



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:35 PM UTC

PDB ID : 3UJS / pdb_00003ujs
Title : Asymmetric complex of human neuron specific enolase-6-PGA/PEP
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Deposited on : 2011-11-08
Resolution : 1.65 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
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

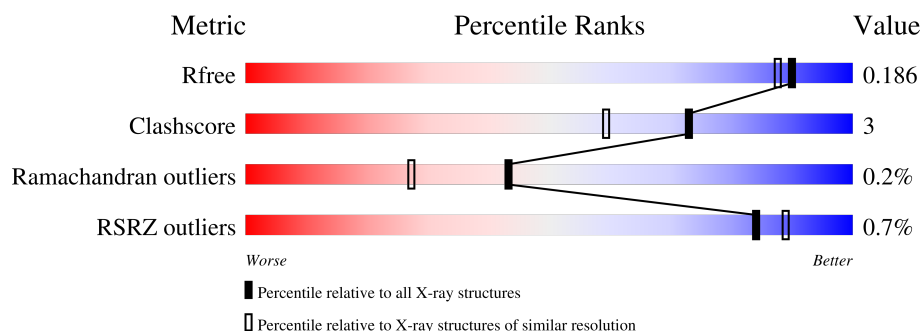
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	443	
1	B	443	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7359 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 Gamma-enolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	433	Total	C	N	O	S	0	0	0
			3251	2058	558	622	13			
1	B	433	Total	C	N	O	S	0	0	0
			3269	2068	556	632	13			

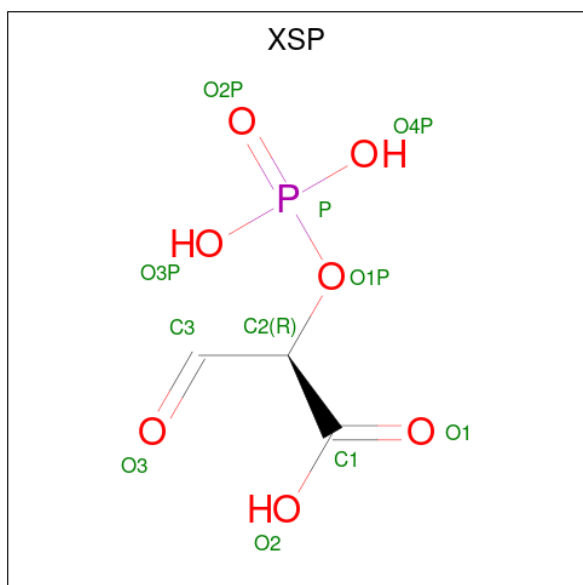
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	434	HIS	-	expression tag	UNP P09104
A	435	HIS	-	expression tag	UNP P09104
A	436	HIS	-	expression tag	UNP P09104
A	437	HIS	-	expression tag	UNP P09104
A	438	HIS	-	expression tag	UNP P09104
A	439	HIS	-	expression tag	UNP P09104
A	440	HIS	-	expression tag	UNP P09104
A	441	HIS	-	expression tag	UNP P09104
A	442	HIS	-	expression tag	UNP P09104
A	443	HIS	-	expression tag	UNP P09104
B	434	HIS	-	expression tag	UNP P09104
B	435	HIS	-	expression tag	UNP P09104
B	436	HIS	-	expression tag	UNP P09104
B	437	HIS	-	expression tag	UNP P09104
B	438	HIS	-	expression tag	UNP P09104
B	439	HIS	-	expression tag	UNP P09104
B	440	HIS	-	expression tag	UNP P09104
B	441	HIS	-	expression tag	UNP P09104
B	442	HIS	-	expression tag	UNP P09104
B	443	HIS	-	expression tag	UNP P09104

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mg	0	0
			2	2		
2	B	2	Total	Mg	0	0
			2	2		

- Molecule 3 is (2R)-3-oxo-2-(phosphonoxy)propanoic acid (CCD ID: XSP) (formula: $C_3H_5O_7P$).



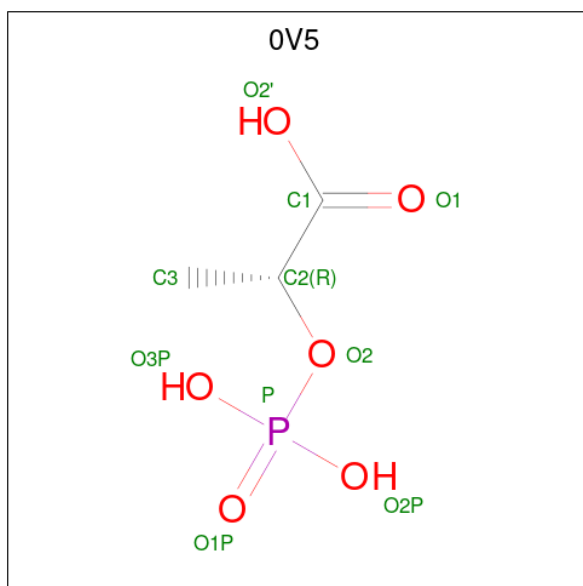
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			11	3	7	1		

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 5 is (2R)-2-(phosphonooxy)propanoic acid (CCD ID: 0V5) (formula: $C_3H_7O_6P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	O	P	0	0
			10	3	6	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	381	Total 381	O 381	0	0
6	B	425	Total 425	O 425	0	0

- Molecule 1: Gamma-enolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	114.45Å 119.82Å 68.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.84 – 1.65 43.84 – 1.65	Depositor EDS
% Data completeness (in resolution range)	99.3 (43.84-1.65) 99.3 (43.84-1.65)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.20 (at 1.65Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.135 , 0.185 (Not available) , 0.186	Depositor DCC
R_{free} test set	5776 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	17.1	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 52.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.017 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7359	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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: XSP, MG, TRS, OV5

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	1.50	14/3306 (0.4%)	1.24	6/4478 (0.1%)
1	B	1.56	9/3324 (0.3%)	1.25	11/4502 (0.2%)
All	All	1.53	23/6630 (0.3%)	1.24	17/8980 (0.2%)

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	143	ILE	CA-CB	6.52	1.62	1.54
1	A	38	ALA	N-CA	6.20	1.53	1.46
1	A	277	ALA	CA-CB	6.10	1.63	1.53
1	A	420	ALA	CA-CB	5.90	1.62	1.53
1	A	415	GLU	CB-CG	5.64	1.69	1.52
1	A	395	GLY	C-O	5.64	1.28	1.23
1	A	215	ASN	CA-C	-5.59	1.47	1.53
1	B	321	VAL	CA-CB	5.55	1.62	1.54
1	A	381	ALA	N-CA	5.43	1.52	1.46
1	B	287	PRO	CA-CB	5.37	1.60	1.53
1	B	150	ASN	CA-CB	5.35	1.59	1.53
1	A	353	ILE	C-O	5.35	1.30	1.24
1	A	299	ASP	N-CA	5.23	1.53	1.46
1	B	45	ALA	N-CA	5.23	1.52	1.46
1	A	106	GLY	N-CA	5.14	1.52	1.45
1	B	17	PRO	C-O	5.14	1.29	1.23
1	B	322	THR	CA-CB	5.13	1.61	1.53
1	A	171	PRO	CA-C	5.10	1.57	1.52
1	A	291	ILE	CA-CB	5.10	1.60	1.54
1	B	73	ALA	C-O	5.10	1.29	1.24
1	A	102	LYS	N-CA	5.09	1.54	1.46
1	B	374	GLU	CA-CB	5.09	1.61	1.53
1	B	231	ASP	CB-CG	5.06	1.64	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	78	SER	CA-CB-OG	-7.81	95.48	111.10
1	B	151	VAL	N-CA-C	6.67	121.22	113.42
1	B	357	LYS	CD-CE-NZ	6.04	131.24	111.90
1	B	153	ASN	N-CA-C	5.86	118.61	109.52
1	A	262	SER	CA-C-N	-5.84	113.94	119.90
1	A	262	SER	C-N-CA	-5.84	113.94	119.90
1	B	365	GLY	N-CA-C	-5.52	103.96	112.85
1	A	104	LYS	CD-CE-NZ	-5.23	95.16	111.90
1	A	428	ARG	N-CA-C	-5.23	105.66	111.36
1	A	72	ILE	N-CA-C	5.23	115.44	110.42
1	B	265	ASP	CA-C-N	5.15	124.87	119.82
1	B	265	ASP	C-N-CA	5.15	124.87	119.82
1	A	177	PHE	CA-CB-CG	-5.12	108.69	113.80
1	B	429	ASN	N-CA-CB	-5.08	104.97	110.71
1	B	73	ALA	CA-C-N	-5.07	113.81	119.19
1	B	73	ALA	C-N-CA	-5.07	113.81	119.19
1	B	19	VAL	CB-CA-C	-5.05	104.65	110.91

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	3251	0	3201	22	0
1	B	3269	0	3220	21	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	11	0	3	0	0
4	A	8	0	12	0	0
5	B	10	0	6	1	0
6	A	381	0	0	4	3
6	B	425	0	0	5	3
All	All	7359	0	6442	41	3

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 3.

All (41) 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:357:LYS:HD2	6:B:932:HOH:O	1.34	1.27
1:A:178:ARG:HD3	1:A:413:GLU:OE1	1.49	1.10
1:B:353:ILE:HG22	1:B:357:LYS:HE2	1.50	0.91
1:B:314:ILE:H	1:B:337:ASN:HD21	1.34	0.73
1:A:101:ASN:H	1:A:101:ASN:HD22	1.42	0.64
1:B:101:ASN:HD22	1:B:101:ASN:H	1.46	0.63
1:B:314:ILE:H	1:B:337:ASN:ND2	1.97	0.63
1:A:314:ILE:H	1:A:337:ASN:HD21	1.48	0.60
1:B:337:ASN:C	1:B:337:ASN:HD22	2.10	0.58
1:B:265:ASP:O	1:B:268:ARG:HG2	2.03	0.57
1:A:314:ILE:H	1:A:337:ASN:ND2	2.03	0.56
1:A:227:LYS:HE2	1:A:231:ASP:OD2	2.07	0.55
1:B:166:GLU:OE2	5:B:602:OV5:H4	2.07	0.54
1:A:215:ASN:CB	1:B:202:ASP:OD2	2.57	0.53
1:A:418:ASP:HA	6:A:1033:HOH:O	2.07	0.53
1:B:125:ARG:HD2	6:B:1070:HOH:O	2.07	0.53
1:B:328:GLU:HG3	6:B:1039:HOH:O	2.10	0.52
1:B:429:ASN:ND2	6:B:1046:HOH:O	2.44	0.51
1:A:95:GLU:CG	6:A:883:HOH:O	2.60	0.50
1:A:313:GLN:HA	1:A:337:ASN:HD21	1.76	0.50
1:B:324:PRO:HG2	6:B:1104:HOH:O	2.12	0.49
1:A:149:PHE:O	1:A:168:MET:HA	2.13	0.48
1:A:23:LEU:C	1:A:23:LEU:HD23	2.39	0.48
1:A:92:LEU:C	1:A:92:LEU:HD23	2.40	0.47
1:B:429:ASN:HD22	1:B:429:ASN:N	2.12	0.46
1:A:142:LEU:N	6:A:895:HOH:O	2.47	0.46
1:A:101:ASN:HD22	1:A:101:ASN:N	2.10	0.46
1:A:164:MET:H	1:A:219:ASN:HD21	1.63	0.45
1:A:337:ASN:HD22	1:A:337:ASN:C	2.24	0.45
1:A:265:ASP:O	1:A:268:ARG:HG2	2.18	0.44
1:B:94:LEU:HD22	1:B:102:LYS:HE3	1.99	0.44
1:A:293:ASP:HA	1:A:303:TRP:CH2	2.52	0.44
1:B:164:MET:H	1:B:219:ASN:HD21	1.65	0.44
1:A:178:ARG:HD2	1:A:410:MET:HA	2.00	0.44
1:B:83:VAL:HG23	1:B:121:GLY:HA2	2.00	0.43
1:B:149:PHE:O	1:B:168:MET:HA	2.18	0.43
1:A:141:ASP:C	6:A:895:HOH:O	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:LEU:CD2	1:A:102:LYS:HE3	2.50	0.41
1:A:400:SER:HB2	1:B:401:GLU:HB3	2.02	0.41
1:B:429:ASN:HD22	1:B:429:ASN:H	1.68	0.41
1:B:370:HIS:CG	1:B:394:THR:HA	2.56	0.40

All (3) 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)
6:A:948:HOH:O	6:B:765:HOH:O[1_556]	1.87	0.33
6:A:1040:HOH:O	6:B:996:HOH:O[1_556]	1.97	0.23
6:A:870:HOH:O	6:B:728:HOH:O[3_545]	2.09	0.11

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	431/443 (97%)	419 (97%)	11 (3%)	1 (0%)	43	27
1	B	431/443 (97%)	422 (98%)	8 (2%)	1 (0%)	43	27
All	All	862/886 (97%)	841 (98%)	19 (2%)	2 (0%)	43	27

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	399	ARG
1	A	399	ARG

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 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$
3	XSP	A	602	2	10,10,10	2.23	2 (20%)	8,14,14	1.67	1 (12%)
4	TRS	A	603	-	7,7,7	0.71	0	9,9,9	1.22	1 (11%)
5	0V5	B	602	2	8,9,9	1.38	1 (12%)	11,13,13	1.84	4 (36%)

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
3	XSP	A	602	2	-	2/8/11/11	-
4	TRS	A	603	-	-	0/9/9/9	-
5	0V5	B	602	2	-	2/9/9/9	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	XSP	O3-C3	5.65	1.41	1.20
5	B	602	OV5	P-O2	2.53	1.64	1.59
3	A	602	XSP	O1-C1	2.15	1.28	1.22

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	XSP	P-O1P-C2	-3.94	112.80	123.21
5	B	602	OV5	O2'-C1-O1	-2.89	117.53	124.08
5	B	602	OV5	O2-C2-C1	2.87	116.26	111.06
5	B	602	OV5	C3-C2-C1	2.72	114.53	109.42
4	A	603	TRS	C2-C-C1	-2.43	104.20	110.66
5	B	602	OV5	O3P-P-O2P	2.33	116.53	107.80

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	XSP	O2-C1-C2-C3
3	A	602	XSP	O1-C1-C2-C3
5	B	602	OV5	O2'-C1-C2-C3
5	B	602	OV5	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	602	OV5	1	0

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	433/443 (97%)	-0.54	2 (0%) 87 91	9, 19, 33, 46	0
1	B	433/443 (97%)	-0.71	4 (0%) 81 86	9, 16, 29, 51	0
All	All	866/886 (97%)	-0.62	6 (0%) 84 89	9, 17, 32, 51	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	158	ALA	3.7
1	A	420	ALA	3.1
1	B	157	HIS	2.2
1	B	202	ASP	2.2
1	A	159	GLY	2.0
1	B	156	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](#)

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($\text{\AA}^2$)	Q<0.9
4	TRS	A	603	8/8	0.88	0.10	28,34,36,36	0
3	XSP	A	602	11/11	0.99	0.04	14,16,27,30	0
2	MG	A	601	1/1	0.99	0.02	17,17,17,17	0
5	0V5	B	602	10/10	0.99	0.04	12,14,17,21	0
2	MG	A	600	1/1	1.00	0.02	16,16,16,16	0
2	MG	B	600	1/1	1.00	0.01	12,12,12,12	0
2	MG	B	601	1/1	1.00	0.04	12,12,12,12	0

6.5 Other polymers [i](#)

There are no such residues in this entry.