



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 5TON / pdb_00005ton
Title : Crystal structure of AAT H143L mutant
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Deposited on : 2016-10-18
Resolution : 1.40 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
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

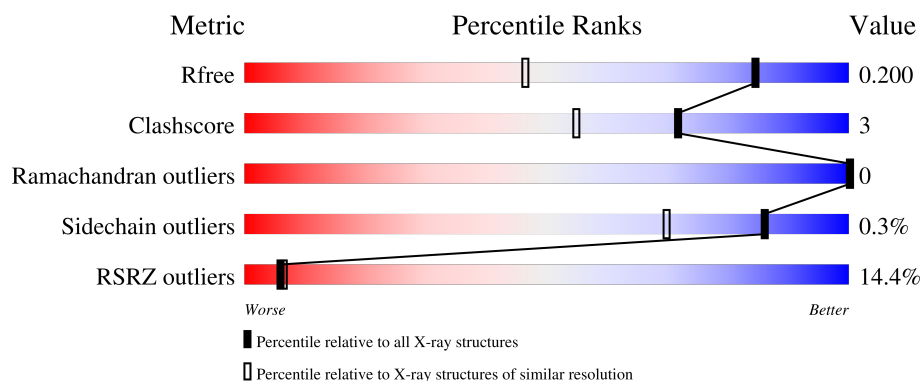
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 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	2563 (1.40-1.40)
Clashscore	190562	2660 (1.40-1.40)
Ramachandran outliers	187476	2611 (1.40-1.40)
Sidechain outliers	187428	2610 (1.40-1.40)
RSRZ outliers	180081	2561 (1.40-1.40)

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	414	6% 96% .
1	B	414	22% 87% 8% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6996 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 Aspartate aminotransferase, cytoplasmic.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	414	Total	C	N	O	P	S	0	6	0
			3342	2127	583	618	1	13			
1	B	396	Total	C	N	O	P	S	0	5	0
			3180	2023	553	588	1	15			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P00503
A	63	ASN	ASP	conflict	UNP P00503
A	143	LEU	HIS	engineered mutation	UNP P00503
A	288	GLN	GLU	conflict	UNP P00503
A	376	GLN	GLU	conflict	UNP P00503
B	-1	GLY	-	expression tag	UNP P00503
B	63	ASN	ASP	conflict	UNP P00503
B	143	LEU	HIS	engineered mutation	UNP P00503
B	288	GLN	GLU	conflict	UNP P00503
B	376	GLN	GLU	conflict	UNP P00503

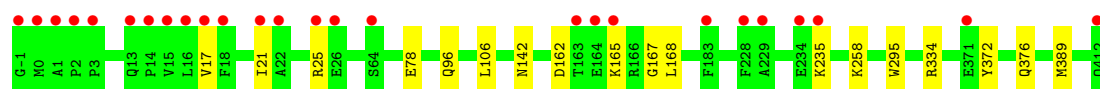
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	284	Total	O	0	0
			284	284		
2	B	190	Total	O	0	0
			190	190		

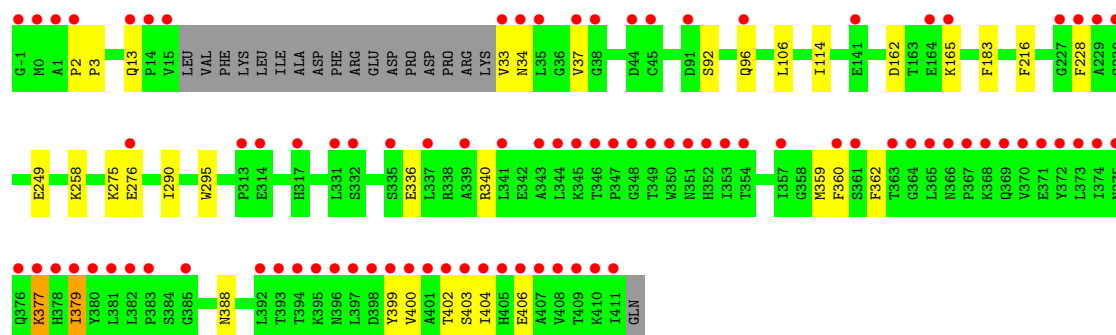
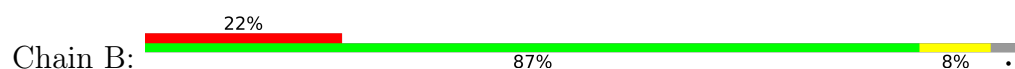
3 Residue-property plots [i](#)

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: Aspartate aminotransferase, cytoplasmic



- Molecule 1: Aspartate aminotransferase, cytoplasmic



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.29Å 124.01Å 129.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.34 – 1.40 35.34 – 1.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (35.34-1.40) 99.9 (35.34-1.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.13 (at 1.40Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155)	Depositor
R, R_{free}	0.184 , 0.198 0.186 , 0.200	Depositor DCC
R_{free} test set	8740 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	10.7	Xtriage
Anisotropy	0.161	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 35.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.012 for -h,l,k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6996	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.26% 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: LLP

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	0.26	0/3404	0.49	0/4623
1	B	0.27	0/3233	0.50	2/4389 (0.0%)
All	All	0.26	0/6637	0.49	2/9012 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	379	ILE	N-CA-CB	5.25	116.45	110.72
1	B	377	LYS	CD-CE-NZ	-5.05	95.73	111.90

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	3342	0	3280	14	0
1	B	3180	0	3121	30	0
2	A	284	0	0	5	0
2	B	190	0	0	3	0
All	All	6996	0	6401	43	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 3.

All (43) 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:165:LYS:NZ	1:A:168:LEU:O	1.85	1.08
1:B:377:LYS:NZ	1:B:379:ILE:HG13	1.98	0.78
1:A:162:ASP:HB3	1:A:165:LYS:HG2	1.68	0.74
1:B:33:VAL:N	2:B:503:HOH:O	2.23	0.71
1:B:34:ASN:O	2:B:501:HOH:O	2.08	0.70
1:B:377:LYS:CE	1:B:379:ILE:HG13	2.23	0.69
1:B:377:LYS:O	1:B:377:LYS:HG2	1.94	0.68
1:A:78:GLU:OE1	2:A:501:HOH:O	2.14	0.64
1:B:377:LYS:HD2	1:B:403:SER:HB3	1.79	0.63
1:A:142[B]:ASN:ND2	2:A:503:HOH:O	2.32	0.62
1:B:340:ARG:HH11	1:B:340:ARG:HG2	1.67	0.59
1:B:228:PHE:HE1	1:B:359:MET:HG2	1.68	0.58
1:B:379:ILE:HD11	1:B:400:VAL:HG22	1.86	0.56
1:B:377:LYS:HZ1	1:B:379:ILE:HG13	1.70	0.56
1:B:13:GLN:O	2:B:502:HOH:O	2.18	0.55
1:A:21:ILE:O	1:A:25:ARG:HG3	2.05	0.55
1:B:92:SER:O	1:B:96:GLN:HG3	2.05	0.55
1:A:165:LYS:HE3	2:A:740:HOH:O	2.08	0.54
1:B:228:PHE:CE1	1:B:359:MET:HG2	2.44	0.53
1:B:377:LYS:HE3	1:B:379:ILE:HG13	1.91	0.53
1:B:162:ASP:CG	1:B:165:LYS:HG2	2.36	0.51
1:B:377:LYS:NZ	1:B:399:TYR:CE2	2.79	0.51
1:B:402:THR:O	1:B:406:GLU:HG3	2.11	0.50
1:B:377:LYS:HE3	1:B:379:ILE:CD1	2.42	0.50
1:B:377:LYS:HD2	1:B:403:SER:CB	2.42	0.49
1:A:165:LYS:HE2	1:A:167:GLY:C	2.39	0.48
1:A:235:LYS:NZ	2:A:505:HOH:O	2.46	0.47
1:A:106:LEU:HD11	1:B:106:LEU:HD11	1.98	0.45
1:A:106:LEU:HD23	1:A:295:TRP:CE2	2.51	0.45
1:B:379:ILE:HD13	1:B:379:ILE:HG21	1.73	0.45
1:B:37:VAL:HG13	1:B:388:ASN:ND2	2.32	0.44
1:B:183:PHE:HA	1:B:216:PHE:O	2.18	0.44
1:B:400:VAL:O	1:B:404:ILE:HG12	2.18	0.43
1:B:336:GLU:OE1	1:B:340:ARG:NH2	2.52	0.43
1:B:106:LEU:HD23	1:B:295:TRP:CE2	2.54	0.43
1:B:359:MET:HE3	1:B:360:PHE:CZ	2.54	0.42
1:B:114:ILE:HD12	1:B:290:ILE:HG22	2.00	0.42
1:A:372:TYR:CD1	1:A:376:GLN:HG3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:GLN:HG2	2:A:514:HOH:O	2.20	0.41
1:A:17:VAL:O	1:A:21:ILE:HG12	2.20	0.41
1:B:2:PRO:HA	1:B:3:PRO:HD3	1.89	0.41
1:A:334:ARG:HA	1:A:389:MET:HE2	2.04	0.40
1:B:249:GLU:CD	1:B:275:LYS:HG3	2.46	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	417/414 (101%)	412 (99%)	5 (1%)	0	100	100
1	B	396/414 (96%)	387 (98%)	9 (2%)	0	100	100
All	All	813/828 (98%)	799 (98%)	14 (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	358/352 (102%)	358 (100%)	0	100	100
1	B	340/352 (97%)	338 (99%)	2 (1%)	78	56
All	All	698/704 (99%)	696 (100%)	2 (0%)	86	70

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	276	GLU
1	B	362	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	171	GLN
1	A	254	GLN
1	A	269	ASN
1	A	317	HIS
1	B	179	ASN
1	B	269	ASN
1	B	322	ASN
1	B	369	GLN
1	B	375	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	LLP	A	258	1	23,24,25	2.40	7 (30%)	25,32,34	1.47	4 (16%)
1	LLP	B	258	1	23,24,25	2.45	7 (30%)	25,32,34	1.48	4 (16%)

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	LLP	A	258	1	-	6/16/17/19	0/1/1/1
1	LLP	B	258	1	-	7/16/17/19	0/1/1/1

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	258	LLP	C4-C4'	7.18	1.61	1.46
1	A	258	LLP	C4-C4'	7.16	1.61	1.46
1	B	258	LLP	C4'-NZ	5.06	1.44	1.27
1	A	258	LLP	C4'-NZ	5.01	1.43	1.27
1	B	258	LLP	C2'-C2	3.82	1.56	1.50
1	B	258	LLP	C4-C5	-3.59	1.37	1.42
1	A	258	LLP	C2'-C2	3.48	1.55	1.50
1	A	258	LLP	C4-C5	-3.34	1.37	1.42
1	A	258	LLP	C6-N1	2.47	1.39	1.34
1	B	258	LLP	C6-N1	2.45	1.39	1.34
1	B	258	LLP	C5'-C5	2.21	1.56	1.50
1	B	258	LLP	P-OP3	-2.15	1.46	1.54
1	A	258	LLP	C5'-C5	2.12	1.56	1.50
1	A	258	LLP	P-OP3	-2.04	1.47	1.54

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	258	LLP	C4-C4'-NZ	-4.76	102.06	124.04
1	B	258	LLP	C4-C4'-NZ	-3.99	105.62	124.04
1	B	258	LLP	C5-C6-N1	-2.80	119.28	123.83
1	B	258	LLP	OP4-C5'-C5	2.76	114.53	109.36
1	A	258	LLP	C5-C6-N1	-2.33	120.04	123.83
1	B	258	LLP	C5'-C5-C6	-2.12	115.91	119.36
1	A	258	LLP	C5'-C5-C6	-2.01	116.08	119.36
1	A	258	LLP	OP4-C5'-C5	2.00	113.11	109.36

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	258	LLP	C5'-OP4-P-OP1
1	B	258	LLP	C5'-OP4-P-OP1
1	B	258	LLP	C5'-OP4-P-OP3

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Mol	Chain	Res	Type	Atoms
1	B	258	LLP	C4-C4'-NZ-CE
1	B	258	LLP	CG-CD-CE-NZ
1	A	258	LLP	CA-CB-CG-CD
1	B	258	LLP	CA-CB-CG-CD
1	A	258	LLP	C3-C4-C4'-NZ
1	B	258	LLP	C3-C4-C4'-NZ
1	A	258	LLP	C5-C4-C4'-NZ
1	A	258	LLP	CD-CE-NZ-C4'
1	B	258	LLP	C5-C4-C4'-NZ
1	A	258	LLP	C5'-OP4-P-OP3

There are no ring outliers.

No monomer is involved in short contacts.

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	413/414 (99%)	0.09	26 (6%) 26 27	4, 11, 27, 47	6 (1%)
1	B	395/414 (95%)	1.11	90 (22%) 2 2	4, 14, 44, 61	11 (2%)
All	All	808/828 (97%)	0.59	116 (14%) 6 6	4, 12, 37, 61	17 (2%)

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	411	ILE	11.0
1	B	379	ILE	8.8
1	B	15	VAL	8.6
1	B	-1	GLY	7.7
1	A	18	PHE	7.2
1	B	377	LYS	7.1
1	B	1	ALA	6.8
1	B	344	LEU	6.8
1	B	373	LEU	6.6
1	B	399	TYR	6.4
1	B	401	ALA	6.4
1	B	398	ASP	6.3
1	B	0	MET	6.1
1	A	-1	GLY	6.1
1	B	374	ILE	5.9
1	B	372	TYR	5.6
1	B	408	VAL	5.6
1	B	371	GLU	5.5
1	B	397	LEU	5.5
1	B	407	ALA	5.4
1	B	37	VAL	5.4
1	B	365	LEU	5.3
1	B	400	VAL	5.3
1	B	380	TYR	5.2

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Mol	Chain	Res	Type	RSRZ
1	B	33	VAL	5.2
1	B	367	PRO	5.2
1	B	339	ALA	5.2
1	B	404	ILE	5.1
1	B	228	PHE	5.1
1	B	368	LYS	5.0
1	B	370	VAL	5.0
1	B	350	TRP	4.9
1	B	34	ASN	4.9
1	B	347	PRO	4.8
1	A	165	LYS	4.8
1	B	341	LEU	4.7
1	A	1	ALA	4.7
1	B	229	ALA	4.7
1	B	378	HIS	4.7
1	B	402	THR	4.6
1	B	345	LYS	4.6
1	A	15	VAL	4.5
1	B	348	GLY	4.5
1	B	343	ALA	4.4
1	B	385	GLY	4.4
1	B	382	LEU	4.2
1	B	375	ASN	4.2
1	B	14	PRO	4.0
1	B	394	THR	4.0
1	B	409	THR	4.0
1	B	376	GLN	3.9
1	A	16	LEU	3.9
1	B	366	ASN	3.9
1	B	405	HIS	3.8
1	B	410	LYS	3.7
1	B	361	SER	3.7
1	B	357	ILE	3.6
1	B	13	GLN	3.6
1	A	229	ALA	3.6
1	A	412	GLN	3.5
1	B	331	LEU	3.5
1	A	2	PRO	3.5
1	B	2	PRO	3.4
1	B	38	GLY	3.4
1	B	96	GLN	3.3
1	B	313	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	25	ARG	3.2
1	B	383	PRO	3.2
1	B	403	SER	3.2
1	B	346	THR	3.1
1	B	353	ILE	3.1
1	B	395	LYS	3.0
1	A	26	GLU	3.0
1	B	364	GLY	2.9
1	A	22	ALA	2.9
1	B	314	GLU	2.9
1	B	349	THR	2.9
1	B	393	THR	2.9
1	B	141	GLU	2.9
1	A	14	PRO	2.8
1	A	13	GLN	2.8
1	A	17	VAL	2.8
1	B	351	ASN	2.8
1	A	228	PHE	2.8
1	B	396	ASN	2.7
1	A	64	SER	2.7
1	B	45	CYS	2.7
1	B	35	LEU	2.7
1	B	335	SER	2.7
1	A	234	GLU	2.6
1	B	369	GLN	2.6
1	B	230	SER	2.6
1	A	183	PHE	2.6
1	B	337	LEU	2.6
1	B	406	GLU	2.6
1	B	360	PHE	2.5
1	B	381	LEU	2.5
1	A	21	ILE	2.5
1	B	354	THR	2.5
1	B	91	ASP	2.4
1	B	363	THR	2.4
1	A	235	LYS	2.4
1	A	3	PRO	2.4
1	B	165	LYS	2.4
1	B	392	LEU	2.3
1	A	371	GLU	2.3
1	B	227	GLY	2.2
1	B	317	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	44	ASP	2.2
1	A	164	GLU	2.2
1	A	0	MET	2.1
1	B	164	GLU	2.1
1	B	276	GLU	2.1
1	B	352	HIS	2.1
1	B	332	SER	2.0
1	A	163	THR	2.0

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	LLP	B	258	24/25	0.97	0.07	7,12,18,24	0
1	LLP	A	258	24/25	0.98	0.07	5,11,16,19	0

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.