Full wwPDB X-ray Structure Validation Report (i)

Jun 16, 2024 – 06:46 AM EDT

PDB ID	:	4YE6
Title	:	The crystal structure of the intact human GlnRS
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Deposited on	:	2015-02-23
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 (i) 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 (1)) were used in the production of this report:

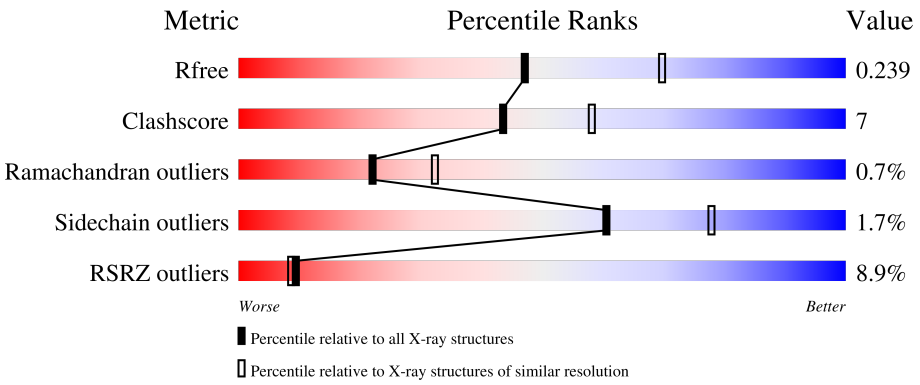
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (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 <=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	776	8%, 76%, 14%, •, 9%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 5477 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 Glutamine–tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	709	5240	3330	921	961	28	0	9	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	expression tag	UNP P47897

- Molecule 2 is water.

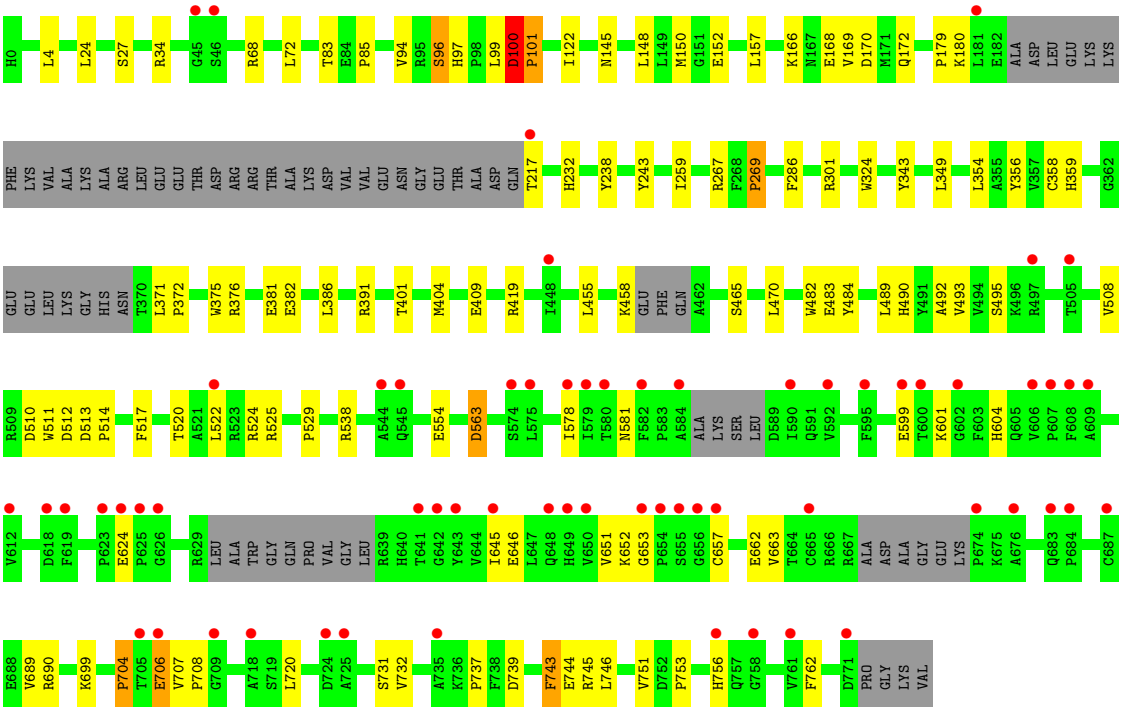
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	237	237	237	0	0

3 Residue-property plots (i)

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: Glutamine–tRNA ligase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	333.68Å 57.98Å 86.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.99 – 2.40 28.99 – 2.36	Depositor EDS
% Data completeness (in resolution range)	99.8 (28.99-2.40) 88.5 (28.99-2.36)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.62 (at 2.36Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.210 , 0.239 0.216 , 0.239	Depositor DCC
R_{free} test set	3358 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å^2)	45.3	Xtriage
Anisotropy	0.227	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 62.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	5477	wwPDB-VP
Average B, all atoms (Å^2)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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	0.50	2/5384 (0.0%)	0.64	2/7336 (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	A	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	706	GLU	CB-CG	8.19	1.67	1.52
1	A	704	PRO	CG-CD	6.22	1.71	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	24	LEU	CA-CB-CG	6.16	129.46	115.30
1	A	645	ILE	N-CA-C	5.38	125.52	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	100	ASP	Peptide
1	A	581	ASN	Peptide
1	A	743	PHE	Peptide

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	5240	0	4741	67	0
2	A	237	0	0	3	0
All	All	5477	0	4741	67	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 (67) 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:96:SER:O	1:A:97:HIS:ND1	1.73	1.20
1:A:68:ARG:NH2	1:A:97:HIS:O	2.07	0.87
1:A:83:THR:HG22	1:A:85:PRO:HD2	1.55	0.86
1:A:96:SER:C	1:A:97:HIS:HD1	1.87	0.78
1:A:404:MET:HE3	1:A:470:LEU:HD13	1.72	0.71
1:A:651:VAL:HG12	1:A:652:LYS:H	1.63	0.63
1:A:99:LEU:O	1:A:101:PRO:HD3	2.00	0.61
1:A:743:PHE:HB3	1:A:746:LEU:HD13	1.84	0.59
1:A:217:THR:HG21	1:A:538:ARG:HG2	1.84	0.59
1:A:525:ARG:NH2	1:A:554:GLU:OE2	2.34	0.58
1:A:324:TRP:CE2	1:A:529:PRO:HG3	2.37	0.58
1:A:4:LEU:O	1:A:34[A]:ARG:NH2	2.23	0.58
1:A:706:GLU:HB3	1:A:708:PRO:HD3	1.85	0.57
1:A:704:PRO:HB2	1:A:707:VAL:HA	1.86	0.56
1:A:508:VAL:HG13	1:A:513:ASP:HB3	1.89	0.54
1:A:238:TYR:HA	1:A:243:TYR:CD2	2.43	0.53
1:A:148:LEU:O	1:A:152:GLU:HG3	2.09	0.53
1:A:68:ARG:HG3	1:A:94:VAL:HG13	1.91	0.52
1:A:179:PRO:HG3	1:A:259:ILE:HG12	1.91	0.52
1:A:653:GLY:N	1:A:657:CYS:O	2.40	0.52
1:A:490:HIS:HB3	1:A:699:LYS:O	2.10	0.52
1:A:356:TYR:CD2	1:A:376:ARG:HA	2.45	0.51
1:A:524:ARG:HE	1:A:753:PRO:HD2	1.74	0.51
1:A:343:TYR:CZ	1:A:391:ARG:HD2	2.46	0.51
1:A:419[A]:ARG:NE	2:A:887:HOH:O	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:745:ARG:H	1:A:746:LEU:HD12	1.76	0.50
1:A:737:PRO:HA	1:A:751:VAL:HB	1.95	0.49
1:A:122:ILE:HA	1:A:157:LEU:HD11	1.95	0.48
1:A:232:HIS:HD2	2:A:984:HOH:O	1.96	0.48
1:A:269:PRO:HA	1:A:301:ARG:O	2.13	0.48
1:A:690:ARG:HB3	1:A:720:LEU:HD21	1.96	0.48
1:A:514:PRO:HB3	1:A:525:ARG:HB2	1.95	0.48
1:A:145:ASN:HB3	1:A:148:LEU:HD13	1.97	0.47
1:A:599:GLU:C	1:A:601:LYS:H	2.18	0.46
1:A:482:TRP:CZ3	1:A:484:TYR:HB3	2.50	0.46
1:A:404:MET:HE1	1:A:470:LEU:HD22	1.96	0.46
1:A:122:ILE:HG12	1:A:157:LEU:HD13	1.98	0.46
1:A:371:LEU:HD12	1:A:372:PRO:HD2	1.98	0.46
1:A:99:LEU:C	1:A:101:PRO:CD	2.85	0.45
1:A:356:TYR:CE2	1:A:358:CYS:HB2	2.52	0.45
1:A:72:LEU:HD11	1:A:94:VAL:HG21	2.00	0.44
1:A:458:LYS:HG2	1:A:483:GLU:HB2	1.99	0.44
1:A:382:GLU:O	1:A:386:LEU:HG	2.18	0.44
1:A:704:PRO:HA	1:A:708:PRO:HD2	2.00	0.44
1:A:510:ASP:HB3	1:A:512[B]:ASP:OD1	2.18	0.44
1:A:180:LYS:N	2:A:1027:HOH:O	2.46	0.44
1:A:359:HIS:HB2	1:A:375:TRP:CH2	2.53	0.44
1:A:517:PHE:HA	1:A:522:LEU:HD21	2.00	0.43
1:A:646:GLU:O	1:A:663:VAL:HA	2.18	0.43
1:A:349[A]:LEU:HG	1:A:354:LEU:HB2	2.00	0.42
1:A:689:VAL:HG22	1:A:762:PHE:HB2	2.00	0.42
1:A:286:PHE:CD2	1:A:455:LEU:HD13	2.53	0.42
1:A:578:ILE:O	1:A:662:GLU:HA	2.20	0.42
1:A:704:PRO:CB	1:A:707:VAL:HA	2.50	0.42
1:A:68:ARG:NH1	1:A:100:ASP:HA	2.35	0.41
1:A:563:ASP:OD1	1:A:563:ASP:N	2.53	0.41
1:A:381[B]:GLU:H	1:A:381[B]:GLU:CD	2.23	0.41
1:A:166:LYS:NZ	1:A:170:ASP:OD2	2.43	0.41
1:A:409:GLU:OE2	1:A:465:SER:HB2	2.20	0.41
1:A:511:TRP:CZ3	1:A:520:THR:HG21	2.55	0.41
1:A:739:ASP:O	1:A:751:VAL:HG23	2.21	0.41
1:A:489:LEU:O	1:A:492:ALA:HB3	2.21	0.41
1:A:150:MET:HG3	1:A:169:VAL:HG21	2.03	0.41
1:A:101:PRO:CD	1:A:101:PRO:O	2.69	0.40
1:A:168:GLU:OE2	1:A:172:GLN:NE2	2.34	0.40
1:A:267:ARG:NH1	1:A:269:PRO:HG3	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:604:HIS:CD2	1:A:731:SER:HB2	2.57	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	704/776 (91%)	647 (92%)	52 (7%)	5 (1%)	22 32

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	100	ASP
1	A	269	PRO
1	A	101	PRO
1	A	624	GLU
1	A	732	VAL

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	479/666 (72%)	471 (98%)	8 (2%)	60 78

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	SER
1	A	96	SER
1	A	401	THR
1	A	493	VAL
1	A	495	SER
1	A	563	ASP
1	A	744	GLU
1	A	756	HIS

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

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 monosaccharides 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 (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	709/776 (91%)	0.25	63 (8%) 9 9	29, 73, 145, 160	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	650	VAL	6.1
1	A	619	PHE	6.0
1	A	643	TYR	5.6
1	A	649	HIS	5.6
1	A	584	ALA	5.5
1	A	623	PRO	5.3
1	A	625	PRO	5.1
1	A	606	VAL	4.8
1	A	656	GLY	4.7
1	A	595	PHE	4.7
1	A	578	ILE	4.6
1	A	608	PHE	4.5
1	A	579	ILE	4.4
1	A	575	LEU	4.1
1	A	609	ALA	3.9
1	A	657	CYS	3.9
1	A	626	GLY	3.9
1	A	676	ALA	3.9
1	A	645	ILE	3.6
1	A	687	CYS	3.4
1	A	580	THR	3.3
1	A	607	PRO	3.3
1	A	599	GLU	3.3
1	A	574	SER	3.3
1	A	674	PRO	3.2
1	A	641	THR	3.2
1	A	684	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	709	GLY	3.2
1	A	217	THR	3.1
1	A	705	THR	3.1
1	A	45	GLY	3.0
1	A	46	SER	3.0
1	A	648	GLN	2.9
1	A	612	VAL	2.8
1	A	618	ASP	2.8
1	A	725	ALA	2.8
1	A	706	GLU	2.8
1	A	735	ALA	2.7
1	A	545	GLN	2.7
1	A	771	ASP	2.7
1	A	497	ARG	2.6
1	A	544	ALA	2.6
1	A	505	THR	2.6
1	A	724	ASP	2.6
1	A	756	HIS	2.6
1	A	590	ILE	2.5
1	A	758	GLY	2.5
1	A	602	GLY	2.5
1	A	653	GLY	2.5
1	A	654	PRO	2.5
1	A	655	SER	2.5
1	A	181	LEU	2.4
1	A	665	CYS	2.4
1	A	624	GLU	2.4
1	A	683	GLN	2.3
1	A	718	ALA	2.3
1	A	522	LEU	2.2
1	A	582	PHE	2.2
1	A	761	VAL	2.1
1	A	600	THR	2.1
1	A	642	GLY	2.0
1	A	592	VAL	2.0
1	A	448	ILE	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 monosaccharides 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.