



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 11:58 pm GMT

PDB ID : 5SVK  
Title : Crystal structure of the ATP-gated human P2X3 ion channel in the ATP-bound, open state  
Authors : Mansoor, S.E.; Lu, W.; Oosterheert, W.; Shekhar, M.; Tajkhorshid, E.; Gouaux, E.  
Deposited on : 2016-08-06  
Resolution : 2.77 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

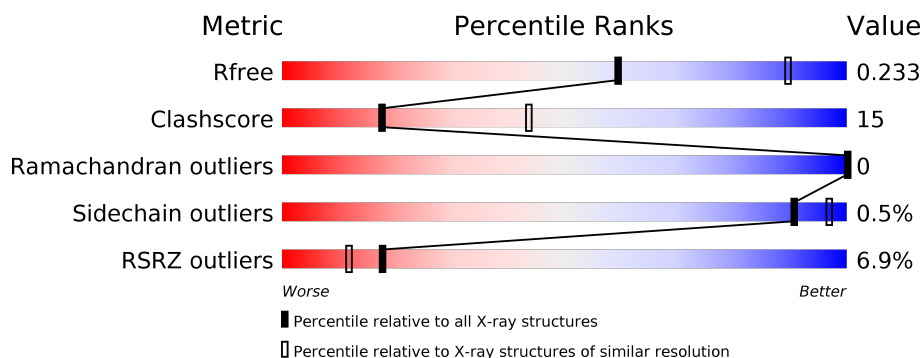
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.77 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))
$R_{free}$	100719	3276 (2.80-2.76)
Clashscore	112137	3771 (2.80-2.76)
Ramachandran outliers	110173	3707 (2.80-2.76)
Sidechain outliers	110143	3709 (2.80-2.76)
RSRZ outliers	101464	3307 (2.80-2.76)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	363	<div> <div>6%</div> <div>72%</div> <div>26%</div> <div>••</div> </div>
1	B	363	<div> <div>8%</div> <div>75%</div> <div>23%</div> <div>•</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	A	405	-	-	-	X
4	MAL	A	407	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5967 atoms, of which 130 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 P2X purinoceptor 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	357	Total	C	N	O	S	0	0	0
			2766	1786	456	506	18			
1	B	357	Total	C	N	O	S	0	0	0
			2737	1772	450	497	18			

There are 14 discrepancies between the modelled and reference sequences:

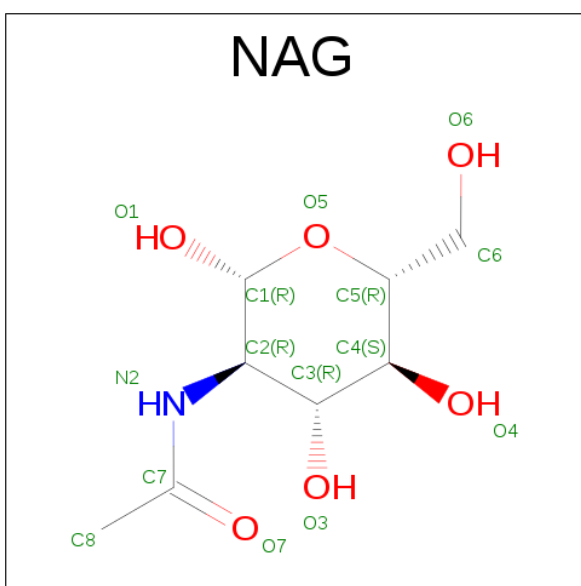
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	GLY	-	expression tag	UNP P56373
A	3	SER	-	expression tag	UNP P56373
A	4	ARG	-	expression tag	UNP P56373
A	5	ALA	-	expression tag	UNP P56373
A	13	PRO	THR	engineered mutation	UNP P56373
A	15	VAL	SER	engineered mutation	UNP P56373
A	16	ILE	VAL	engineered mutation	UNP P56373
B	2	GLY	-	expression tag	UNP P56373
B	3	SER	-	expression tag	UNP P56373
B	4	ARG	-	expression tag	UNP P56373
B	5	ALA	-	expression tag	UNP P56373
B	13	PRO	THR	engineered mutation	UNP P56373
B	15	VAL	SER	engineered mutation	UNP P56373
B	16	ILE	VAL	engineered mutation	UNP P56373

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 43	C 10	H 12	N 5	O 13	P 3	0	0
2	B	1	Total 43	C 10	H 12	N 5	O 13	P 3	0	0

- Molecule 3 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



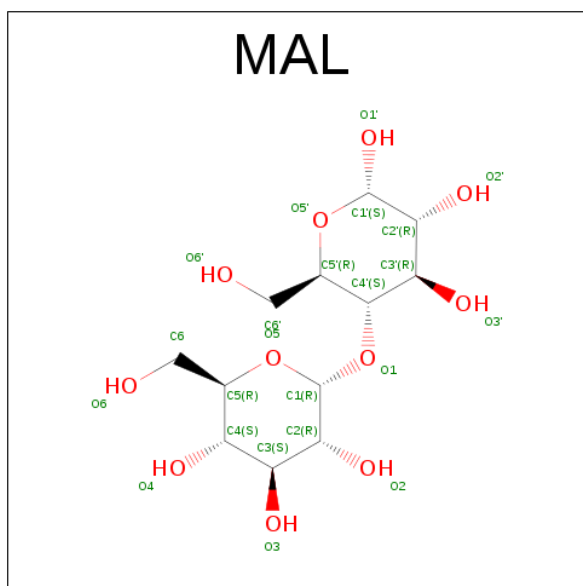
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 28	C 8	H 14	N 1	O 5	0	0
3	A	1	Total 28	C 8	H 14	N 1	O 5	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	B	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	B	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	B	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

- Molecule 4 is MALTOSE (three-letter code: MAL) (formula:  $C_{12}H_{22}O_{11}$ ).



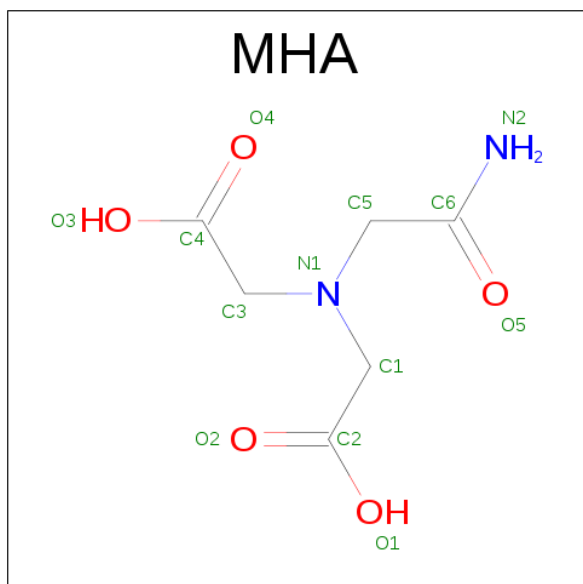
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			23	12	11		
4	A	1	Total	C	O	0	0
			23	12	11		
4	B	1	Total	C	O	0	0
			23	12	11		
4	B	1	Total	C	O	0	0
			23	12	11		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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

- Molecule 6 is (CARBAMOYLMETHYL-CARBOXYMETHYL-AMINO)-ACETIC ACID (three-letter code: MHA) (formula:  $C_6H_{10}N_2O_5$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	H	N	O	0	0
			21	6	8	2	5		

- Molecule 7 is water.

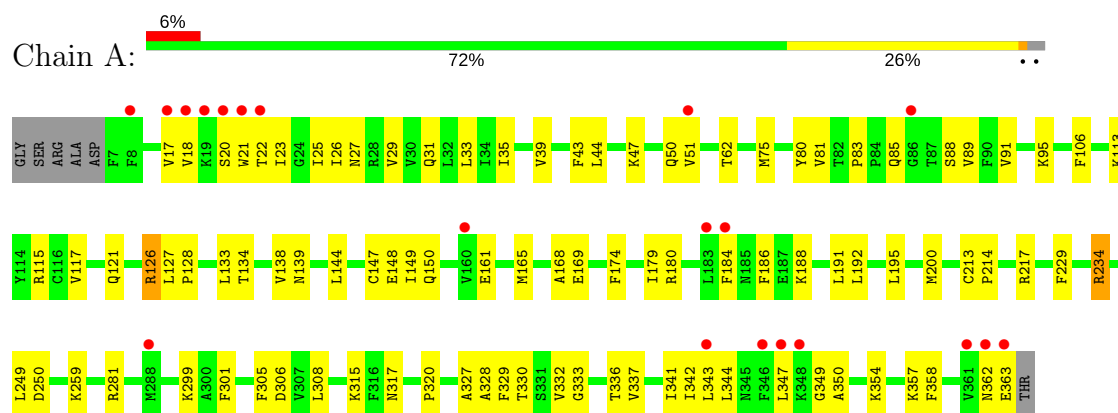
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	39	Total 39	O 39	0	0
7	B	22	Total 22	O 22	0	0



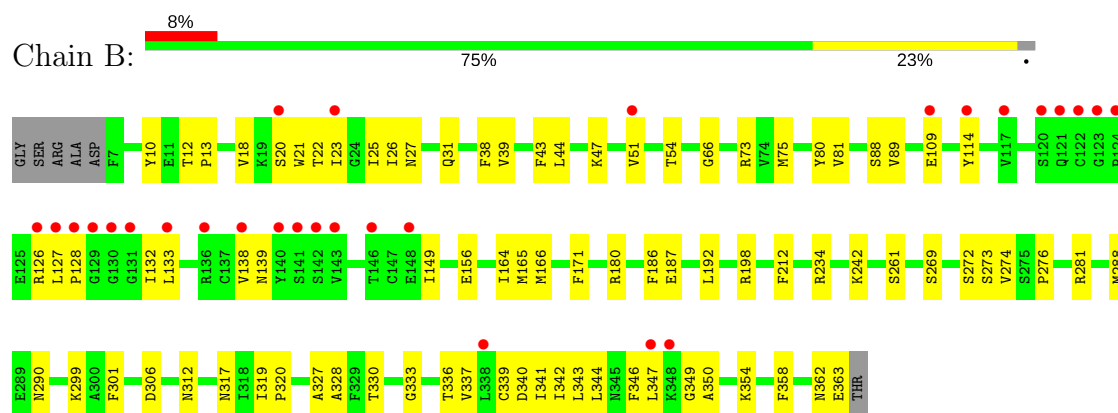
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: P2X purinoceptor 3



#### • Molecule 1: P2X purinoceptor 3



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	173.15Å 173.15Å 173.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.29 – 2.77 43.29 – 2.77	Depositor EDS
% Data completeness (in resolution range)	93.9 (43.29-2.77) 99.3 (43.29-2.77)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.53 (at 2.77Å)	Xtriage
Refinement program	PHENIX (1.10_2142: ???)	Depositor
R, $R_{free}$	0.201 , 0.228 0.203 , 0.233	Depositor DCC
$R_{free}$ test set	2184 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	78.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 61.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.024 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5967	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: MHA, MAL, NAG, ATP, 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	0.27	0/2828	0.49	0/3838
1	B	0.27	0/2800	0.49	0/3804
All	All	0.27	0/5628	0.49	0/7642

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	2766	0	2735	93	1
1	B	2737	0	2670	79	2
2	A	31	12	12	1	0
2	B	31	12	12	0	0
3	A	56	56	52	2	0
3	B	42	42	39	1	0
4	A	46	0	44	2	0
4	B	46	0	44	1	0
5	A	4	0	6	0	0
5	B	4	0	6	2	0
6	A	13	8	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	39	0	0	1	0
7	B	22	0	0	0	0
All	All	5837	130	5628	174	2

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 15.

All (174) 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:343:LEU:HD12	1:B:344:LEU:HD12	1.49	0.93
1:A:127:LEU:HD23	1:A:128:PRO:HD3	1.51	0.93
1:A:343:LEU:HD12	1:A:344:LEU:HD12	1.47	0.92
1:A:23:ILE:HA	1:A:26:ILE:HG22	1.56	0.85
1:B:23:ILE:HA	1:B:26:ILE:HG22	1.58	0.85
1:A:89:VAL:HG22	1:A:306:ASP:HB3	1.60	0.80
1:B:75:MET:HB2	1:B:165:MET:HE1	1.63	0.80
1:B:26:ILE:CD1	1:B:342:ILE:HD13	2.13	0.79
1:A:343:LEU:HA	1:A:347:LEU:HD22	1.64	0.78
1:A:26:ILE:HD11	1:A:342:ILE:HD13	1.68	0.75
1:B:23:ILE:HG12	1:B:347:LEU:HD21	1.66	0.75
1:B:133:LEU:HD13	1:B:149:ILE:HG22	1.66	0.75
1:A:343:LEU:CD1	1:A:344:LEU:HD12	2.16	0.74
1:A:23:ILE:HA	1:A:26:ILE:CG2	2.18	0.74
1:B:26:ILE:HD11	1:B:342:ILE:HD13	1.69	0.74
1:A:89:VAL:HG22	1:A:306:ASP:CB	2.16	0.73
1:A:337:VAL:O	1:A:341:ILE:HG12	1.91	0.71
1:B:337:VAL:O	1:B:341:ILE:HG12	1.91	0.70
1:A:75:MET:HG3	1:A:165:MET:HE3	1.73	0.70
1:B:343:LEU:CD1	1:B:344:LEU:HD12	2.19	0.70
1:A:23:ILE:CG1	1:A:347:LEU:HD21	2.22	0.69
1:A:138:VAL:HG12	1:A:139:ASN:H	1.59	0.67
1:B:288:MET:CE	5:B:407:EDO:H22	2.24	0.67
1:B:23:ILE:CG1	1:B:347:LEU:HD21	2.23	0.67
4:B:405:MAL:O2	4:B:405:MAL:O3'	2.06	0.66
1:A:26:ILE:CD1	1:A:342:ILE:HD13	2.25	0.66
1:A:88:SER:O	1:A:306:ASP:HA	1.95	0.66
1:B:89:VAL:HG22	1:B:306:ASP:HB3	1.78	0.65
1:A:23:ILE:HD11	1:A:347:LEU:HD21	1.77	0.65
1:B:23:ILE:HA	1:B:26:ILE:CG2	2.25	0.65
1:A:23:ILE:HG13	1:A:343:LEU:HD23	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:288:MET:HE3	5:B:407:EDO:H22	1.78	0.64
1:A:350:ALA:O	1:A:354:LYS:HG3	1.98	0.63
1:A:51:VAL:HG23	1:A:317:ASN:HB3	1.81	0.63
1:A:51:VAL:HG23	1:A:317:ASN:CB	2.30	0.62
1:A:281:ARG:NH2	2:A:401:ATP:O3G	2.32	0.62
1:A:117:VAL:HG12	1:A:121:GLN:OE1	2.00	0.62
1:A:23:ILE:CA	1:A:26:ILE:HG22	2.29	0.61
1:B:23:ILE:HG13	1:B:343:LEU:HD23	1.81	0.61
1:A:327:ALA:O	1:A:330:THR:HG22	2.00	0.61
1:B:75:MET:HG3	1:B:165:MET:HE3	1.82	0.61
1:B:343:LEU:HD22	1:B:347:LEU:HD22	1.82	0.61
1:B:127:LEU:N	1:B:128:PRO:HD2	2.16	0.61
1:A:27:ASN:O	1:A:31:GLN:HG3	2.00	0.60
1:B:26:ILE:HD13	1:B:342:ILE:HD13	1.82	0.60
1:A:127:LEU:N	1:A:128:PRO:HD2	2.16	0.60
1:A:113:LYS:O	1:A:126:ARG:NH1	2.35	0.60
1:A:342:ILE:O	1:A:347:LEU:HD13	2.02	0.60
1:B:18:VAL:HG12	1:B:20:SER:H	1.65	0.60
1:A:138:VAL:HG12	1:A:139:ASN:N	2.15	0.59
1:A:50:GLN:HB2	1:A:315:LYS:O	2.02	0.59
1:B:242:LYS:HE3	1:B:261:SER:HB2	1.83	0.59
1:B:75:MET:HB2	1:B:165:MET:CE	2.31	0.59
1:A:299:LYS:HE2	1:A:301:PHE:CZ	2.38	0.59
1:A:362:ASN:O	1:A:363:GLU:HB2	2.03	0.59
1:A:191:LEU:HD23	1:A:214:PRO:HG3	1.83	0.58
1:A:343:LEU:HD12	1:A:344:LEU:CD1	2.26	0.58
1:B:88:SER:O	1:B:306:ASP:HA	2.03	0.58
1:A:18:VAL:HG12	1:A:20:SER:H	1.69	0.58
1:B:272:SER:OG	1:B:274:VAL:HG12	2.03	0.58
1:A:328:ALA:O	1:A:332:VAL:HG13	2.03	0.57
1:B:327:ALA:O	1:B:330:THR:HG22	2.04	0.57
1:B:164:ILE:CG2	1:B:234:ARG:HG2	2.35	0.57
1:B:180:ARG:HB2	1:B:187:GLU:HG2	1.87	0.56
1:B:51:VAL:HG23	1:B:317:ASN:HB3	1.88	0.56
1:A:357:LYS:HD3	1:A:358:PHE:CE1	2.41	0.56
1:A:329:PHE:O	1:A:332:VAL:HG22	2.05	0.56
1:A:127:LEU:HD23	1:A:128:PRO:CD	2.31	0.56
1:A:21:TRP:O	1:A:25:ILE:HG23	2.05	0.56
1:A:35:ILE:HD11	1:A:332:VAL:HG11	1.87	0.56
1:A:50:GLN:HB2	1:A:315:LYS:C	2.27	0.55
1:A:23:ILE:CD1	1:A:347:LEU:HD21	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:327:ALA:HA	1:A:330:THR:HG22	1.89	0.54
1:B:22:THR:O	1:B:25:ILE:HG13	2.07	0.54
1:B:43:PHE:O	1:B:47:LYS:HA	2.06	0.54
1:A:342:ILE:HG22	1:A:347:LEU:HD11	1.88	0.54
1:B:138:VAL:HG12	1:B:139:ASN:N	2.23	0.54
1:A:127:LEU:N	1:A:128:PRO:CD	2.71	0.54
1:B:127:LEU:N	1:B:128:PRO:CD	2.71	0.54
1:B:138:VAL:HG12	1:B:139:ASN:H	1.73	0.54
1:A:75:MET:HB2	1:A:165:MET:HE1	1.89	0.54
1:B:327:ALA:HA	1:B:330:THR:HG22	1.89	0.54
1:B:109:GLU:HG2	1:B:114:TYR:CD1	2.43	0.54
1:B:343:LEU:HD12	1:B:344:LEU:CD1	2.31	0.53
1:B:39:VAL:O	1:B:44:LEU:HG	2.08	0.53
1:B:299:LYS:HE2	1:B:301:PHE:CZ	2.43	0.53
1:B:344:LEU:HD21	1:B:358:PHE:HE1	1.74	0.53
1:A:179:ILE:HG13	1:A:188:LYS:O	2.08	0.53
1:B:73:ARG:NH1	1:B:75:MET:SD	2.82	0.52
1:B:23:ILE:CA	1:B:26:ILE:HG22	2.37	0.52
1:B:180:ARG:HA	1:B:186:PHE:O	2.09	0.52
1:A:250:ASP:HB3	4:A:407:MAL:H3'	1.91	0.52
1:A:343:LEU:HD22	1:A:347:LEU:HD22	1.92	0.52
1:B:290:ASN:ND2	3:B:404:NAG:O7	2.43	0.52
1:A:22:THR:O	1:A:25:ILE:HG13	2.09	0.52
1:B:156:GLU:OE2	1:B:281:ARG:NH1	2.42	0.52
1:B:350:ALA:O	1:B:354:LYS:HG3	2.09	0.51
1:A:133:LEU:HD23	1:A:149:ILE:HG22	1.93	0.50
1:A:191:LEU:HD23	1:A:214:PRO:CG	2.41	0.50
1:A:39:VAL:O	1:A:44:LEU:HG	2.10	0.50
1:B:89:VAL:HG22	1:B:306:ASP:CB	2.41	0.50
1:B:12:THR:OG1	1:B:13:PRO:HD2	2.11	0.50
1:B:27:ASN:O	1:B:31:GLN:HG3	2.12	0.49
1:A:184:PHE:CD2	1:A:249:LEU:HD12	2.47	0.49
1:A:192:LEU:HD13	3:A:403:NAG:H5	1.94	0.49
3:A:402:NAG:H61	1:B:273:SER:HB2	1.93	0.49
1:A:347:LEU:C	1:A:349:GLY:H	2.16	0.49
1:B:126:ARG:C	1:B:128:PRO:HD2	2.33	0.49
1:A:43:PHE:O	1:A:47:LYS:HA	2.13	0.49
1:A:317:ASN:OD1	1:A:320:PRO:HD2	2.12	0.49
1:B:66:GLY:HA3	1:B:171:PHE:CD1	2.48	0.48
1:B:281:ARG:NH1	1:B:299:LYS:HD2	2.29	0.48
1:B:333:GLY:O	1:B:336:THR:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:336:THR:O	1:B:340:ASP:HB2	2.13	0.48
1:B:132:ILE:N	1:B:132:ILE:HD12	2.29	0.48
1:B:80:TYR:CE1	1:B:81:VAL:HG23	2.49	0.48
1:A:75:MET:HG3	1:A:165:MET:CE	2.42	0.47
1:B:21:TRP:O	1:B:25:ILE:HG23	2.14	0.47
1:A:174:PHE:CE1	1:A:214:PRO:HB2	2.50	0.47
1:B:343:LEU:HD13	1:B:343:LEU:C	2.35	0.47
1:B:269:SER:HB3	1:B:276:PRO:O	2.15	0.47
1:A:127:LEU:CD2	1:A:128:PRO:HD3	2.34	0.46
1:B:180:ARG:HD2	1:B:187:GLU:OE2	2.16	0.46
1:A:138:VAL:CG1	1:A:139:ASN:H	2.26	0.46
1:A:115:ARG:HG3	1:A:144:LEU:CD1	2.46	0.46
1:A:343:LEU:HA	1:A:347:LEU:CD2	2.39	0.46
1:A:195:LEU:HD21	1:A:200:MET:SD	2.56	0.45
1:A:134:THR:OG1	1:A:148:GLU:HB3	2.15	0.45
1:B:347:LEU:C	1:B:349:GLY:H	2.19	0.45
1:A:95:LYS:HB3	1:A:301:PHE:HB2	1.98	0.45
1:A:161:GLU:OE2	1:A:234:ARG:HG2	2.17	0.45
1:A:80:TYR:CE1	1:A:81:VAL:HG23	2.52	0.45
1:B:75:MET:HG3	1:B:165:MET:CE	2.46	0.45
1:B:344:LEU:HD21	1:B:358:PHE:CE1	2.52	0.45
1:B:344:LEU:O	1:B:350:ALA:HB1	2.17	0.44
1:B:51:VAL:HG23	1:B:317:ASN:CB	2.47	0.44
1:A:29:VAL:O	1:A:33:LEU:HG	2.18	0.44
1:B:346:PHE:C	1:B:347:LEU:HD12	2.37	0.44
1:B:133:LEU:HD13	1:B:149:ILE:CG2	2.43	0.44
1:B:339:CYS:HA	1:B:342:ILE:HD12	2.00	0.44
1:A:169:GLU:HG2	1:A:217:ARG:NH2	2.33	0.44
1:A:327:ALA:C	1:A:330:THR:HG22	2.39	0.43
1:B:54:THR:HG22	1:B:312:ASN:CB	2.48	0.43
1:B:80:TYR:CD1	1:B:81:VAL:HG23	2.53	0.43
1:B:164:ILE:HG21	1:B:234:ARG:HG2	2.00	0.43
1:A:62:THR:HA	1:A:174:PHE:O	2.18	0.43
1:A:259:LYS:HG3	7:A:525:HOH:O	2.18	0.43
1:A:83:PRO:HB2	1:A:85:GLN:OE1	2.18	0.43
1:B:164:ILE:HD11	1:B:166:MET:SD	2.59	0.43
1:A:106:PHE:CE1	1:A:150:GLN:HB2	2.54	0.42
1:B:27:ASN:HA	1:B:339:CYS:SG	2.59	0.42
1:B:327:ALA:C	1:B:330:THR:HG22	2.39	0.42
1:B:327:ALA:HA	1:B:330:THR:CG2	2.48	0.42
1:A:133:LEU:HD22	1:A:147:CYS:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:ILE:HG12	1:A:347:LEU:HD21	2.00	0.42
1:A:333:GLY:O	1:A:336:THR:HG23	2.19	0.42
1:A:80:TYR:CD1	1:A:81:VAL:HG23	2.54	0.42
1:B:319:ILE:HB	1:B:320:PRO:CD	2.50	0.42
1:A:180:ARG:HA	1:A:186:PHE:O	2.18	0.42
1:A:89:VAL:HA	1:A:305:PHE:O	2.19	0.42
1:A:191:LEU:CD2	1:A:214:PRO:CG	2.98	0.42
1:A:17:VAL:HG12	1:A:17:VAL:O	2.19	0.42
4:A:407:MAL:H1'	4:A:407:MAL:H6'1	1.77	0.42
1:A:81:VAL:HA	1:A:91:VAL:O	2.20	0.42
1:A:115:ARG:HG3	1:A:144:LEU:HD11	2.02	0.41
1:A:213:CYS:HA	1:A:214:PRO:HD3	1.92	0.41
1:B:362:ASN:O	1:B:363:GLU:CB	2.68	0.41
1:A:89:VAL:HG22	1:A:306:ASP:HB2	2.00	0.41
1:A:149:ILE:HD12	1:A:149:ILE:C	2.41	0.41
1:A:75:MET:HB2	1:A:165:MET:CE	2.50	0.40
1:B:38:PHE:CE2	1:B:328:ALA:HA	2.55	0.40
1:A:138:VAL:CG1	1:A:139:ASN:N	2.82	0.40
1:A:168:ALA:HB3	1:A:229:PHE:HZ	1.86	0.40
1:B:192:LEU:HD11	1:B:212:PHE:CD1	2.57	0.40

All (2) 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)
1:A:200:MET:O	1:B:198:ARG:NH2[6_577]	2.08	0.12
1:B:10:TYR:OH	1:B:340:ASP:OD1[12_774]	2.17	0.03

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	355/363 (98%)	346 (98%)	9 (2%)	0	100	100
1	B	355/363 (98%)	346 (98%)	9 (2%)	0	100	100
All	All	710/726 (98%)	692 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	302/318 (95%)	299 (99%)	3 (1%)	80	94
1	B	291/318 (92%)	291 (100%)	0	100	100
All	All	593/636 (93%)	590 (100%)	3 (0%)	91	97

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	126	ARG
1	A	234	ARG
1	A	308	LEU

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

### 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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

16 ligands 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
2	ATP	A	401	-	27,33,33	0.93	1 (3%)	25,52,52	1.67	2 (8%)
3	NAG	A	402	1	14,14,15	0.16	0	15,19,21	0.76	1 (6%)
3	NAG	A	403	1	14,14,15	0.24	0	15,19,21	0.47	0
3	NAG	A	404	1	14,14,15	0.16	0	15,19,21	0.60	0
3	NAG	A	405	1	14,14,15	1.17	1 (7%)	15,19,21	1.06	2 (13%)
4	MAL	A	406	-	24,24,24	0.53	0	35,35,35	0.55	0
4	MAL	A	407	-	24,24,24	0.53	0	35,35,35	0.62	0
5	EDO	A	408	-	3,3,3	0.47	0	2,2,2	0.37	0
6	MHA	A	409	-	6,12,12	1.89	1 (16%)	9,15,15	1.72	4 (44%)
2	ATP	B	401	-	27,33,33	0.90	1 (3%)	25,52,52	1.65	2 (8%)
3	NAG	B	402	1	14,14,15	0.27	0	15,19,21	0.54	0
3	NAG	B	403	1	14,14,15	0.35	0	15,19,21	0.52	0
3	NAG	B	404	1	14,14,15	0.55	0	15,19,21	1.26	1 (6%)
4	MAL	B	405	-	24,24,24	0.52	0	35,35,35	0.52	0
4	MAL	B	406	-	24,24,24	0.54	0	35,35,35	0.97	1 (2%)
5	EDO	B	407	-	3,3,3	0.46	0	2,2,2	0.33	0

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
2	ATP	A	401	-	-	0/18/38/38	0/3/3/3
3	NAG	A	402	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	403	1	-	0/6/23/26	0/1/1/1
3	NAG	A	404	1	-	0/6/23/26	0/1/1/1
3	NAG	A	405	1	-	0/6/23/26	0/1/1/1
4	MAL	A	406	-	-	0/8/48/48	0/2/2/2
4	MAL	A	407	-	-	0/8/48/48	0/2/2/2
5	EDO	A	408	-	-	0/1/1/1	0/0/0/0
6	MHA	A	409	-	-	0/8/12/12	0/0/0/0
2	ATP	B	401	-	-	0/18/38/38	0/3/3/3
3	NAG	B	402	1	-	0/6/23/26	0/1/1/1
3	NAG	B	403	1	-	0/6/23/26	0/1/1/1
3	NAG	B	404	1	-	0/6/23/26	0/1/1/1
4	MAL	B	405	-	-	0/8/48/48	0/2/2/2
4	MAL	B	406	-	-	0/8/48/48	0/2/2/2
5	EDO	B	407	-	-	0/1/1/1	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	405	NAG	O5-C1	-4.09	1.37	1.43
2	B	401	ATP	C5-C4	2.67	1.46	1.40
2	A	401	ATP	C5-C4	2.74	1.46	1.40
6	A	409	MHA	C6-N2	4.06	1.46	1.32

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	ATP	N3-C2-N1	-6.64	123.08	128.86
2	B	401	ATP	N3-C2-N1	-6.51	123.18	128.86
2	B	401	ATP	C4-C5-N7	-2.60	106.90	109.41
6	A	409	MHA	C6-C5-N1	-2.49	109.69	114.00
6	A	409	MHA	C2-C1-N1	-2.44	110.01	113.48
6	A	409	MHA	C4-C3-N1	-2.43	110.02	113.48
2	A	401	ATP	C4-C5-N7	-2.37	107.12	109.41
3	A	405	NAG	C3-C4-C5	2.38	114.41	110.22
3	A	405	NAG	C4-C3-C2	2.49	114.66	111.02
3	A	402	NAG	C1-O5-C5	2.50	115.61	112.17
6	A	409	MHA	C5-C6-N2	2.65	120.13	115.81
3	B	404	NAG	C8-C7-N2	3.03	121.59	116.11
4	B	406	MAL	C1-C2-C3	3.34	116.19	109.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	ATP	1	0
3	A	402	NAG	1	0
3	A	403	NAG	1	0
4	A	407	MAL	2	0
3	B	404	NAG	1	0
4	B	405	MAL	1	0
5	B	407	EDO	2	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

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	357/363 (98%)	0.31	20 (5%) 25 19	46, 82, 134, 168	0
1	B	357/363 (98%)	0.45	29 (8%) 13 8	48, 89, 153, 181	0
All	All	714/726 (98%)	0.38	49 (6%) 18 12	46, 86, 141, 181	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	140	TYR	7.2
1	B	130	GLY	7.2
1	B	141	SER	5.6
1	B	146	THR	4.6
1	A	347	LEU	4.3
1	B	123	GLY	4.2
1	B	120	SER	4.2
1	B	347	LEU	4.1
1	B	114	TYR	4.0
1	B	126	ARG	3.8
1	B	131	GLY	3.8
1	B	142	SER	3.7
1	B	128	PRO	3.7
1	A	20	SER	3.6
1	A	8	PHE	3.6
1	A	19	LYS	3.3
1	A	346	PHE	3.3
1	A	362	ASN	3.3
1	A	363	GLU	3.2
1	B	124	PRO	3.2
1	B	136	ARG	3.1
1	A	343	LEU	3.0
1	B	348	LYS	3.0
1	B	129	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	51	VAL	2.9
1	B	121	GLN	2.9
1	A	361	VAL	2.9
1	A	184	PHE	2.9
1	A	51	VAL	2.9
1	A	348	LYS	2.9
1	A	21	TRP	2.8
1	B	133	LEU	2.8
1	A	183	LEU	2.7
1	B	122	CYS	2.6
1	B	138	VAL	2.6
1	A	18	VAL	2.6
1	B	338	LEU	2.5
1	B	143	VAL	2.5
1	B	109	GLU	2.5
1	B	127	LEU	2.5
1	A	160	VAL	2.4
1	A	86	GLY	2.4
1	B	20	SER	2.3
1	A	17	VAL	2.3
1	A	22	THR	2.2
1	B	117	VAL	2.1
1	B	148	GLU	2.1
1	A	288	MET	2.1
1	B	23	ILE	2.1

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	A	405	14/15	0.82	0.50	11.16	123,172,212,213	0
4	MAL	A	407	23/23	0.82	0.41	2.27	104,146,153,157	0
4	MAL	A	406	23/23	0.82	0.32	1.52	121,151,166,168	0
4	MAL	B	405	23/23	0.93	0.32	1.37	120,134,144,151	0
3	NAG	A	403	14/15	0.94	0.20	0.16	99,123,156,166	0
2	ATP	B	401	31/31	0.98	0.19	-0.47	53,64,80,86	0
2	ATP	A	401	31/31	0.98	0.18	-0.76	52,63,79,84	0
3	NAG	A	402	14/15	0.96	0.16	-0.84	53,75,105,109	0
3	NAG	B	403	14/15	0.94	0.15	-0.89	68,92,156,156	0
4	MAL	B	406	23/23	0.62	0.38	-	120,139,152,157	0
3	NAG	B	402	14/15	0.92	0.14	-	88,132,167,179	0
3	NAG	A	404	14/15	0.89	0.42	-	117,147,171,174	0
3	NAG	B	404	14/15	0.63	0.39	-	117,147,171,174	0
5	EDO	B	407	4/4	0.70	0.30	-	95,97,100,100	0
6	MHA	A	409	13/13	0.82	0.23	-	104,110,129,129	21
5	EDO	A	408	4/4	0.76	0.19	-	95,99,110,112	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.