



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:18 PM UTC

PDB ID : 6YUE / pdb_00006yue
Title : Fragment of nitrate/nitrite sensor histidine kinase NarQ (R50S variant)
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Deposited on : 2020-04-27
Resolution : 2.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
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)
Validation Pipeline (wwPDB-VP)	:	2.49

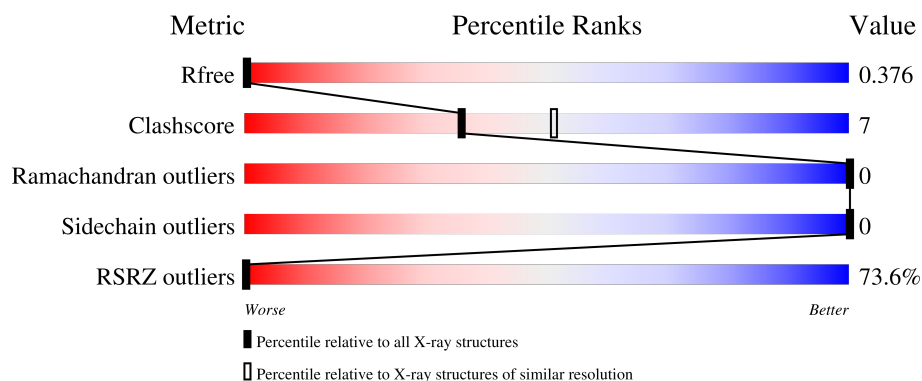
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	236	71% 81% 15% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1840 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 Nitrate/nitrite sensor protein NarQ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	227	Total	C	N	O	S	0	12	1
			1831	1186	319	321	5			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	SER	ARG	engineered mutation	UNP P27896
A	231	HIS	-	expression tag	UNP P27896
A	232	HIS	-	expression tag	UNP P27896
A	233	HIS	-	expression tag	UNP P27896
A	234	HIS	-	expression tag	UNP P27896
A	235	HIS	-	expression tag	UNP P27896
A	236	HIS	-	expression tag	UNP P27896

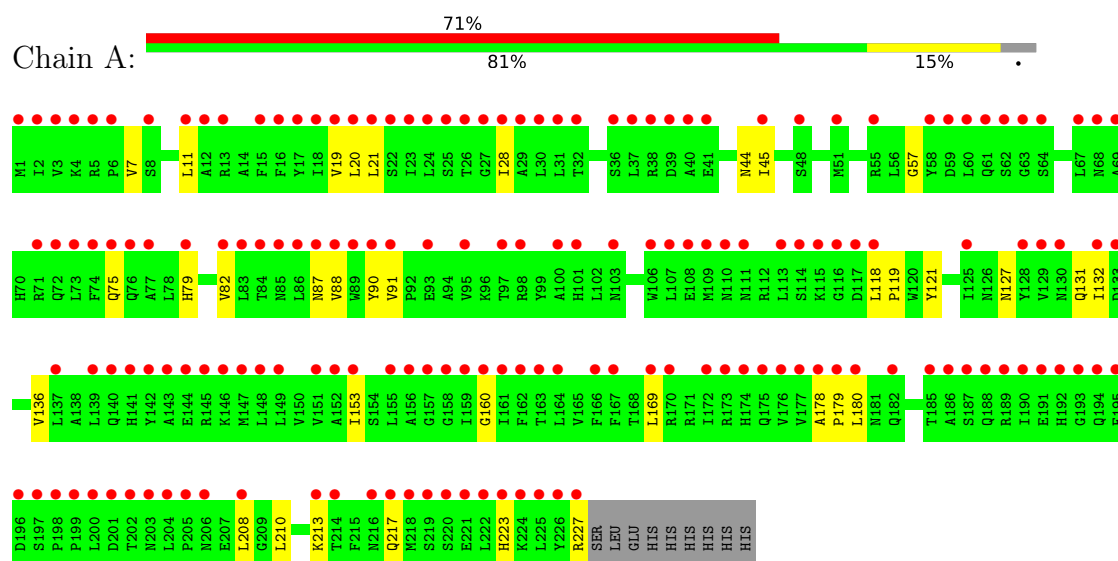
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	9	Total	O	0	0
			9	9		

3 Residue-property plots

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

- Molecule 1: Nitrate/nitrite sensor protein NarQ



4 Data and refinement statistics

Property	Value	Source
Space group	F 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	57.93Å 73.70Å 236.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.70 – 2.40 44.70 – 2.40	Depositor EDS
% Data completeness (in resolution range)	66.0 (44.70-2.40) 66.0 (44.70-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.77 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.285 , 0.367 0.288 , 0.376	Depositor DCC
R_{free} test set	337 reflections (3.31%)	wwPDB-VP
Wilson B-factor (Å ²)	40.6	Xtriage
Anisotropy	0.576	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 29.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	1840	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.98% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.33	0/1906	0.67	0/2597

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	1831	0	1885	27	0
2	A	9	0	0	1	0
All	All	1840	0	1885	27	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 7.

All (27) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:LEU:HB3	1:A:119:PRO:HD3	1.90	0.54
1:A:132:ILE:O	1:A:136:VAL:HG23	2.10	0.52
1:A:178:ALA:HB3	1:A:179:PRO:CD	2.40	0.52
1:A:75[B]:GLN:HE21	1:A:79:HIS:CE1	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:LEU:HG	1:A:208:LEU:HD21	1.90	0.52
1:A:87:ASN:OD1	2:A:302:HOH:O	2.20	0.50
1:A:44:ASN:OD1	1:A:44:ASN:C	2.56	0.49
1:A:179:PRO:HB2	1:A:208:LEU:HD22	1.95	0.49
1:A:57:GLY:HA3	1:A:121:TYR:CZ	2.47	0.49
1:A:178:ALA:HB3	1:A:179:PRO:HD3	1.95	0.48
1:A:118:LEU:N	1:A:119:PRO:CD	2.77	0.47
1:A:28:ILE:HG22	1:A:153[A]:ILE:HD13	1.98	0.46
1:A:88[B]:VAL:CG1	1:A:91:VAL:HG23	2.45	0.46
1:A:45:ILE:HD12	1:A:82:VAL:HG11	1.97	0.46
1:A:210:LEU:C	1:A:210:LEU:HD23	2.41	0.45
1:A:21:LEU:HD21	1:A:160:GLY:HA3	1.98	0.45
1:A:28:ILE:CG2	1:A:153[A]:ILE:HD13	2.46	0.45
1:A:179:PRO:HB2	1:A:208:LEU:CD2	2.49	0.43
1:A:19:VAL:O	1:A:20:LEU:C	2.61	0.43
1:A:88[A]:VAL:HG11	1:A:90:TYR:CE2	2.54	0.42
1:A:7[A]:VAL:HG12	1:A:11:LEU:CD1	2.50	0.42
1:A:213:LYS:O	1:A:217:GLN:HG2	2.19	0.42
1:A:57:GLY:HA3	1:A:121:TYR:CE1	2.55	0.41
1:A:88[B]:VAL:HG12	1:A:91:VAL:HG23	2.02	0.41
1:A:223:HIS:O	1:A:227:ARG:N	2.51	0.41
1:A:127:ASN:O	1:A:131[B]:GLN:HG2	2.21	0.40

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	237/236 (100%)	232 (98%)	5 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	201/205 (98%)	201 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	ASN
1	A	122	GLN
1	A	140	GLN
1	A	141	HIS
1	A	181	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	227/236 (96%)	3.01	167 (73%) 0 0	15, 36, 64, 78	20 (8%)

All (167) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	226	TYR	9.7
1	A	224	LYS	8.7
1	A	227	ARG	8.7
1	A	225[A]	LEU	8.4
1	A	1	MET	7.9
1	A	218	MET	6.3
1	A	37	LEU	6.3
1	A	223	HIS	6.3
1	A	39	ASP	6.3
1	A	118	LEU	6.0
1	A	217	GLN	5.8
1	A	219	SER	5.7
1	A	61	GLN	5.6
1	A	222	LEU	5.6
1	A	141	HIS	5.6
1	A	60	LEU	5.1
1	A	203	ASN	5.0
1	A	173	ARG	4.9
1	A	62	SER	4.8
1	A	13	ARG	4.8
1	A	143	ALA	4.8
1	A	199	PRO	4.8
1	A	76	GLN	4.8
1	A	90	TYR	4.8
1	A	21	LEU	4.7
1	A	89	TRP	4.7
1	A	195	PHE	4.7

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Mol	Chain	Res	Type	RSRZ
1	A	190	ILE	4.7
1	A	185	THR	4.6
1	A	191	GLU	4.5
1	A	144	GLU	4.5
1	A	221	GLU	4.4
1	A	59	ASP	4.4
1	A	23	ILE	4.3
1	A	28	ILE	4.3
1	A	194	GLN	4.3
1	A	193	GLY	4.3
1	A	189	ARG	4.3
1	A	198	PRO	4.2
1	A	40	ALA	4.2
1	A	140	GLN	4.2
1	A	116	GLY	4.2
1	A	158	GLY	4.1
1	A	106	TRP	4.1
1	A	147	MET	4.1
1	A	115	LYS	4.0
1	A	159	ILE	4.0
1	A	148	LEU	3.9
1	A	82	VAL	3.9
1	A	103	ASN	3.8
1	A	4	LYS	3.8
1	A	192	HIS	3.8
1	A	36	SER	3.7
1	A	88[A]	VAL	3.7
1	A	27	GLY	3.7
1	A	182	GLN	3.7
1	A	24	LEU	3.7
1	A	213	LYS	3.7
1	A	214	THR	3.7
1	A	22	SER	3.7
1	A	180	LEU	3.6
1	A	216	ASN	3.6
1	A	38	ARG	3.6
1	A	86	LEU	3.6
1	A	220	SER	3.6
1	A	145	ARG	3.5
1	A	97	THR	3.5
1	A	137	LEU	3.5
1	A	208	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	2	ILE	3.5
1	A	25	SER	3.4
1	A	156	ALA	3.4
1	A	196	ASP	3.4
1	A	87	ASN	3.4
1	A	93	GLU	3.4
1	A	117	ASP	3.3
1	A	11	LEU	3.3
1	A	200	LEU	3.3
1	A	26	THR	3.3
1	A	197	SER	3.3
1	A	15	PHE	3.2
1	A	75[A]	GLN	3.2
1	A	109	MET	3.2
1	A	67	LEU	3.2
1	A	164	LEU	3.2
1	A	205	PRO	3.2
1	A	201	ASP	3.1
1	A	157	GLY	3.1
1	A	166	PHE	3.1
1	A	188	GLN	3.0
1	A	155	LEU	3.0
1	A	172	ILE	3.0
1	A	41	GLU	3.0
1	A	107	LEU	3.0
1	A	5	ARG	3.0
1	A	178	ALA	3.0
1	A	163	THR	3.0
1	A	79	HIS	3.0
1	A	20	LEU	3.0
1	A	139	LEU	3.0
1	A	132	ILE	2.9
1	A	55	ARG	2.9
1	A	162	PHE	2.9
1	A	98	ARG	2.9
1	A	74	PHE	2.9
1	A	108	GLU	2.9
1	A	202	THR	2.9
1	A	17	TYR	2.9
1	A	71	ARG	2.9
1	A	64	SER	2.8
1	A	31	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	133	ASP	2.8
1	A	170	ARG	2.8
1	A	130[A]	ASN	2.8
1	A	30	LEU	2.8
1	A	142	TYR	2.8
1	A	153[A]	ILE	2.7
1	A	77	ALA	2.7
1	A	16	PHE	2.7
1	A	186	ALA	2.7
1	A	63	GLY	2.7
1	A	110	ASN	2.7
1	A	3	VAL	2.7
1	A	114	SER	2.7
1	A	68	ASN	2.7
1	A	45	ILE	2.6
1	A	152	ALA	2.6
1	A	179	PRO	2.6
1	A	6	PRO	2.6
1	A	85	ASN	2.6
1	A	149	LEU	2.5
1	A	129	VAL	2.5
1	A	204	LEU	2.5
1	A	167	PHE	2.5
1	A	95	VAL	2.4
1	A	161	ILE	2.4
1	A	169[A]	LEU	2.4
1	A	206	ASN	2.4
1	A	18	ILE	2.4
1	A	83	LEU	2.3
1	A	72	GLN	2.3
1	A	175	GLN	2.3
1	A	128	TYR	2.3
1	A	176	VAL	2.3
1	A	111	ASN	2.3
1	A	160	GLY	2.3
1	A	8[A]	SER	2.3
1	A	146	LYS	2.2
1	A	32	THR	2.2
1	A	113	LEU	2.2
1	A	19	VAL	2.2
1	A	91	VAL	2.2
1	A	187	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	29	ALA	2.2
1	A	100	ALA	2.2
1	A	177	VAL	2.1
1	A	101	HIS	2.1
1	A	174[A]	HIS	2.1
1	A	69	ALA	2.1
1	A	125	ILE	2.1
1	A	58	TYR	2.1
1	A	84	THR	2.1
1	A	51	MET	2.1
1	A	151	VAL	2.1
1	A	12	ALA	2.0
1	A	73	LEU	2.0
1	A	48	SER	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.