



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:12 PM GMT

PDB ID : 4WZA  
Title : Asymmetric Nucleotide Binding in the Nitrogenase Complex  
Authors : Tezcan, F.A.; Kaiser, J.T.; Howard, J.B.; Rees, D.C.  
Deposited on : 2014-11-19  
Resolution : 1.90 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

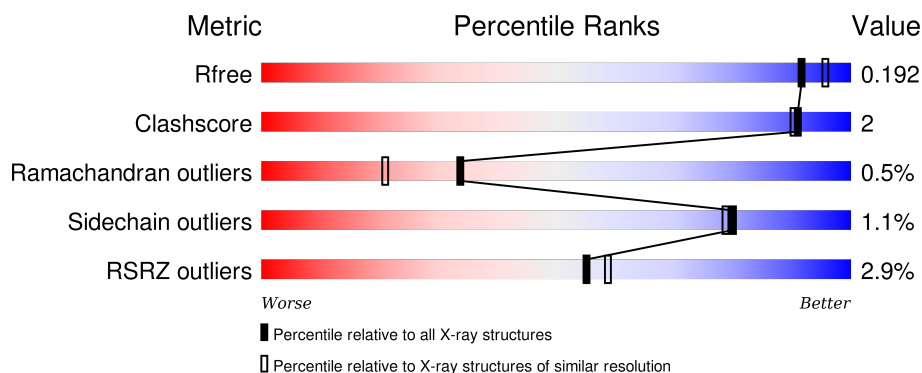
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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.




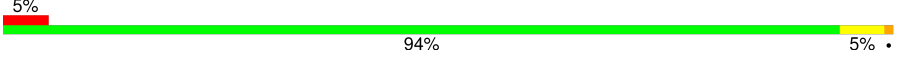
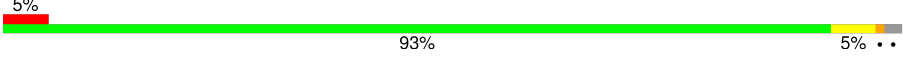
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . 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	477	 3% 92% 8%
1	C	477	 % 93% 7%
2	B	522	 95% 5%
2	D	522	 95% 5%
3	E	276	 7% 92% 8%

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
3	F	276	 8% 90% 8% ••
3	G	276	 5% 94% 5% •
3	H	276	 5% 93% 5% ••

## 2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 26654 atoms, of which 0 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 Nitrogenase molybdenum-iron protein alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	477	Total	C	N	O	S	4	0	0
			3791	2410	647	709	25			
1	C	477	Total	C	N	O	S	0	0	0
			3791	2410	647	709	25			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	440	GLN	GLU	variant	UNP P07328
C	440	GLN	GLU	variant	UNP P07328

- Molecule 2 is a protein called Nitrogenase molybdenum-iron protein beta chain.

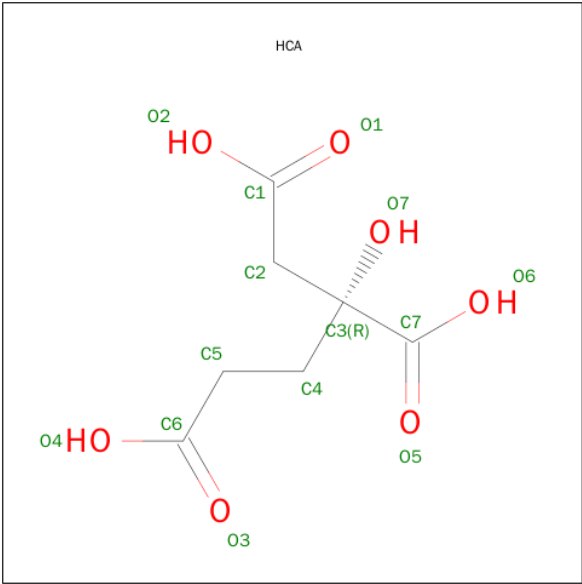
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	522	Total	C	N	O	S	0	0	0
			4174	2666	705	775	28			
2	D	522	Total	C	N	O	S	0	1	0
			4183	2671	706	778	28			

- Molecule 3 is a protein called Nitrogenase iron protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	276	Total	C	N	O	S	100	0	0
			2090	1306	355	408	21			
3	F	271	Total	C	N	O	S	52	0	0
			2053	1283	350	400	20			
3	G	276	Total	C	N	O	S	29	0	0
			2089	1306	355	407	21			
3	H	271	Total	C	N	O	S	53	0	0
			2053	1283	350	400	20			

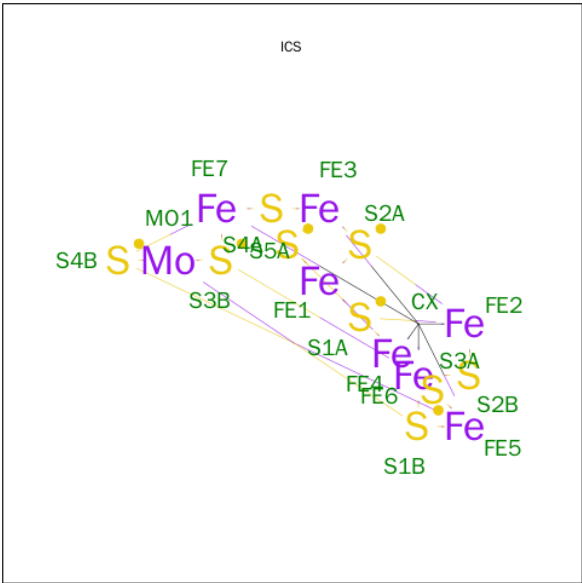
- Molecule 4 is 3-HYDROXY-3-CARBOXY-ADIPIC ACID (three-letter code: HCA) (for-

mula: C<sub>7</sub>H<sub>10</sub>O<sub>7</sub>).



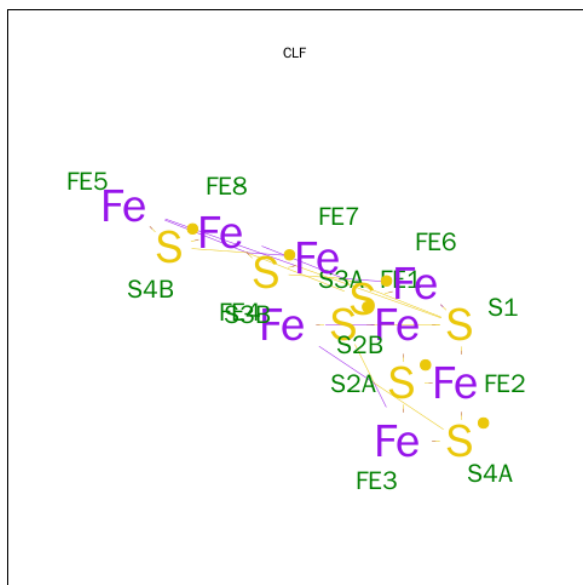
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			14	7	7		
4	C	1	Total	C	O	0	0
			14	7	7		

- Molecule 5 is iron-sulfur-molybdenum cluster with interstitial carbon (three-letter code: ICS) (formula: CFe<sub>7</sub>MoS<sub>9</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	Fe	Mo	S	
			18	1	7	1	9	
5	C	1	Total	C	Fe	Mo	S	
			18	1	7	1	9	

- Molecule 6 is FE(8)-S(7) CLUSTER (three-letter code: CLF) (formula:  $\text{Fe}_8\text{S}_7$ ).

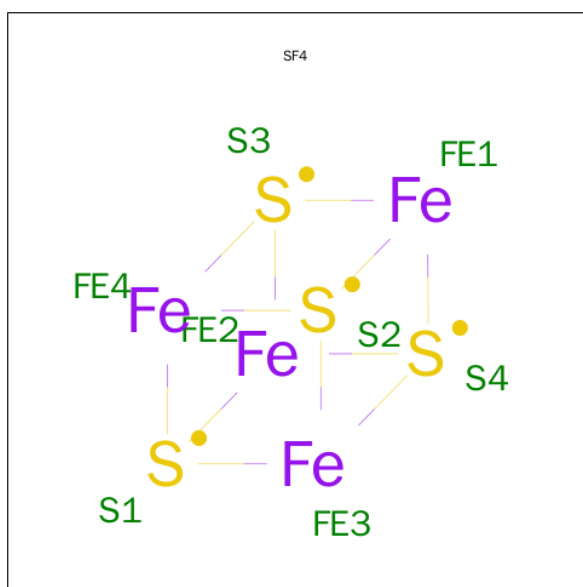


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	Fe	S		
			15	8	7	0	0
6	C	1	Total	Fe	S		
			15	8	7	0	0

- Molecule 7 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Fe		
			1	1	0	0
7	D	1	Total	Fe		
			1	1	0	0

- Molecule 8 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula:  $\text{Fe}_4\text{S}_4$ ).

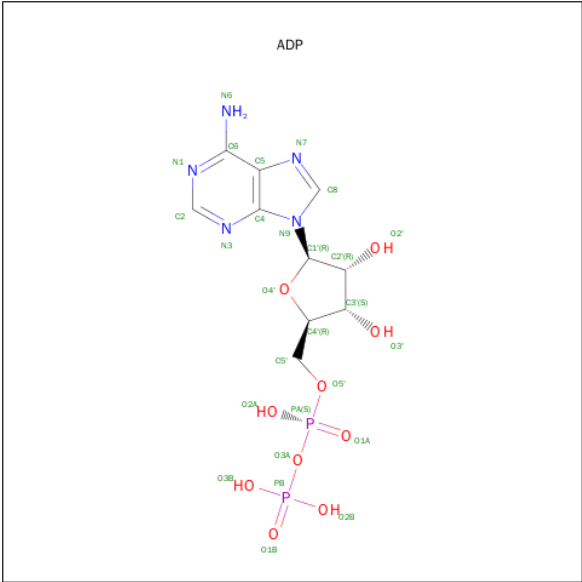


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	E	1	Total	Fe	S	0	0
			8	4	4		
8	G	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

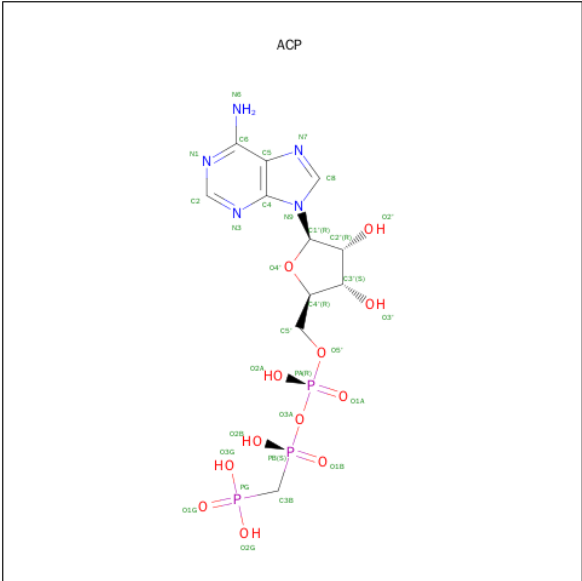
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	H	1	Total	Mg	0	0
			1	1		
9	G	1	Total	Mg	0	0
			1	1		
9	F	1	Total	Mg	0	0
			1	1		
9	E	1	Total	Mg	0	0
			1	1		

- Molecule 10 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	E	1	Total 27	C 10	N 5	O 10	P 2	0	0
10	G	1	Total 27	C 10	N 5	O 10	P 2	0	0

- Molecule 11 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: C<sub>11</sub>H<sub>18</sub>N<sub>5</sub>O<sub>12</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	F	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

Continued on next page...



*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	H	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

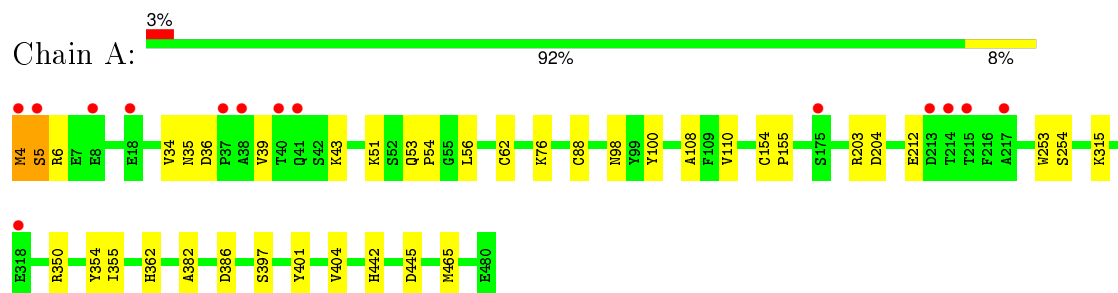
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	297	Total	O	0	0
			297	297		
12	B	525	Total	O	0	0
			525	525		
12	C	424	Total	O	0	0
			424	424		
12	D	510	Total	O	0	0
			510	510		
12	E	79	Total	O	0	0
			79	79		
12	F	95	Total	O	0	0
			95	95		
12	G	130	Total	O	0	0
			130	130		
12	H	138	Total	O	0	0
			138	138		

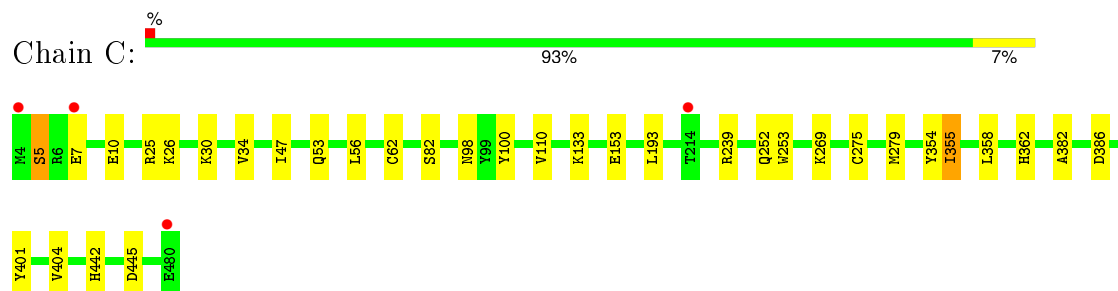
### 3 Residue-property plots [i](#)

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.

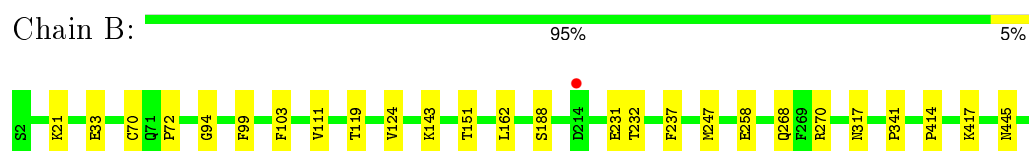
- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain



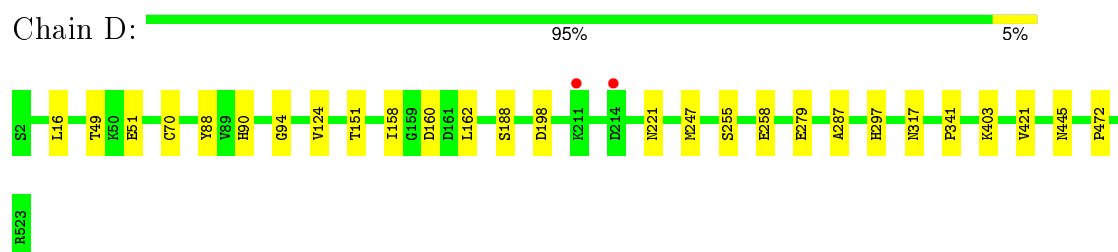
- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain



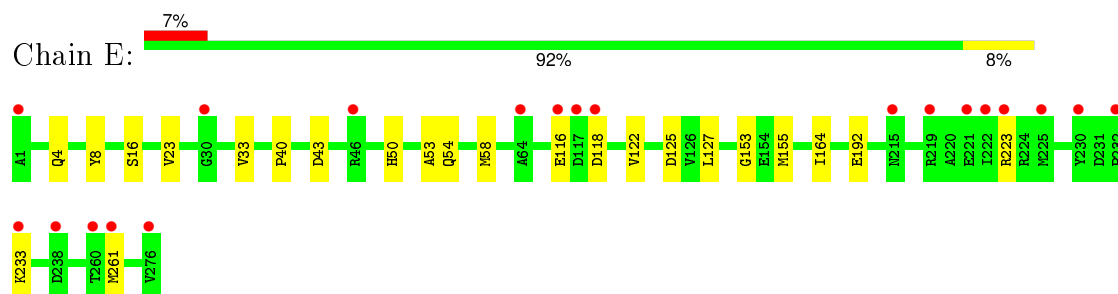
- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



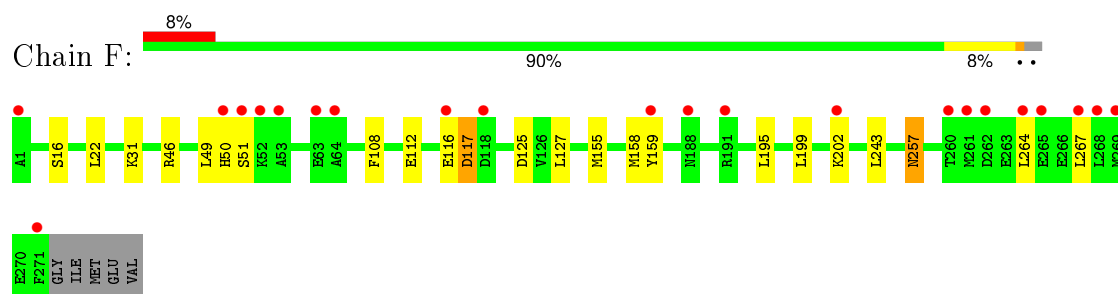
- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



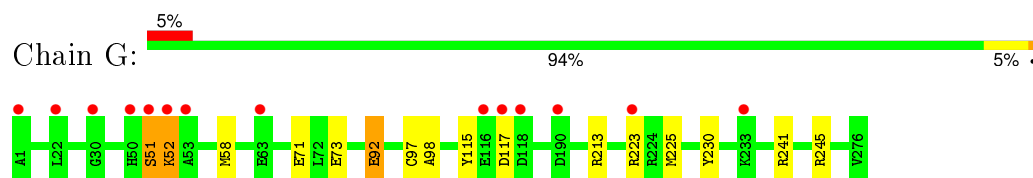
- Molecule 3: Nitrogenase iron protein 1



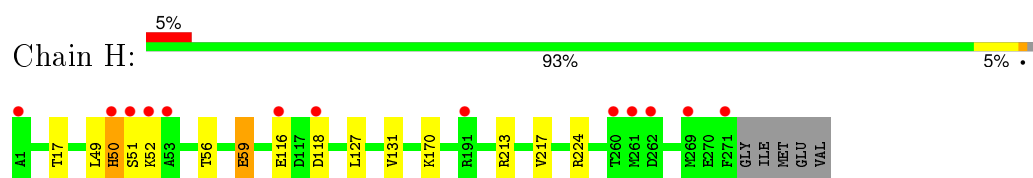
- Molecule 3: Nitrogenase iron protein 1



- Molecule 3: Nitrogenase iron protein 1



- Molecule 3: Nitrogenase iron protein 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	110.20Å 120.41Å 264.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.84 – 1.90 19.84 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.7 (19.84-1.90) 97.7 (19.84-1.90)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.94 (at 1.90Å)	Xtriage
Refinement program	phenix	Depositor
R, $R_{free}$	0.145 , 0.187 0.151 , 0.192	Depositor DCC
$R_{free}$ test set	13601 reflections (5.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	20.0	Xtriage
Anisotropy	0.515	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 58.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 269420 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	26654	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.80% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, ADP, HCA, SF4, ACP, FE, ICS, CLF

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	0.46	0/3879	0.58	0/5229
1	C	0.51	0/3879	0.60	0/5229
2	B	0.51	0/4280	0.59	0/5786
2	D	0.53	0/4289	0.60	0/5798
3	E	0.36	0/2114	0.52	0/2846
3	F	0.38	0/2077	0.55	0/2798
3	G	0.43	0/2113	0.57	0/2846
3	H	0.41	0/2077	0.55	0/2798
All	All	0.47	0/24708	0.58	0/33330

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	3791	0	3731	22	0
1	C	3791	0	3731	18	0
2	B	4174	0	4088	19	0
2	D	4183	0	4093	14	0
3	E	2090	0	2107	10	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	2053	0	2069	14	0
3	G	2089	0	2107	11	0
3	H	2053	0	2069	8	0
4	A	14	0	6	3	0
4	C	14	0	6	2	0
5	A	18	0	0	0	0
5	C	18	0	0	0	0
6	A	15	0	0	0	0
6	C	15	0	0	0	0
7	B	1	0	0	0	0
7	D	1	0	0	0	0
8	E	8	0	0	0	0
8	G	8	0	0	0	0
9	E	1	0	0	0	0
9	F	1	0	0	0	0
9	G	1	0	0	0	0
9	H	1	0	0	0	0
10	E	27	0	12	0	0
10	G	27	0	12	0	0
11	F	31	0	14	0	0
11	H	31	0	14	0	0
12	A	297	0	0	5	0
12	B	525	0	0	5	0
12	C	424	0	0	2	0
12	D	510	0	0	2	0
12	E	79	0	0	1	0
12	F	95	0	0	2	0
12	G	130	0	0	1	0
12	H	138	0	0	0	0
All	All	26654	0	24059	107	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 107 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)
3:F:257:ASN:ND2	12:F:1371:HOH:O	2.25	0.70
2:B:317:ASN:ND2	12:B:2007:HOH:O	2.23	0.70
3:H:49:LEU:O	3:H:51:SER:N	2.29	0.66
3:F:202:LYS:HE3	3:F:267:LEU:HD21	1.79	0.63

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:213:ARG:NH2	12:G:1394:HOH:O	2.33	0.62

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	475/477 (100%)	459 (97%)	14 (3%)	2 (0%)	39	27
1	C	475/477 (100%)	457 (96%)	16 (3%)	2 (0%)	39	27
2	B	520/522 (100%)	511 (98%)	9 (2%)	0	100	100
2	D	521/522 (100%)	511 (98%)	9 (2%)	1 (0%)	52	42
3	E	274/276 (99%)	261 (95%)	10 (4%)	3 (1%)	17	6
3	F	269/276 (98%)	257 (96%)	10 (4%)	2 (1%)	26	14
3	G	274/276 (99%)	263 (96%)	9 (3%)	2 (1%)	26	14
3	H	269/276 (98%)	256 (95%)	11 (4%)	2 (1%)	26	14
All	All	3077/3102 (99%)	2975 (97%)	88 (3%)	14 (0%)	34	21

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	E	50	HIS
3	F	50	HIS
3	G	52	LYS
3	H	50	HIS
3	E	54	GLN

### 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	407/407 (100%)	400 (98%)	7 (2%)	68	64
1	C	407/407 (100%)	402 (99%)	5 (1%)	78	76
2	B	454/454 (100%)	454 (100%)	0	100	100
2	D	455/454 (100%)	452 (99%)	3 (1%)	88	88
3	E	222/222 (100%)	219 (99%)	3 (1%)	74	71
3	F	218/222 (98%)	214 (98%)	4 (2%)	66	61
3	G	222/222 (100%)	219 (99%)	3 (1%)	74	71
3	H	218/222 (98%)	215 (99%)	3 (1%)	74	71
All	All	2603/2610 (100%)	2575 (99%)	28 (1%)	80	79

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	16	LEU
3	E	155	MET
3	H	59	GLU
2	D	88	TYR
2	D	258	GLU

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

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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



## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 6 are monoatomic - leaving 12 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	$\# Z  > 2$
4	HCA	A	1494	-	4,13,13	0.78	0	3,18,18	2.16	1 (33%)
5	ICS	A	1496	1	6,30,30	1.70	2 (33%)	0,78,78	0.00	-
6	CLF	A	1498	1,2	0,24,24	0.00	-	0,57,57	0.00	-
4	HCA	C	1494	-	4,13,13	0.54	0	3,18,18	1.86	1 (33%)
5	ICS	C	1496	1	6,30,30	1.88	2 (33%)	0,78,78	0.00	-
6	CLF	C	1498	1,2	0,24,24	0.00	-	0,57,57	0.00	-
8	SF4	E	1290	3	0,12,12	0.00	-	0,24,24	0.00	-
10	ADP	E	1292	9	22,29,29	1.08	2 (9%)	27,45,45	1.96	5 (18%)
11	ACP	F	1292	9	25,33,33	1.71	4 (16%)	31,52,52	1.99	5 (16%)
8	SF4	G	1290	3	0,12,12	0.00	-	0,24,24	0.00	-
10	ADP	G	1292	9	22,29,29	1.05	1 (4%)	27,45,45	1.84	5 (18%)
11	ACP	H	1292	9	25,33,33	1.66	5 (20%)	31,52,52	1.82	5 (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
4	HCA	A	1494	-	-	0/7/17/17	0/0/0/0
5	ICS	A	1496	1	-	0/0/204/204	0/0/13/13
6	CLF	A	1498	1,2	-	0/0/132/132	0/12/10/10
4	HCA	C	1494	-	-	0/7/17/17	0/0/0/0
5	ICS	C	1496	1	-	0/0/204/204	0/0/13/13
6	CLF	C	1498	1,2	-	0/0/132/132	0/12/10/10

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	SF4	E	1290	3	-	0/0/48/48	0/6/5/5
10	ADP	E	1292	9	-	0/12/32/32	0/3/3/3
11	ACP	F	1292	9	-	0/15/38/38	0/3/3/3
8	SF4	G	1290	3	-	0/0/48/48	0/6/5/5
10	ADP	G	1292	9	-	0/12/32/32	0/3/3/3
11	ACP	H	1292	9	-	0/15/38/38	0/3/3/3

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1496	ICS	S2B-FE6	-2.79	2.18	2.24
5	C	1496	ICS	S2B-FE6	-2.78	2.18	2.24
5	C	1496	ICS	S5A-FE7	-2.62	2.18	2.24
11	H	1292	ACP	PG-O2G	-2.53	1.48	1.54
11	F	1292	ACP	PG-O2G	-2.40	1.49	1.54

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	E	1292	ADP	N3-C2-N1	-7.47	123.17	128.89
11	F	1292	ACP	N3-C2-N1	-7.07	123.48	128.89
11	H	1292	ACP	N3-C2-N1	-6.51	123.91	128.89
10	G	1292	ADP	N3-C2-N1	-6.49	123.92	128.89
4	A	1494	HCA	C3-C2-C1	-3.43	109.47	114.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1494	HCA	3	0
4	C	1494	HCA	2	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	477/477 (100%)	-0.30	14 (2%) 55 59	13, 25, 46, 72	1 (0%)
1	C	477/477 (100%)	-0.48	4 (0%) 87 88	12, 20, 40, 85	0
2	B	522/522 (100%)	-0.55	1 (0%) 95 95	12, 19, 36, 51	0
2	D	522/522 (100%)	-0.59	2 (0%) 93 93	11, 19, 32, 48	0
3	E	271/276 (98%)	0.36	20 (7%) 17 19	20, 42, 65, 107	17 (6%)
3	F	270/276 (97%)	0.37	22 (8%) 15 16	19, 39, 80, 101	13 (4%)
3	G	276/276 (100%)	-0.14	14 (5%) 32 35	14, 30, 53, 76	10 (3%)
3	H	271/276 (98%)	-0.02	13 (4%) 34 37	14, 30, 70, 84	18 (6%)
All	All	3086/3102 (99%)	-0.27	90 (2%) 55 59	11, 24, 53, 107	59 (1%)

The worst 5 of 90 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	53	ALA	7.2
3	E	117	ASP	6.6
3	H	53	ALA	6.5
3	F	261	MET	6.3
3	F	159	TYR	6.3

### 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, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
9	MG	H	1291	1/1	0.99	0.08	0.78	23,23,23,23	0
4	HCA	A	1494	14/14	0.96	0.08	0.53	15,17,23,24	0
9	MG	E	1291	1/1	0.79	0.12	0.32	39,39,39,39	0
4	HCA	C	1494	14/14	0.98	0.07	0.07	11,15,19,20	0
9	MG	G	1291	1/1	0.86	0.07	-0.41	32,32,32,32	0
10	ADP	G	1292	27/27	0.98	0.07	-0.63	19,27,35,40	0
10	ADP	E	1292	27/27	0.96	0.09	-0.66	27,39,43,47	0
11	ACP	F	1292	31/31	0.97	0.07	-0.80	20,32,39,49	0
9	MG	F	1291	1/1	0.92	0.06	-0.88	27,27,27,27	0
11	ACP	H	1292	31/31	0.98	0.07	-1.09	16,23,30,41	0
6	CLF	A	1498	15/15	0.99	0.05	-1.50	13,15,16,17	0
6	CLF	C	1498	15/15	1.00	0.04	-1.99	11,13,13,14	0
5	ICS	A	1496	18/18	0.99	0.05	-2.28	15,18,20,20	0
5	ICS	C	1496	18/18	1.00	0.04	-2.42	12,14,16,16	0
7	FE	D	1492	1/1	0.99	0.02	-2.49	21,21,21,21	1
8	SF4	E	1290	8/8	0.99	0.04	-2.51	16,18,19,22	0
7	FE	B	1492	1/1	0.99	0.03	-2.77	25,25,25,25	1
8	SF4	G	1290	8/8	0.99	0.04	-2.90	12,14,15,16	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.