	NDP	N7A-C8A-N9A	-2.42	107.50	114.36
2	F	401	NDP	O4B-C1B-C2B	2.41	109.20	106.95
2	F	401	NDP	C1B-N9A-C4A	-2.37	122.54	126.64
2	G	401	NDP	C2B-C1B-N9A	-2.36	104.79	113.74
2	D	401	NDP	N7A-C8A-N9A	-2.36	107.70	114.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	401	NDP	C6N-N1N-C2N	2.35	122.51	119.44
2	K	401	NDP	C6N-N1N-C2N	2.35	122.51	119.44
2	O	401	NDP	O4B-C1B-N9A	2.33	110.61	108.44
2	M	401	NDP	C2A-N3A-C4A	2.33	120.64	114.01
2	H	401	NDP	C2A-N3A-C4A	2.32	120.60	114.01
2	I	401	NDP	O4B-C1B-C2B	2.31	109.11	106.95
2	N	401	NDP	O4B-C1B-C2B	2.31	109.11	106.95
2	B	401	NDP	O4B-C1B-C2B	2.31	109.10	106.95
2	H	401	NDP	O2X-P2B-O2B	2.30	113.72	107.09
2	P	401	NDP	O2B-P2B-O1X	2.30	113.23	106.79
2	O	401	NDP	C8A-N9A-C4A	2.30	108.65	106.90
2	H	401	NDP	N7A-C8A-N9A	-2.29	107.87	114.36
2	D	401	NDP	C1B-N9A-C4A	-2.29	122.68	126.64
2	D	401	NDP	O3D-C3D-C2D	-2.29	104.40	111.83
2	K	401	NDP	C2B-C1B-N9A	-2.28	105.08	113.74
2	I	401	NDP	N6A-C6A-N1A	2.27	123.82	119.36
2	O	401	NDP	C2A-N3A-C4A	2.26	120.44	114.01
2	D	401	NDP	O4B-C1B-N9A	2.25	110.53	108.44
2	J	401	NDP	C2B-C1B-N9A	-2.24	105.23	113.74
2	I	401	NDP	PN-O3-PA	-2.24	125.12	131.68
2	A	401	NDP	O4B-C1B-N9A	2.21	110.50	108.44
2	P	401	NDP	C2A-N3A-C4A	2.21	120.30	114.01
2	C	401	NDP	O7N-C7N-N7N	-2.21	117.36	122.93
2	O	401	NDP	O4B-C1B-C2B	2.20	109.01	106.95
2	C	401	NDP	PN-O3-PA	-2.19	125.25	131.68
2	O	401	NDP	N7A-C8A-N9A	-2.18	108.19	114.36
2	C	401	NDP	N7A-C8A-N9A	-2.17	108.21	114.36
2	F	401	NDP	C6N-N1N-C2N	2.17	122.29	119.44
2	C	401	NDP	C1D-N1N-C2N	-2.16	117.34	121.02
2	P	401	NDP	PN-O3-PA	-2.15	125.39	131.68
2	P	401	NDP	O3-PN-O5D	-2.14	93.83	103.41
2	C	401	NDP	O3X-P2B-O2X	2.14	115.94	107.61
2	M	401	NDP	C3N-C2N-N1N	-2.14	120.02	123.05
2	I	401	NDP	C5A-C6A-N6A	-2.13	115.91	120.72
2	J	401	NDP	C8A-N9A-C4A	2.11	108.51	106.90
2	H	401	NDP	O2X-P2B-O1X	-2.11	103.54	110.44
2	L	401	NDP	C2A-N3A-C4A	2.11	120.01	114.01
2	O	401	NDP	O2B-P2B-O1X	2.10	112.67	106.79
2	B	401	NDP	N6A-C6A-N1A	2.10	123.49	119.36
2	I	401	NDP	N7A-C8A-N9A	-2.09	108.44	114.36
2	A	401	NDP	C2A-N3A-C4A	2.08	119.94	114.01
2	N	401	NDP	O2B-P2B-O1X	2.08	112.60	106.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	401	NDP	N7A-C8A-N9A	-2.08	108.48	114.36
2	I	401	NDP	C2B-C1B-N9A	-2.06	105.91	113.74
2	O	401	NDP	P2B-O2B-C2B	2.06	126.30	121.96
2	A	401	NDP	C5A-C4A-N3A	-2.05	121.23	125.70
2	M	401	NDP	C1B-N9A-C4A	-2.04	123.12	126.64
2	L	401	NDP	O4B-C1B-N9A	-2.04	106.55	108.44
2	P	401	NDP	C4A-C5A-N7A	-2.03	107.78	109.52
2	C	401	NDP	N6A-C6A-N1A	2.03	123.35	119.36
2	P	401	NDP	C5A-C4A-N3A	-2.02	121.29	125.70
2	A	401	NDP	N7A-C8A-N9A	-2.03	108.63	114.36
2	N	401	NDP	C4B-O4B-C1B	2.00	111.92	109.75

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	333/370 (90%)	-0.54	0 100 100	25, 35, 57, 68	0
1	B	333/370 (90%)	-0.58	0 100 100	27, 37, 56, 71	0
1	C	333/370 (90%)	-0.58	1 (0%) 91 94	27, 36, 53, 66	0
1	D	333/370 (90%)	-0.55	0 100 100	27, 37, 58, 70	0
1	E	333/370 (90%)	-0.54	0 100 100	27, 38, 57, 73	0
1	F	333/370 (90%)	-0.58	0 100 100	25, 36, 55, 72	0
1	G	333/370 (90%)	-0.52	0 100 100	30, 40, 57, 71	0
1	H	333/370 (90%)	-0.61	0 100 100	27, 38, 55, 71	0
1	I	333/370 (90%)	-0.56	0 100 100	28, 39, 57, 69	0
1	J	333/370 (90%)	-0.55	0 100 100	31, 41, 57, 68	0
1	K	333/370 (90%)	-0.49	0 100 100	28, 44, 64, 71	0
1	L	333/370 (90%)	-0.38	2 (0%) 86 89	29, 45, 68, 76	0
1	M	333/370 (90%)	-0.42	0 100 100	34, 48, 64, 71	0
1	N	333/370 (90%)	-0.51	0 100 100	31, 45, 63, 73	0
1	O	333/370 (90%)	-0.29	2 (0%) 86 89	28, 51, 68, 75	0
1	P	333/370 (90%)	-0.32	1 (0%) 91 94	30, 50, 68, 75	0
All	All	5328/5920 (90%)	-0.50	6 (0%) 93 96	25, 41, 63, 76	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	P	304	ASN	3.0
1	L	11	LEU	2.3
1	O	309	ALA	2.3
1	O	310	ASP	2.2
1	C	77	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	L	16	LEU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	NDP	E	401	48/48	0.11	1.29	25,35,55,61	0
2	NDP	C	401	48/48	0.11	0.92	21,30,40,49	0
3	ZN	F	402	1/1	0.11	0.57	34,34,34,34	0
3	ZN	L	402	1/1	0.12	0.57	39,39,39,39	0
2	NDP	B	401	48/48	0.10	0.51	23,35,50,58	0
2	NDP	J	401	48/48	0.10	0.51	30,41,51,63	0
3	ZN	E	402	1/1	0.12	0.51	29,29,29,29	0
3	ZN	H	402	1/1	0.11	0.43	34,34,34,34	0
3	ZN	B	402	1/1	0.12	0.38	30,30,30,30	0
2	NDP	F	401	48/48	0.10	0.33	23,31,36,40	0
3	ZN	O	402	1/1	0.10	0.32	49,49,49,49	0
2	NDP	H	401	48/48	0.10	0.30	24,34,50,58	0
3	ZN	I	402	1/1	0.11	0.29	32,32,32,32	0
3	ZN	D	402	1/1	0.11	0.28	31,31,31,31	0
3	ZN	J	402	1/1	0.11	0.26	33,33,33,33	0
2	NDP	N	401	48/48	0.10	0.25	21,39,56,62	0
3	ZN	A	402	1/1	0.11	0.23	30,30,30,30	0
2	NDP	O	401	48/48	0.10	0.08	35,48,61,64	0
3	ZN	P	402	1/1	0.10	0.07	45,45,45,45	0
2	NDP	D	401	48/48	0.10	-0.01	23,35,49,58	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	ZN	C	402	1/1	0.11	-0.02	32,32,32,32	0
3	ZN	M	402	1/1	0.10	-0.02	50,50,50,50	0
3	ZN	G	402	1/1	0.10	-0.05	36,36,36,36	0
2	NDP	I	401	48/48	0.10	-0.05	25,36,47,56	0
3	ZN	N	402	1/1	0.10	-0.09	46,46,46,46	0
2	NDP	A	401	48/48	0.10	-0.17	24,32,49,52	0
2	NDP	K	401	48/48	0.10	-0.17	29,38,53,62	0
2	NDP	L	401	48/48	0.10	-0.18	28,43,60,68	0
2	NDP	G	401	48/48	0.10	-0.18	26,38,53,64	0
2	NDP	P	401	48/48	0.10	-0.20	35,43,54,60	0
2	NDP	M	401	48/48	0.09	-0.45	32,47,59,64	0
3	ZN	K	402	1/1	0.10	-0.49	36,36,36,36	0

6.5 Other polymers ⓘ

There are no such residues in this entry.