



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 02:55 PM UTC

PDB ID : 6GQ3 / pdb_00006gq3
Title : Human asparagine synthetase (ASNS) in complex with 6-diazo-5-oxo-L-norleucine (DON) at 1.85 Å resolution
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Deposited on : 2018-06-07
Resolution : 1.85 Å (reported)

This is a Full wwPDB X-ray Structure Validation 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

<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
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)
Validation Pipeline (wwPDB-VP)	:	2.49

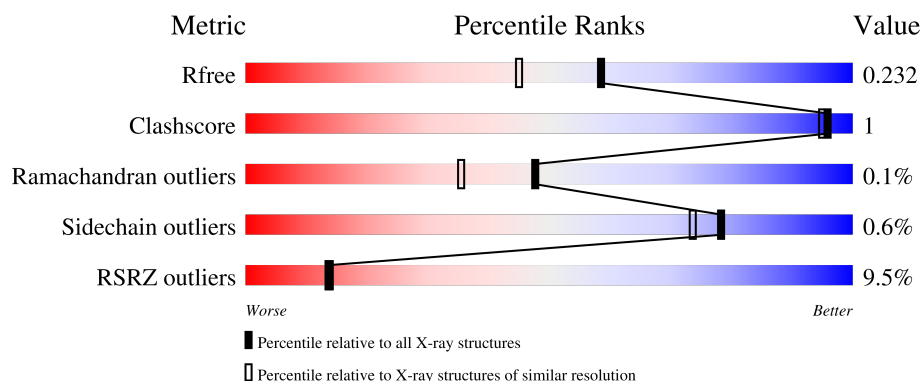
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	561	7% 88% 9%
1	B	561	10% 88% 9%

2 Entry composition [i](#)

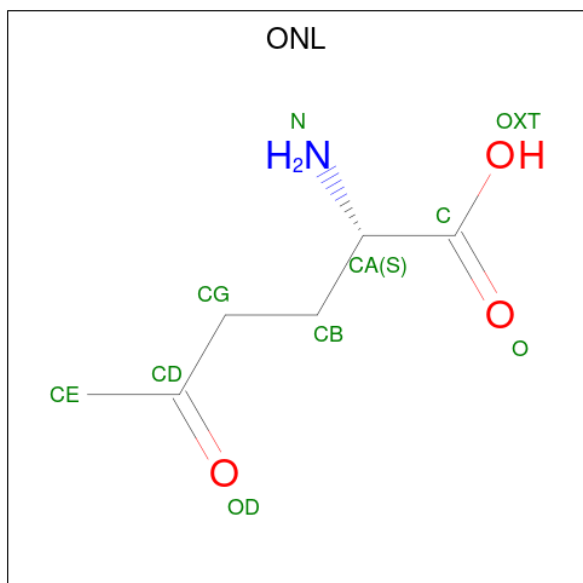
There are 6 unique types of molecules in this entry. The entry contains 8899 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Asparagine synthetase [glutamine-hydrolyzing].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	509	Total	C	N	O	S	0	3	0
			4135	2666	695	751	23			
1	B	509	Total	C	N	O	S	0	2	0
			4128	2661	694	750	23			

- Molecule 2 is 5-OXO-L-NORLEUCINE (CCD ID: ONL) (formula: C₆H₁₁NO₃).



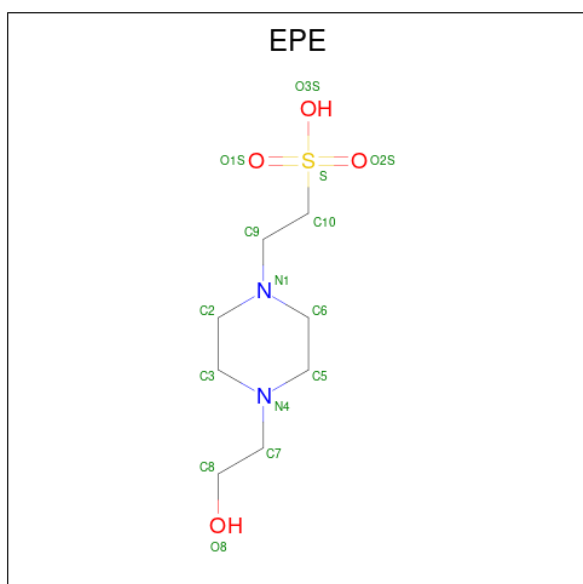
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	6	1	3		
2	B	1	Total	C	N	O	0	0
			10	6	1	3		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
4	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		
5	B	1	Total	Cl	0	0
			1	1		

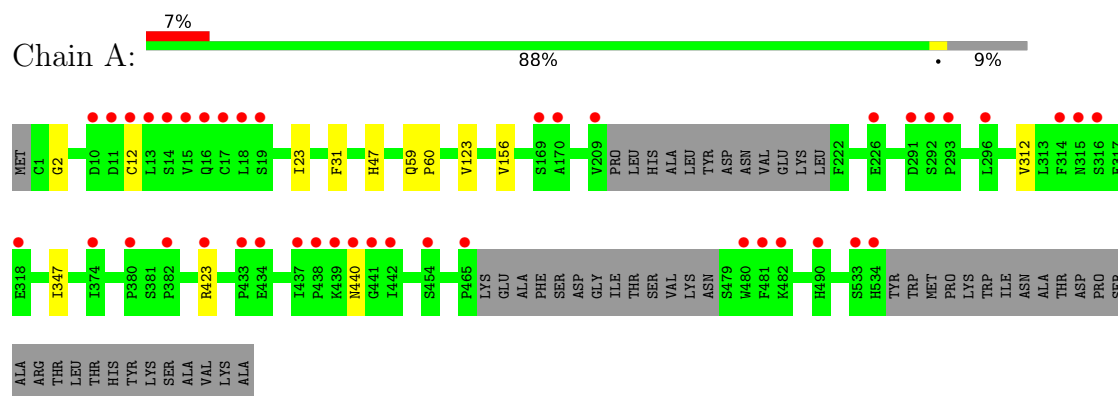
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	301	Total	O	0	0
			301	301		
6	B	267	Total	O	0	0
			267	267		

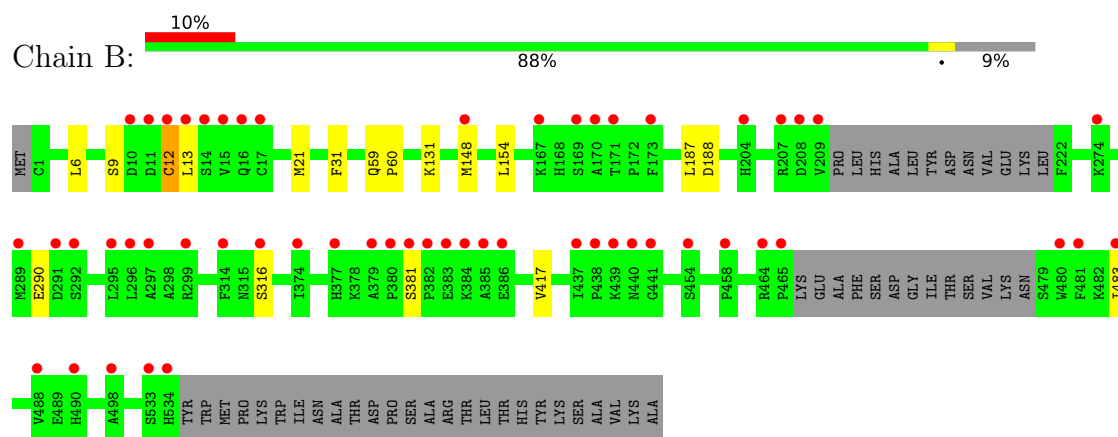
3 Residue-property plots [i](#)

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: Asparagine synthetase [glutamine-hydrolyzing]



- Molecule 1: Asparagine synthetase [glutamine-hydrolyzing]



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.70Å 83.52Å 110.29Å 90.00° 90.65° 90.00°	Depositor
Resolution (Å)	33.65 – 1.85 33.65 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.8 (33.65-1.85) 99.8 (33.65-1.85)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.178 , 0.225 0.187 , 0.232	Depositor DCC
R_{free} test set	4876 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	22.1	Xtriage
Anisotropy	0.429	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.119 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8899	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.30% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, EPE, ONL, EDO

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	0.74	0/4245	0.86	0/5738
1	B	0.69	0/4238	0.85	1/5728 (0.0%)
All	All	0.72	0/8483	0.85	1/11466 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	381	SER	N-CA-C	6.27	113.65	108.07

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	4135	0	4080	6	0
1	B	4128	0	4072	12	0
2	A	10	0	8	0	0
2	B	10	0	8	0	0
3	A	12	0	18	0	0
3	B	4	0	6	0	0
4	A	15	0	18	0	0
4	B	15	0	18	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	301	0	0	1	0
6	B	267	0	0	0	0
All	All	8899	0	8228	18	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 1.

All (18) 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:148:MET:HE3	1:B:154:LEU:HD13	1.65	0.77
1:B:316:SER:HB2	1:B:483:ILE:HG21	1.69	0.75
1:B:148:MET:HE2	1:B:154:LEU:HB2	1.75	0.66
1:B:148:MET:CE	1:B:154:LEU:HD13	2.31	0.61
1:B:148:MET:HE1	1:B:187:LEU:CD2	2.31	0.59
1:B:148:MET:HE1	1:B:187:LEU:HD21	1.90	0.53
1:B:59:GLN:HA	1:B:60:PRO:C	2.37	0.49
1:B:9:SER:HB3	1:B:12:CYS:HB3	1.94	0.49
1:B:12:CYS:O	1:B:12:CYS:SG	2.71	0.48
1:A:423:ARG:NE	6:A:702:HOH:O	2.46	0.48
1:A:59:GLN:HA	1:A:60:PRO:C	2.38	0.48
1:A:31:PHE:CD1	1:A:47:HIS:CE1	3.03	0.47
1:B:6:LEU:HD12	1:B:12:CYS:HB2	1.98	0.46
1:A:123[B]:VAL:HG21	1:A:156:VAL:HG21	1.98	0.44
1:B:21:MET:HE1	1:B:31:PHE:CE2	2.52	0.44
1:B:131:LYS:NZ	1:B:188:ASP:OD1	2.52	0.42
1:A:2:GLY:HA3	1:A:23:ILE:HD12	2.03	0.41
1:A:312:VAL:HG21	1:A:347:ILE:CD1	2.51	0.41

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	506/561 (90%)	496 (98%)	10 (2%)	0	100	100
1	B	505/561 (90%)	488 (97%)	16 (3%)	1 (0%)	43	31
All	All	1011/1122 (90%)	984 (97%)	26 (3%)	1 (0%)	48	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	13	LEU

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	448/490 (91%)	446 (100%)	2 (0%)	84	82
1	B	447/490 (91%)	444 (99%)	3 (1%)	76	70
All	All	895/980 (91%)	890 (99%)	5 (1%)	78	73

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	CYS
1	A	440	ASN
1	B	12	CYS
1	B	290	GLU
1	B	417	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	GLN
1	A	279	GLN

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Mol	Chain	Res	Type
1	A	502	GLN
1	A	519	GLN
1	B	85	GLN
1	B	272	GLN
1	B	371	GLN
1	B	485	GLN

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](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	EPE	A	605	-	15,15,15	2.00	1 (6%)	19,20,20	1.15	2 (10%)
2	ONL	B	601	1	8,9,9	0.77	0	8,11,11	1.34	1 (12%)
3	EDO	B	602	-	3,3,3	0.46	0	2,2,2	0.17	0
3	EDO	A	602	-	3,3,3	0.45	0	2,2,2	0.31	0
3	EDO	A	604	-	3,3,3	0.44	0	2,2,2	0.37	0
3	EDO	A	603	-	3,3,3	0.34	0	2,2,2	0.53	0
2	ONL	A	601	1	8,9,9	0.68	0	8,11,11	1.39	1 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EPE	B	603	-	15,15,15	2.01	1 (6%)	19,20,20	1.07	1 (5%)

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	EPE	A	605	-	-	5/9/19/19	0/1/1/1
2	ONL	B	601	1	-	2/9/9/9	-
3	EDO	B	602	-	-	0/1/1/1	-
3	EDO	A	602	-	-	0/1/1/1	-
3	EDO	A	604	-	-	1/1/1/1	-
3	EDO	A	603	-	-	0/1/1/1	-
2	ONL	A	601	1	-	2/9/9/9	-
4	EPE	B	603	-	-	2/9/19/19	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	603	EPE	C10-S	-7.41	1.67	1.77
4	A	605	EPE	C10-S	-7.18	1.67	1.77

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	605	EPE	O1S-S-C10	3.29	111.70	106.73
2	B	601	ONL	CB-CG-CD	-3.28	109.66	114.77
2	A	601	ONL	CB-CG-CD	-2.99	110.10	114.77
4	B	603	EPE	O1S-S-C10	2.64	110.72	106.73
4	A	605	EPE	O3S-S-C10	2.02	109.96	106.00

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	ONL	CE-CD-CG-CB
2	A	601	ONL	CE-CD-CG-CB
2	B	601	ONL	OD-CD-CG-CB
4	A	605	EPE	C9-C10-S-O1S

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Mol	Chain	Res	Type	Atoms
4	B	603	EPE	C9-C10-S-O2S
2	A	601	ONL	OD-CD-CG-CB
4	A	605	EPE	C10-C9-N1-C2
4	A	605	EPE	C9-C10-S-O3S
4	B	603	EPE	C9-C10-S-O3S
4	A	605	EPE	C9-C10-S-O2S
4	A	605	EPE	C10-C9-N1-C6
3	A	604	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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	509/561 (90%)	0.06	42 (8%) 17 18	7, 22, 74, 133	3 (0%)
1	B	509/561 (90%)	0.45	55 (10%) 11 10	12, 30, 91, 138	3 (0%)
All	All	1018/1122 (90%)	0.25	97 (9%) 14 14	7, 26, 86, 138	6 (0%)

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	209	VAL	7.0
1	A	12	CYS	6.9
1	A	481	PHE	6.0
1	B	13	LEU	6.0
1	B	12	CYS	5.8
1	B	380	PRO	5.7
1	A	314	PHE	5.5
1	B	481	PHE	5.4
1	B	382	PRO	4.6
1	A	438	PRO	4.6
1	A	13	LEU	4.5
1	A	437	ILE	4.5
1	B	437	ILE	4.5
1	A	534	HIS	4.1
1	B	438	PRO	4.1
1	B	374	ILE	4.1
1	B	15	VAL	4.0
1	A	16	GLN	3.9
1	B	207	ARG	3.8
1	B	14	SER	3.8
1	A	441	GLY	3.8
1	B	16	GLN	3.8
1	B	296	LEU	3.8
1	A	14	SER	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	465	PRO	3.7
1	B	488	VAL	3.7
1	B	379	ALA	3.6
1	B	490	HIS	3.6
1	B	11	ASP	3.6
1	B	534	HIS	3.4
1	B	148	MET	3.4
1	A	315	ASN	3.3
1	B	385	ALA	3.3
1	A	11	ASP	3.3
1	B	439	LYS	3.2
1	B	440	ASN	3.2
1	A	18	LEU	3.2
1	A	10	ASP	3.2
1	A	490	HIS	3.2
1	B	208	ASP	3.1
1	A	382	PRO	3.1
1	B	292	SER	3.1
1	B	498	ALA	3.1
1	A	439	LYS	3.1
1	A	19	SER	3.1
1	B	204	HIS	3.1
1	A	15	VAL	3.0
1	B	173	PHE	3.0
1	A	209	VAL	2.9
1	B	441	GLY	2.9
1	B	295	LEU	2.9
1	A	374	ILE	2.8
1	A	170	ALA	2.8
1	A	480	TRP	2.8
1	B	169	SER	2.7
1	B	289	MET	2.7
1	A	169	SER	2.7
1	B	464	ARG	2.7
1	B	377	HIS	2.7
1	A	423	ARG	2.7
1	B	381	SER	2.6
1	B	170	ALA	2.6
1	B	10	ASP	2.6
1	A	292	SER	2.6
1	A	533	SER	2.6
1	A	316	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	314	PHE	2.5
1	A	440	ASN	2.5
1	A	434	GLU	2.5
1	A	17	CYS	2.4
1	A	291	ASP	2.4
1	B	386	GLU	2.4
1	A	454	SER	2.4
1	B	171	THR	2.4
1	A	293	PRO	2.4
1	B	297	ALA	2.3
1	A	482	LYS	2.3
1	B	480	TRP	2.3
1	B	274	LYS	2.3
1	B	458	PRO	2.3
1	B	316	SER	2.3
1	B	17	CYS	2.3
1	A	296	LEU	2.3
1	B	454	SER	2.2
1	B	384	LYS	2.2
1	A	442	ILE	2.2
1	B	299	ARG	2.2
1	A	318	GLU	2.2
1	B	383	GLU	2.2
1	B	533	SER	2.1
1	B	465	PRO	2.1
1	A	226	GLU	2.1
1	B	291	ASP	2.1
1	A	380	PRO	2.0
1	A	433	PRO	2.0
1	B	167	LYS	2.0
1	B	483	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 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
4	EPE	B	603	15/15	0.87	0.13	28,41,103,105	0
4	EPE	A	605	15/15	0.90	0.12	25,35,71,200	0
3	EDO	A	604	4/4	0.90	0.17	28,33,75,88	0
3	EDO	A	603	4/4	0.91	0.10	25,28,37,39	0
3	EDO	A	602	4/4	0.92	0.09	25,28,33,34	0
2	ONL	B	601	10/10	0.94	0.07	15,19,25,32	0
3	EDO	B	602	4/4	0.96	0.07	23,30,31,33	0
2	ONL	A	601	10/10	0.97	0.06	10,12,18,25	0
5	CL	A	606	1/1	1.00	0.02	13,13,13,13	0
5	CL	B	604	1/1	1.00	0.03	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.