



wwPDB X-ray Structure Validation Summary Report ⓘ

May 24, 2020 – 07:18 am BST

PDB ID : 3MYR
Title : Crystal structure of [NiFe] hydrogenase from *Allochromatium vinosum* in its Ni-A state
Authors : Ogata, H.; Kellers, P.; Lubitz, W.
Deposited on : 2010-05-11
Resolution : 2.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

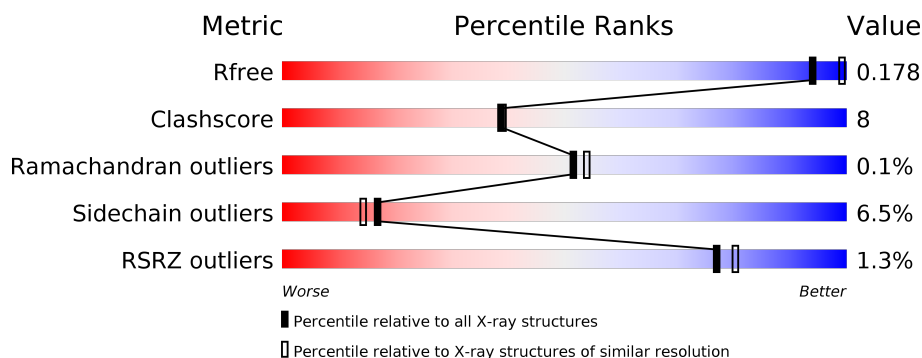
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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.



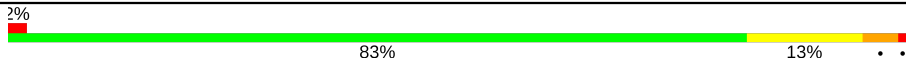

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	269	<div> <div>85%</div> <div>10%</div> <div>••</div> </div>
1	C	269	<div> <div>83%</div> <div>13%</div> <div>•</div> </div>
1	E	269	<div> <div>82%</div> <div>14%</div> <div>••</div> </div>
1	G	269	<div> <div>86%</div> <div>11%</div> <div>••</div> </div>
2	B	561	<div> <div>85%</div> <div>12%</div> <div>•</div> </div>
2	D	561	<div> <div>83%</div> <div>14%</div> <div>•</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	561	 2% 83% 13% . .
2	H	561	 82% 13% . .

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	NFV	B	2005	-	-	X	-
7	NFV	D	2005	-	-	X	-
7	NFV	F	2005	-	-	X	-
7	NFV	H	2005	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 27720 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 Hydrogenase (NiFe) small subunit HydA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	268	Total	C	N	O	S	0	0	0
			2038	1293	348	381	16			
1	C	269	Total	C	N	O	S	0	0	0
			2047	1299	349	383	16			
1	E	268	Total	C	N	O	S	0	0	0
			2038	1293	348	381	16			
1	G	268	Total	C	N	O	S	0	0	0
			2038	1293	348	381	16			

- Molecule 2 is a protein called Nickel-dependent hydrogenase large subunit.

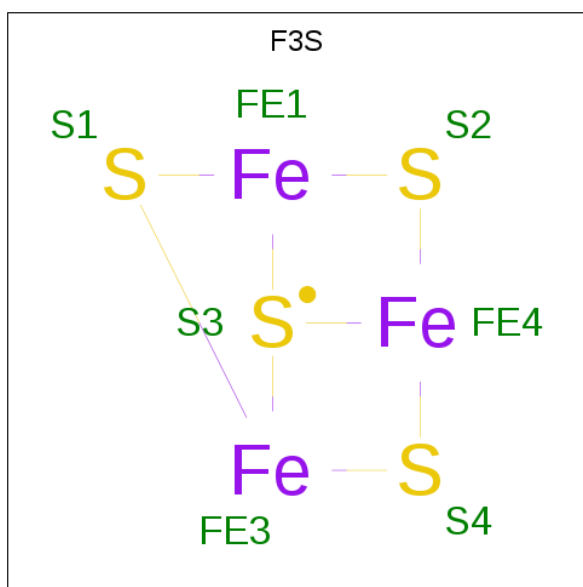
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	559	Total	C	N	O	S	0	0	0
			4363	2765	773	811	14			
2	D	561	Total	C	N	O	S	0	0	0
			4377	2773	775	814	15			
2	F	561	Total	C	N	O	S	0	0	0
			4377	2773	775	814	15			
2	H	559	Total	C	N	O	S	0	0	0
			4363	2765	773	811	14			

- Molecule 3 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



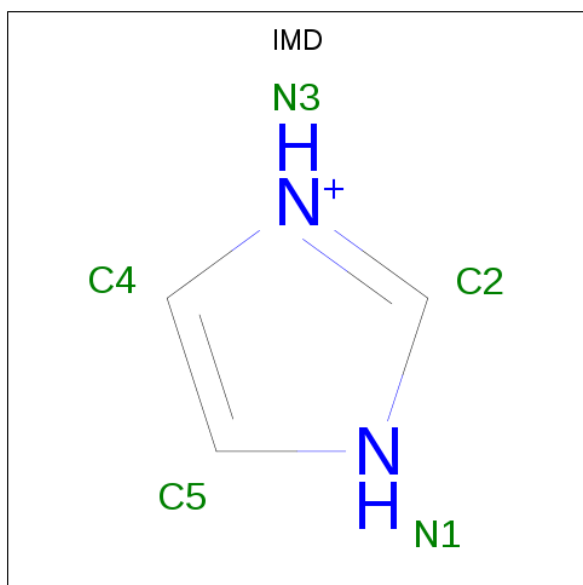
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	1
			10	5	5		
3	A	1	Total	Fe	S	0	0
			8	4	4		
3	C	1	Total	Fe	S	0	1
			10	5	5		
3	C	1	Total	Fe	S	0	0
			8	4	4		
3	E	1	Total	Fe	S	0	1
			10	5	5		
3	E	1	Total	Fe	S	0	0
			8	4	4		
3	G	1	Total	Fe	S	0	1
			10	5	5		
3	G	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 4 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe₃S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Fe	S	0	0
			7	3	4		
4	C	1	Total	Fe	S	0	0
			7	3	4		
4	E	1	Total	Fe	S	0	0
			7	3	4		
4	G	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 5 is IMIDAZOLE (three-letter code: IMD) (formula: C₃H₅N₂).

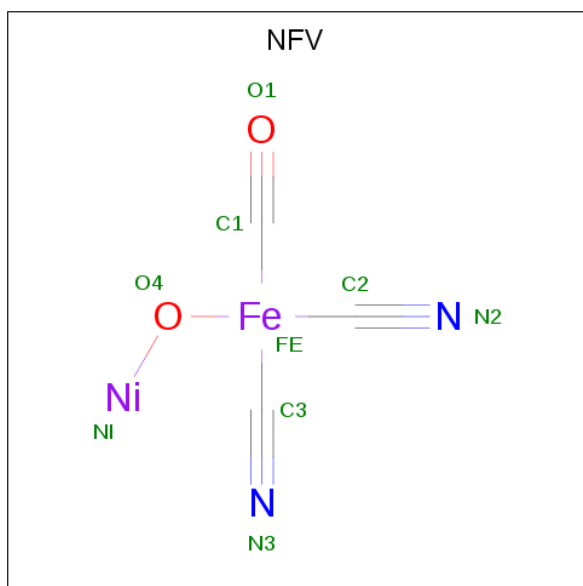


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N 5 3 2	0	0
5	G	1	Total C N 5 3 2	0	0

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	G	1	Total Cl 1 1	0	0
6	A	1	Total Cl 1 1	0	0
6	C	1	Total Cl 1 1	0	0
6	E	1	Total Cl 1 1	0	0

- Molecule 7 is NI-FE OXIDIZED ACTIVE CENTER (three-letter code: NFV) (formula: C₃FeN₂NiO₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total C Fe N Ni O 9 3 1 2 1 2	0	0
7	D	1	Total C Fe N Ni O 9 3 1 2 1 2	0	0
7	F	1	Total C Fe N Ni O 9 3 1 2 1 2	0	0

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
7	H	1	Total	C	Fe	N	Ni	O	0	0
			9	3	1	2	1	2		

- Molecule 8 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	H	1	Total	Mg	0	0
			1	1		
8	B	1	Total	Mg	0	0
			1	1		
8	D	1	Total	Mg	0	0
			1	1		
8	F	1	Total	Mg	0	0
			1	1		

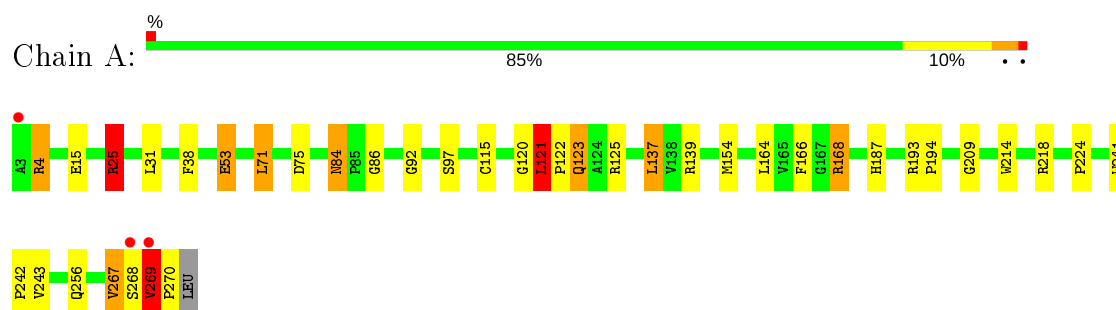
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	199	Total	O	0	0
			199	199		
9	B	379	Total	O	0	0
			379	379		
9	C	157	Total	O	0	0
			157	157		
9	D	281	Total	O	0	0
			281	281		
9	E	115	Total	O	0	0
			115	115		
9	F	286	Total	O	0	0
			286	286		
9	G	179	Total	O	0	0
			179	179		
9	H	329	Total	O	0	0
			329	329		

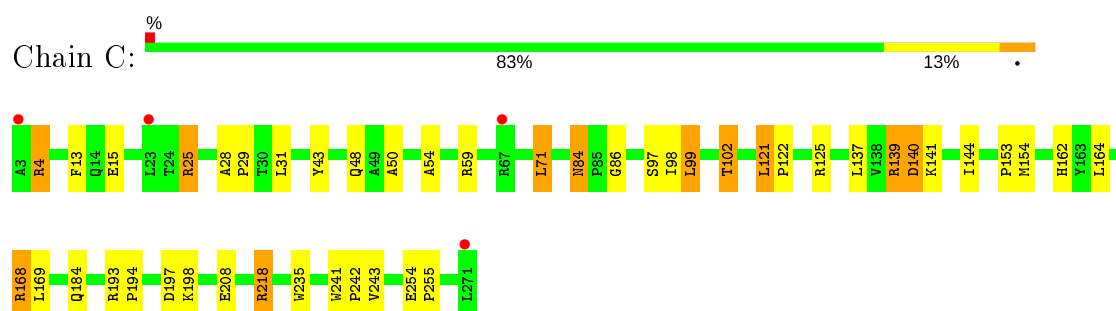
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

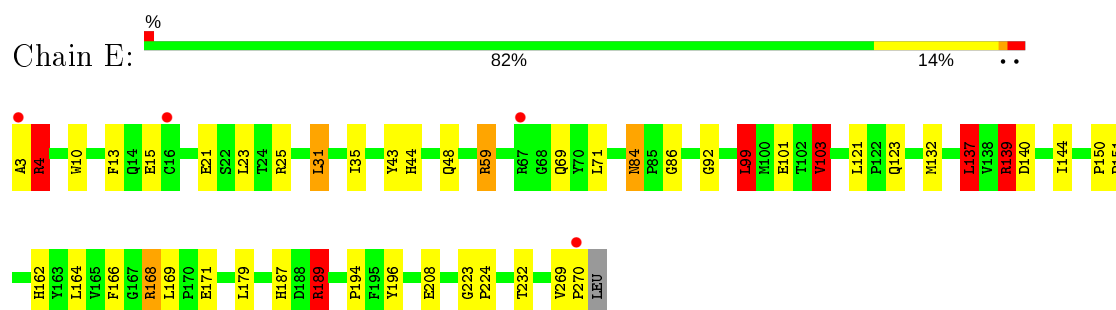
- Molecule 1: Hydrogenase (NiFe) small subunit HydA



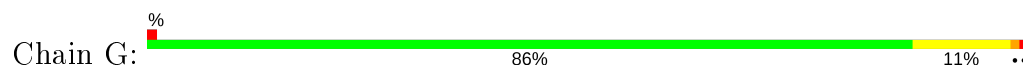
- Molecule 1: Hydrogenase (NiFe) small subunit HydA

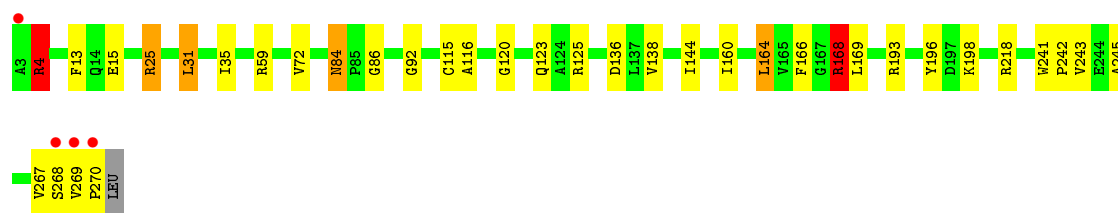


- Molecule 1: Hydrogenase (NiFe) small subunit HydA



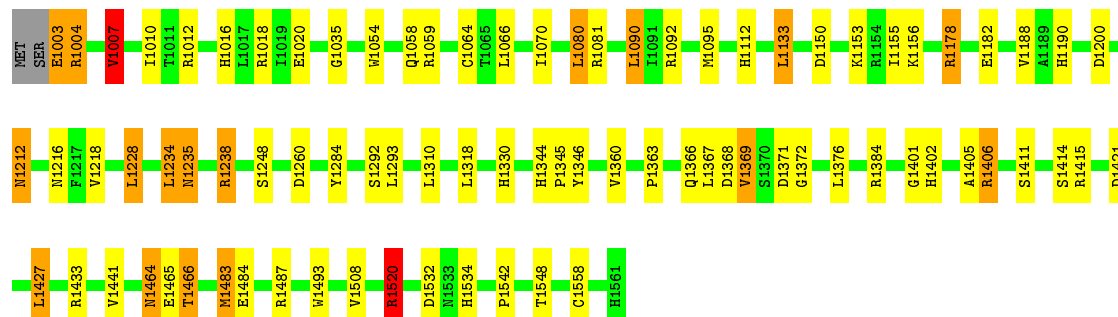
- Molecule 1: Hydrogenase (NiFe) small subunit HydA





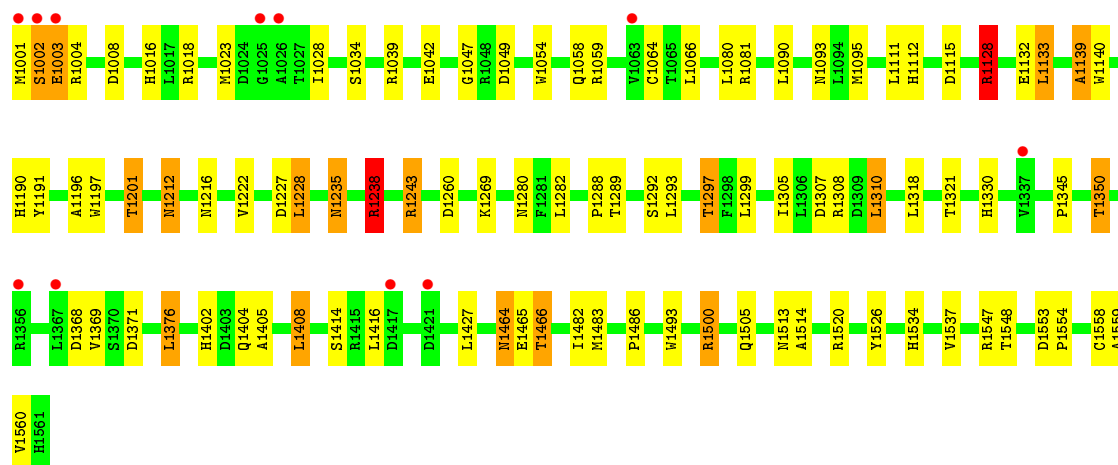
• Molecule 2: Nickel-dependent hydrogenase large subunit

Chain B: 85% 12%



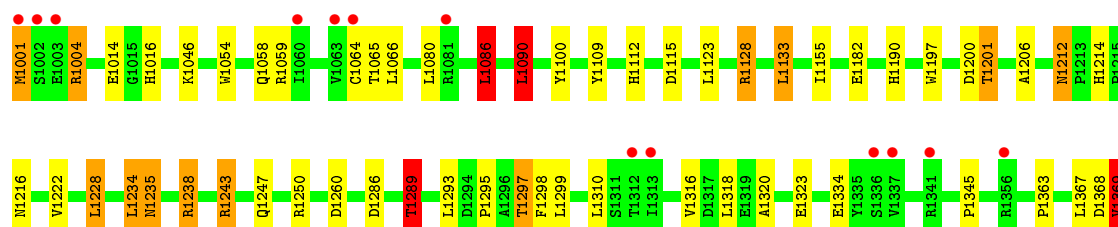
• Molecule 2: Nickel-dependent hydrogenase large subunit

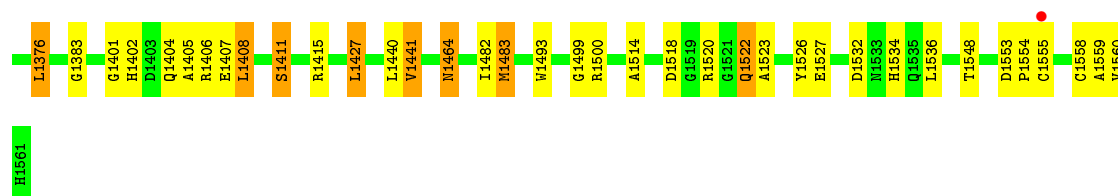
Chain D: 2% 83% 14%



• Molecule 2: Nickel-dependent hydrogenase large subunit

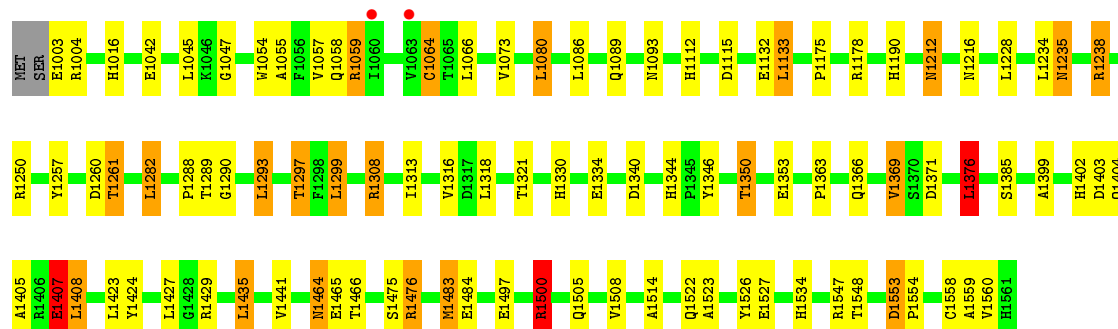
Chain F: 2% 83% 13%





• Molecule 2: Nickel-dependent hydrogenase large subunit

Chain H: 82% 13%



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	205.75Å 216.96Å 119.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.10 48.05 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-2.10) 99.6 (48.05-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.80 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0102, CNS	Depositor
R, R_{free}	0.138 , 0.168 0.151 , 0.178	Depositor DCC
R_{free} test set	15482 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	26.3	Xtriage
Anisotropy	0.405	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 39.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	27720	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.03% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, IMD, CL, SF4, NFV, F3S

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	1.22	6/2099 (0.3%)	1.04	10/2866 (0.3%)
1	C	1.12	2/2108 (0.1%)	0.96	6/2877 (0.2%)
1	E	1.07	3/2099 (0.1%)	1.00	9/2866 (0.3%)
1	G	1.15	3/2099 (0.1%)	0.99	10/2866 (0.3%)
2	B	1.12	11/4476 (0.2%)	1.00	24/6097 (0.4%)
2	D	1.00	3/4490 (0.1%)	0.97	17/6115 (0.3%)
2	F	1.02	4/4490 (0.1%)	0.94	18/6115 (0.3%)
2	H	1.09	4/4476 (0.1%)	1.01	23/6097 (0.4%)
All	All	1.09	36/26337 (0.1%)	0.99	117/35899 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	E	0	1
1	G	0	1
All	All	0	3

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	53	GLU	CG-CD	10.78	1.68	1.51
2	B	1003	GLU	CG-CD	-7.87	1.40	1.51
1	C	208	GLU	CG-CD	7.27	1.62	1.51
2	H	1064	CYS	CB-SG	7.07	1.94	1.82
2	B	1465	GLU	CG-CD	6.92	1.62	1.51

The worst 5 of 117 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	D	1128	ARG	NE-CZ-NH2	15.65	128.13	120.30
1	E	189	ARG	NE-CZ-NH2	14.94	127.77	120.30
2	H	1004	ARG	NE-CZ-NH2	-12.68	113.96	120.30
2	D	1128	ARG	NE-CZ-NH1	-11.63	114.48	120.30
1	E	189	ARG	NE-CZ-NH1	-11.24	114.68	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	25	ARG	Sidechain
1	E	139	ARG	Peptide
1	G	25	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2038	0	1934	25	0
1	C	2047	0	1945	30	0
1	E	2038	0	1934	32	0
1	G	2038	0	1934	25	0
2	B	4363	0	4242	54	0
2	D	4377	0	4256	77	0
2	F	4377	0	4256	79	0
2	H	4363	0	4242	71	0
3	A	18	0	0	1	0
3	C	18	0	0	1	0
3	E	18	0	0	0	0
3	G	18	0	0	0	0
4	A	7	0	0	0	0
4	C	7	0	0	0	0
4	E	7	0	0	0	0
4	G	7	0	0	0	0
5	A	5	0	5	1	0
5	G	5	0	5	0	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	E	1	0	0	0	0
6	G	1	0	0	0	0
7	B	9	0	0	5	0
7	D	9	0	0	5	0
7	F	9	0	0	5	0
7	H	9	0	0	5	0
8	B	1	0	0	0	0
8	D	1	0	0	0	0
8	F	1	0	0	0	0
8	H	1	0	0	0	0
9	A	199	0	0	2	0
9	B	379	0	0	7	0
9	C	157	0	0	5	0
9	D	281	0	0	6	0
9	E	115	0	0	1	0
9	F	286	0	0	9	0
9	G	179	0	0	1	0
9	H	329	0	0	7	0
All	All	27720	0	24753	380	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 8.

The worst 5 of 380 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)
7:H:2005:NFV:C2	7:H:2005:NFV:C1	2.27	1.13
2:D:1464:ASN:HD21	2:D:1466:THR:HG23	1.04	1.12
2:B:1464:ASN:HD21	2:B:1466:THR:HG23	1.09	1.09
7:F:2005:NFV:C2	7:F:2005:NFV:C1	2.30	1.08
1:C:144:ILE:HD11	1:C:169:LEU:HD22	1.32	1.08

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	266/269 (99%)	254 (96%)	11 (4%)	1 (0%)	34	32
1	C	267/269 (99%)	259 (97%)	7 (3%)	1 (0%)	34	32
1	E	266/269 (99%)	256 (96%)	9 (3%)	1 (0%)	34	32
1	G	266/269 (99%)	254 (96%)	12 (4%)	0	100	100
2	B	557/561 (99%)	546 (98%)	11 (2%)	0	100	100
2	D	559/561 (100%)	539 (96%)	19 (3%)	1 (0%)	47	49
2	F	559/561 (100%)	540 (97%)	19 (3%)	0	100	100
2	H	557/561 (99%)	543 (98%)	14 (2%)	0	100	100
All	All	3297/3320 (99%)	3191 (97%)	102 (3%)	4 (0%)	51	54

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	ARG
1	C	4	ARG
2	D	1002	SER
1	E	4	ARG

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	213/214 (100%)	199 (93%)	14 (7%)	16	14
1	C	214/214 (100%)	197 (92%)	17 (8%)	12	9
1	E	213/214 (100%)	200 (94%)	13 (6%)	18	16
1	G	213/214 (100%)	203 (95%)	10 (5%)	26	25
2	B	452/454 (100%)	426 (94%)	26 (6%)	20	17
2	D	454/454 (100%)	421 (93%)	33 (7%)	14	11
2	F	454/454 (100%)	421 (93%)	33 (7%)	14	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	H	452/454 (100%)	424 (94%)	28 (6%)	18	15
All	All	2665/2672 (100%)	2491 (94%)	174 (6%)	17	14

5 of 174 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	1321	THR
1	E	103	VAL
2	H	1318	LEU
2	D	1414	SER
2	D	1520	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 102 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	1402	HIS
1	E	184	GLN
2	H	1402	HIS
2	D	1454	ASN
2	D	1534	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 30 ligands modelled in this entry, 8 are monoatomic - leaving 22 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
7	NFV	F	2005	2	3,8,8	1.95	1 (33%)	-		
7	NFV	D	2005	2	3,8,8	2.81	1 (33%)	-		
4	F3S	A	2003	1	0,9,9	0.00	-	-		
3	SF4	G	2002	1	0,12,12	0.00	-	-		
3	SF4	C	2002	1	0,12,12	0.00	-	-		
3	SF4	C	2001[B]	1	0,12,12	0.00	-	-		
5	IMD	A	3002	-	3,5,5	0.71	0	4,5,5	0.38	0
3	SF4	G	2001[B]	1	0,12,12	0.00	-	-		
3	SF4	C	2001[A]	1	0,12,12	0.00	-	-		
3	SF4	G	2001[A]	1	0,12,12	0.00	-	-		
4	F3S	E	2003	1	0,9,9	0.00	-	-		
7	NFV	H	2005	2	3,8,8	2.36	2 (66%)	-		
4	F3S	C	2003	1	0,9,9	0.00	-	-		
3	SF4	A	2002	1	0,12,12	0.00	-	-		
7	NFV	B	2005	2	3,8,8	3.16	2 (66%)	-		
5	IMD	G	3001	-	3,5,5	0.53	0	4,5,5	0.86	0
3	SF4	A	2001[A]	1	0,12,12	0.00	-	-		
3	SF4	A	2001[B]	1	0,12,12	0.00	-	-		
3	SF4	E	2002	1	0,12,12	0.00	-	-		
3	SF4	E	2001[A]	1	0,12,12	0.00	-	-		
3	SF4	E	2001[B]	1	0,12,12	0.00	-	-		
4	F3S	G	2003	1	0,9,9	0.00	-	-		

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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SF4	G	2001[B]	1	-	-	0/6/5/5
3	SF4	E	2001[A]	1	-	-	0/6/5/5
3	SF4	C	2001[A]	1	-	-	0/6/5/5
5	IMD	G	3001	-	-	-	0/1/1/1
4	F3S	C	2003	1	-	-	0/3/3/3
3	SF4	G	2001[A]	1	-	-	0/6/5/5
4	F3S	E	2003	1	-	-	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SF4	A	2001[A]	1	-	-	0/6/5/5
4	F3S	A	2003	1	-	-	0/3/3/3
3	SF4	A	2001[B]	1	-	-	0/6/5/5
3	SF4	E	2001[B]	1	-	-	0/6/5/5
3	SF4	G	2002	1	-	-	0/6/5/5
5	IMD	A	3002	-	-	-	0/1/1/1
3	SF4	E	2002	1	-	-	0/6/5/5
3	SF4	C	2002	1	-	-	0/6/5/5
3	SF4	A	2002	1	-	-	0/6/5/5
3	SF4	C	2001[B]	1	-	-	0/6/5/5
4	F3S	G	2003	1	-	-	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	2005	NFV	O1-C1	4.40	1.24	1.16
7	D	2005	NFV	O1-C1	4.17	1.24	1.16
7	H	2005	NFV	O1-C1	3.08	1.22	1.16
7	F	2005	NFV	O1-C1	2.75	1.21	1.16
7	B	2005	NFV	C2-N2	2.58	1.18	1.13

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	F	2005	NFV	5	0
7	D	2005	NFV	5	0
3	C	2002	SF4	1	0
5	A	3002	IMD	1	0
7	H	2005	NFV	5	0
3	A	2002	SF4	1	0
7	B	2005	NFV	5	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, 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	268/269 (99%)	-0.36	3 (1%) 80 84	14, 22, 39, 78	0
1	C	269/269 (100%)	-0.33	4 (1%) 73 77	15, 27, 45, 62	0
1	E	268/269 (99%)	-0.33	4 (1%) 73 77	20, 31, 49, 76	0
1	G	268/269 (99%)	-0.45	4 (1%) 73 77	17, 25, 43, 87	0
2	B	559/561 (99%)	-0.60	0 100 100	16, 25, 40, 55	0
2	D	561/561 (100%)	-0.30	11 (1%) 65 69	19, 32, 50, 84	0
2	F	561/561 (100%)	-0.32	14 (2%) 57 62	20, 31, 47, 80	0
2	H	559/561 (99%)	-0.47	2 (0%) 92 93	19, 28, 44, 58	0
All	All	3313/3320 (99%)	-0.40	42 (1%) 77 80	14, 28, 47, 87	0

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	1002	SER	5.0
1	G	3	ALA	5.0
1	E	3	ALA	4.6
2	F	1001	MET	4.6
1	G	270	PRO	4.3

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 [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	IMD	A	3002	5/5	0.93	0.11	37,38,39,42	0
5	IMD	G	3001	5/5	0.94	0.11	38,39,40,42	0
8	MG	B	2006	1/1	0.96	0.03	13,13,13,13	0
8	MG	D	2006	1/1	0.96	0.09	17,17,17,17	0
8	MG	H	2006	1/1	0.96	0.04	16,16,16,16	0
8	MG	F	2006	1/1	0.97	0.06	18,18,18,18	0
3	SF4	E	2001[A]	8/8	0.98	0.07	18,22,23,27	2
3	SF4	E	2001[B]	8/8	0.98	0.07	19,22,24,27	2
3	SF4	E	2002	8/8	0.98	0.04	14,16,18,18	0
7	NFV	D	2005	9/9	0.99	0.07	13,17,19,22	0
3	SF4	G	2002	8/8	0.99	0.03	14,15,15,15	0
6	CL	E	2004	1/1	0.99	0.13	24,24,24,24	0
3	SF4	C	2001[B]	8/8	0.99	0.08	16,19,22,26	2
6	CL	C	2004	1/1	0.99	0.12	20,20,20,20	0
3	SF4	A	2001[A]	8/8	0.99	0.11	15,18,21,21	2
7	NFV	F	2005	9/9	0.99	0.06	15,18,21,22	0
3	SF4	A	2001[B]	8/8	0.99	0.11	15,19,21,22	2
3	SF4	G	2001[B]	8/8	0.99	0.10	18,20,22,26	2
3	SF4	C	2001[A]	8/8	0.99	0.08	16,18,22,22	2
6	CL	A	2004	1/1	0.99	0.09	20,20,20,20	0
3	SF4	G	2001[A]	8/8	0.99	0.10	16,20,22,24	2
4	F3S	G	2003	7/7	0.99	0.04	14,15,16,16	0
4	F3S	E	2003	7/7	0.99	0.05	16,17,18,19	0
7	NFV	H	2005	9/9	1.00	0.09	13,15,20,22	0
4	F3S	A	2003	7/7	1.00	0.07	12,13,14,16	0
6	CL	G	2004	1/1	1.00	0.12	21,21,21,21	0
3	SF4	C	2002	8/8	1.00	0.04	14,15,16,17	0
4	F3S	C	2003	7/7	1.00	0.07	14,15,16,16	0
3	SF4	A	2002	8/8	1.00	0.04	12,13,14,14	0
7	NFV	B	2005	9/9	1.00	0.10	13,16,20,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.