



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 08:33 PM UTC

PDB ID : 1GN9 / pdb_00001gn9
Title : Hybrid Cluster Protein from *Desulfovibrio desulfuricans* ATCC 27774 X-ray structure at 2.6Å resolution using synchrotron radiation at a wavelength of 1.722Å
Authors : Macedo, S.; Mitchell, E.P.; Romao, C.V.; Cooper, S.J.; Coelho, R.; Liu, M.Y.; Xavier, A.V.; Legall, J.; Bailey, S.; Garner, D.C.; Hagen, W.R.; Teixeira, M.; Carrondo, M.A.; Lindley, P.
Deposited on : 2001-10-04
Resolution : 2.60 Å(reported)

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

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A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

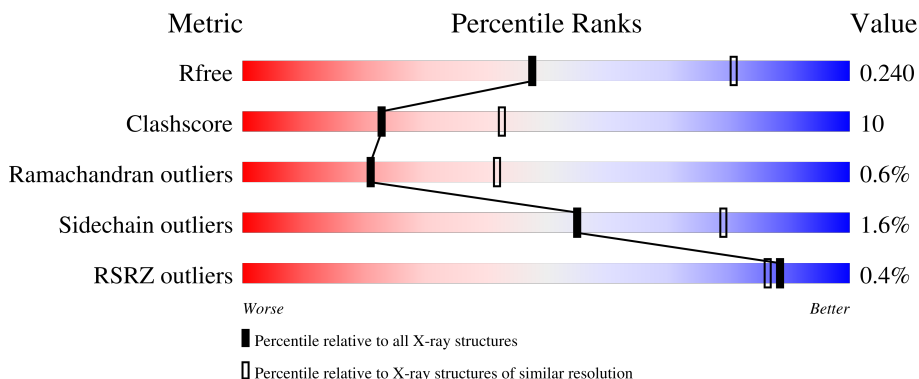
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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

Mol	Chain	Length	Quality of chain
1	A	544	 75% 24% .
1	B	544	 74% 24% .

2 Entry composition [i](#)

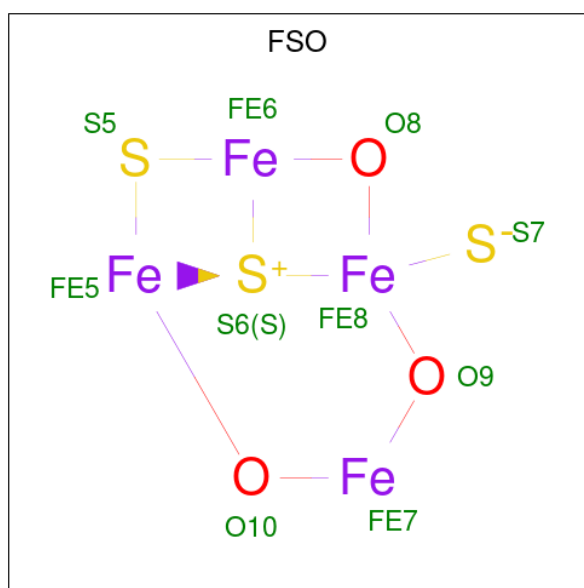
There are 4 unique types of molecules in this entry. The entry contains 8413 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 HYBRID CLUSTER PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	543	Total	C	N	O	S	0	0	0
			4087	2601	689	775	22			
1	B	543	Total	C	N	O	S	0	1	0
			4095	2604	689	780	22			

- Molecule 2 is IRON/SULFUR/OXYGEN HYBRID CLUSTER (CCD ID: FSO) (formula: $\text{Fe}_4\text{O}_3\text{S}_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	Fe	O	S	0	0
			7	4	1	2		
2	B	1	Total	Fe	O	S	0	0
			8	4	2	2		

- Molecule 3 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			8	4	4		
3	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	100	Total	O	0	0
			100	100		
4	B	100	Total	O	0	0
			100	100		

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

Chain A: 75% 24%

G438	D439	R445	V446	L447	D448	M453	S455	Y456	S457	I461	E467	V468	D473	D476	I479	V480	I483	K489	I492	L507	L511	P512	A513	F514	L515	A520	K521	V524	E525	I529	G530	S534	D537	A541	F542	F543	I548
N286	A287	V288	Q291	F295	L304	N307	C308	Y316	V320	I325	V326	I338	G339	E340	H341	K342	D343	F344	I348	G367	H371	L375	I382	I390	K392	F393	C399	R402	A403	S407	T420	V421	K429	Y430	A434	K434	L437
T134	T135	D136	D137	V138	R140	S141	L142	I146	L150	Y156	V162	L170	D171	M174	D183	L186	G202	D210	T214	Y217	P220	T223	K224	L236	T237	S238	D244	L249	V259	H262	L266	P267	Y270	Y271	K281	I132	

Chain B:

Amino Acid	Percentage
S1	74%
N2	74%
A3	74%
N4	74%
Y7	74%
Q8	74%
E11	74%
T12	24%
V13	24%
G17	74%
A32	74%
L33	74%
Q34	74%
L44	74%
I47	74%
D59	24%
H60	24%
R61	74%
F71	74%
A72	74%
I73	74%
I74	74%
D80	74%
I83	74%
E86	74%
R87	74%
H88	74%
R89	74%
N90	74%
T91	74%
C92	74%
K95	74%
K96	74%
D104	74%
E115	74%
K119	74%
A126	74%
G130	74%
D136	74%
D137	74%
D138	74%
N139	74%
F148	74%
A162	74%
K165	74%
E176	74%
K180	74%
T181	74%
L182	74%
V188	74%
V192	24%
G202	24%
M206	74%
A207	74%
L208	74%
A211	74%
T223	74%
N226	74%
I227	74%
G228	74%
L236	74%
I237	74%
S238	74%
G239	74%
H240	74%
D241	24%
L242	74%
R243	74%
E245	74%
M247	74%
L248	74%
T252	74%
Y260	74%
T261	74%
H262	74%
M265	74%
L266	74%
P267	74%
A268	74%
A307	74%
G398	74%
C399	74%
D400	74%
R406	74%
S407	74%
Y408	74%
Y409	24%
T410	74%
C427	74%
A428	74%
K434	74%
L437	74%
R445	74%
S465	74%
Y466	74%
S467	74%
V460	74%
I461	74%
A462	74%
L463	74%
K466	74%
I479	74%
I483	74%
A484	74%
E487	74%
Q488	24%
K489	74%
G490	74%
V491	74%
I492	74%
V493	74%
A496	74%
L497	74%
L498	74%
S499	74%
L500	74%
G501	74%
V502	74%
K503	74%
N518	74%
K521	74%
V524	74%
E525	74%
Q526	74%
F527	74%
N528	74%
I529	74%
T533	74%
S534	74%
F542	74%
F543	74%
GLY	74%

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.40Å 61.80Å 72.20Å 82.70° 73.70° 87.30°	Depositor
Resolution (Å)	25.01 – 2.60 25.01 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.3 (25.01-2.60) 96.3 (25.01-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.15 (at 2.60Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.193 , 0.260 (Not available) , 0.240	Depositor DCC
R_{free} test set	1440 reflections (2.61%)	wwPDB-VP
Wilson B-factor (Å ²)	12.5	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	8413	wwPDB-VP
Average B, all atoms (Å ²)	10.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.50% 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: SF4, FSO, CSS

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	0.42	0/4157	0.91	8/5637 (0.1%)
1	B	0.42	0/4165	0.93	16/5649 (0.3%)
All	All	0.42	0/8322	0.92	24/11286 (0.2%)

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	455	SER	N-CA-C	-9.40	101.07	112.54
1	B	137	ASP	N-CA-C	8.69	120.37	111.07
1	B	455	SER	N-CA-C	-8.37	102.97	113.01
1	A	407	SER	N-CA-C	-7.46	103.44	112.54
1	A	307	ASN	N-CA-C	-6.81	101.36	110.55

There are no chirality outliers.

There are no planarity outliers.

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	4087	0	4079	85	0
1	B	4095	0	4071	85	0
2	A	7	0	0	0	0
2	B	8	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	8	0	0	0	0
3	B	8	0	0	0	0
4	A	100	0	0	3	1
4	B	100	0	0	6	1
All	All	8413	0	8150	170	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 170 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:365:ILE:HD11	1:B:434:LYS:HE3	1.56	0.84
1:B:498:LEU:HD21	1:B:529:ILE:HD11	1.63	0.81
1:A:382:ILE:HD13	1:A:468:VAL:HG11	1.66	0.78
1:B:87:ARG:HA	1:B:90:MET:HE3	1.63	0.78
1:A:488:GLN:H	1:A:488:GLN:CD	1.93	0.77

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2033:HOH:O	4:B:2066:HOH:O[1_454]	1.95	0.25

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	540/544 (99%)	503 (93%)	32 (6%)	5 (1%)	14	30
1	B	541/544 (99%)	513 (95%)	27 (5%)	1 (0%)	43	66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1081/1088 (99%)	1016 (94%)	59 (6%)	6 (1%)	21	42

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	281	LYS
1	A	133	ALA
1	A	132	MET
1	A	542	PHE
1	A	131	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	426/432 (99%)	418 (98%)	8 (2%)	50	75
1	B	426/432 (99%)	420 (99%)	6 (1%)	59	81
All	All	852/864 (99%)	838 (98%)	14 (2%)	55	79

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	467	GLU
1	B	7	TYR
1	B	487	GLU
1	B	281	LYS
1	B	318	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	46	GLN
1	B	69	ASN
1	B	526	GLN

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Mol	Chain	Res	Type
1	B	269	HIS
1	B	518	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	CSS	B	399	2,1	4,6,7	1.17	0	2,6,8	0.69	0
1	CSS	A	399	2,1	4,6,7	1.49	1 (25%)	2,6,8	0.62	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSS	B	399	2,1	-	0/1/5/7	-
1	CSS	A	399	2,1	-	0/1/5/7	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	399	CSS	CA-N	-2.61	1.40	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	399	CSS	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	FSO	B	600	1	0,9,12	-	-	-		
3	SF4	B	650	1	0,12,12	-	-	-		
2	FSO	A	600	1	0,7,12	-	-	-		
3	SF4	A	650	1	0,12,12	-	-	-		

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	FSO	B	600	1	-	-	0/2/2/3
3	SF4	B	650	1	-	-	0/6/5/5
2	FSO	A	600	1	-	-	0/1/1/3
3	SF4	A	650	1	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	542/544 (99%)	-0.35	0	100 100	2, 10, 20, 35	0
1	B	542/544 (99%)	-0.35	4 (0%)	84 82	2, 10, 21, 44	1 (0%)
All	All	1084/1088 (99%)	-0.35	4 (0%)	88 86	2, 10, 21, 44	1 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	336	GLY	3.9
1	B	339	GLY	3.8
1	B	338	ILE	2.4
1	B	318	ASP	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CSS	B	399	7/8	0.97	0.06	7,7,18,18	0
1	CSS	A	399	7/8	0.98	0.06	6,6,8,15	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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
3	SF4	B	650	8/8	0.88	0.07	10,10,10,10	0
3	SF4	A	650	8/8	0.89	0.07	9,9,9,9	0
2	FSO	B	600	8/10	0.90	0.11	8,17,17,17	0
2	FSO	A	600	7/10	0.92	0.09	8,16,16,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.