Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:14 PM GMT

PDB ID	:	4KZT
Title	:	Structure mmNAGS bound with L-arginine
Authors	:	Zhao, G.; Jin, Z.; Allewell, N.M.; Tuchman, M.; Shi, D.
Deposited on	:	2013-05-30
Resolution	:	2.80 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

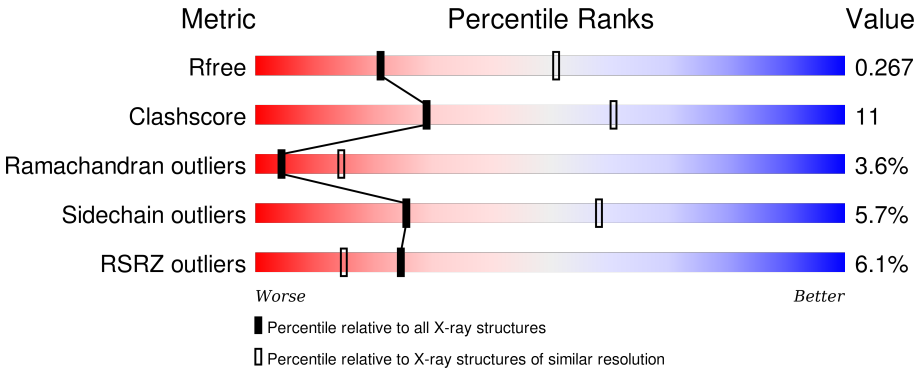
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.80 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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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 >=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 <=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	461	7% 64% 25% • 7%
1	B	461	4% 66% 24% • 7%
1	X	461	7% 70% 21% • 7%
1	Y	461	5% 66% 25% • 7%

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	PEG	X	502	-	-	-	X
3	PEG	Y	502	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13338 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 N-acetylglutamate kinase / N-acetylglutamate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	431	Total	C	N	O	S	0	0	0
			3311	2079	597	626	9			
1	B	431	Total	C	N	O	S	0	0	0
			3311	2079	597	626	9			
1	X	431	Total	C	N	O	S	0	0	0
			3311	2079	597	626	9			
1	Y	431	Total	C	N	O	S	0	0	0
			3311	2079	597	626	9			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q0ASS9
A	-18	GLY	-	EXPRESSION TAG	UNP Q0ASS9
A	-17	SER	-	EXPRESSION TAG	UNP Q0ASS9
A	-16	SER	-	EXPRESSION TAG	UNP Q0ASS9
A	-15	HIS	-	EXPRESSION TAG	UNP Q0ASS9
A	-14	HIS	-	EXPRESSION TAG	UNP Q0ASS9
A	-13	HIS	-	EXPRESSION TAG	UNP Q0ASS9
A	-12	HIS	-	EXPRESSION TAG	UNP Q0ASS9
A	-11	HIS	-	EXPRESSION TAG	UNP Q0ASS9
A	-10	HIS	-	EXPRESSION TAG	UNP Q0ASS9
A	-9	SER	-	EXPRESSION TAG	UNP Q0ASS9
A	-8	SER	-	EXPRESSION TAG	UNP Q0ASS9
A	-7	GLY	-	EXPRESSION TAG	UNP Q0ASS9
A	-6	LEU	-	EXPRESSION TAG	UNP Q0ASS9
A	-5	VAL	-	EXPRESSION TAG	UNP Q0ASS9
A	-4	PRO	-	EXPRESSION TAG	UNP Q0ASS9
A	-3	ARG	-	EXPRESSION TAG	UNP Q0ASS9
A	-2	GLY	-	EXPRESSION TAG	UNP Q0ASS9
A	-1	SER	-	EXPRESSION TAG	UNP Q0ASS9
A	0	HIS	-	EXPRESSION TAG	UNP Q0ASS9
A	106	MET	ILE	ENGINEERED MUTATION	UNP Q0ASS9

Continued on next page...

Continued from previous page...

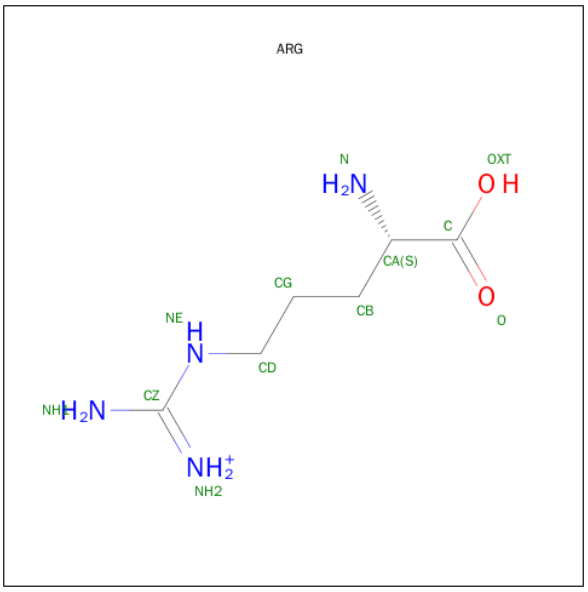
Chain	Residue	Modelled	Actual	Comment	Reference
A	294	MET	ILE	ENGINEERED MUTATION	UNP Q0ASS9
A	376	MET	LEU	ENGINEERED MUTATION	UNP Q0ASS9
B	-19	MET	-	EXPRESSION TAG	UNP Q0ASS9
B	-18	GLY	-	EXPRESSION TAG	UNP Q0ASS9
B	-17	SER	-	EXPRESSION TAG	UNP Q0ASS9
B	-16	SER	-	EXPRESSION TAG	UNP Q0ASS9
B	-15	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	-14	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	-13	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	-12	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	-11	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	-10	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	-9	SER	-	EXPRESSION TAG	UNP Q0ASS9
B	-8	SER	-	EXPRESSION TAG	UNP Q0ASS9
B	-7	GLY	-	EXPRESSION TAG	UNP Q0ASS9
B	-6	LEU	-	EXPRESSION TAG	UNP Q0ASS9
B	-5	VAL	-	EXPRESSION TAG	UNP Q0ASS9
B	-4	PRO	-	EXPRESSION TAG	UNP Q0ASS9
B	-3	ARG	-	EXPRESSION TAG	UNP Q0ASS9
B	-2	GLY	-	EXPRESSION TAG	UNP Q0ASS9
B	-1	SER	-	EXPRESSION TAG	UNP Q0ASS9
B	0	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	106	MET	ILE	ENGINEERED MUTATION	UNP Q0ASS9
B	294	MET	ILE	ENGINEERED MUTATION	UNP Q0ASS9
B	376	MET	LEU	ENGINEERED MUTATION	UNP Q0ASS9
X	-19	MET	-	EXPRESSION TAG	UNP Q0ASS9
X	-18	GLY	-	EXPRESSION TAG	UNP Q0ASS9
X	-17	SER	-	EXPRESSION TAG	UNP Q0ASS9
X	-16	SER	-	EXPRESSION TAG	UNP Q0ASS9
X	-15	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	-14	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	-13	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	-12	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	-11	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	-10	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	-9	SER	-	EXPRESSION TAG	UNP Q0ASS9
X	-8	SER	-	EXPRESSION TAG	UNP Q0ASS9
X	-7	GLY	-	EXPRESSION TAG	UNP Q0ASS9
X	-6	LEU	-	EXPRESSION TAG	UNP Q0ASS9
X	-5	VAL	-	EXPRESSION TAG	UNP Q0ASS9
X	-4	PRO	-	EXPRESSION TAG	UNP Q0ASS9
X	-3	ARG	-	EXPRESSION TAG	UNP Q0ASS9

Continued on next page...

Continued from previous page...

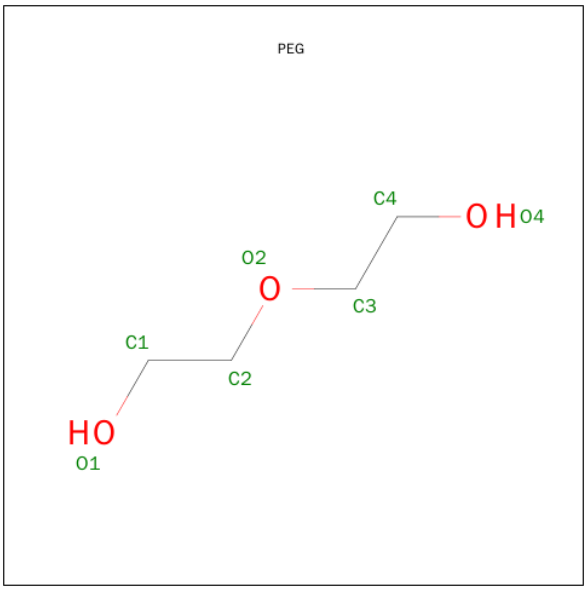
Chain	Residue	Modelled	Actual	Comment	Reference
X	-2	GLY	-	EXPRESSION TAG	UNP Q0ASS9
X	-1	SER	-	EXPRESSION TAG	UNP Q0ASS9
X	0	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	106	MET	ILE	ENGINEERED MUTATION	UNP Q0ASS9
X	294	MET	ILE	ENGINEERED MUTATION	UNP Q0ASS9
X	376	MET	LEU	ENGINEERED MUTATION	UNP Q0ASS9
Y	-19	MET	-	EXPRESSION TAG	UNP Q0ASS9
Y	-18	GLY	-	EXPRESSION TAG	UNP Q0ASS9
Y	-17	SER	-	EXPRESSION TAG	UNP Q0ASS9
Y	-16	SER	-	EXPRESSION TAG	UNP Q0ASS9
Y	-15	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	-14	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	-13	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	-12	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	-11	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	-10	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	-9	SER	-	EXPRESSION TAG	UNP Q0ASS9
Y	-8	SER	-	EXPRESSION TAG	UNP Q0ASS9
Y	-7	GLY	-	EXPRESSION TAG	UNP Q0ASS9
Y	-6	LEU	-	EXPRESSION TAG	UNP Q0ASS9
Y	-5	VAL	-	EXPRESSION TAG	UNP Q0ASS9
Y	-4	PRO	-	EXPRESSION TAG	UNP Q0ASS9
Y	-3	ARG	-	EXPRESSION TAG	UNP Q0ASS9
Y	-2	GLY	-	EXPRESSION TAG	UNP Q0ASS9
Y	-1	SER	-	EXPRESSION TAG	UNP Q0ASS9
Y	0	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	106	MET	ILE	ENGINEERED MUTATION	UNP Q0ASS9
Y	294	MET	ILE	ENGINEERED MUTATION	UNP Q0ASS9
Y	376	MET	LEU	ENGINEERED MUTATION	UNP Q0ASS9

- Molecule 2 is ARGININE (three-letter code: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O 12 6 4 2	0	0
2	B	1	Total C N O 12 6 4 2	0	0
2	X	1	Total C N O 12 6 4 2	0	0
2	Y	1	Total C N O 12 6 4 2	0	0

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 7 4 3	0	0
3	B	1	Total C O 7 4 3	0	0
3	X	1	Total C O 7 4 3	0	0
3	Y	1	Total C O 7 4 3	0	0

- Molecule 4 is water.

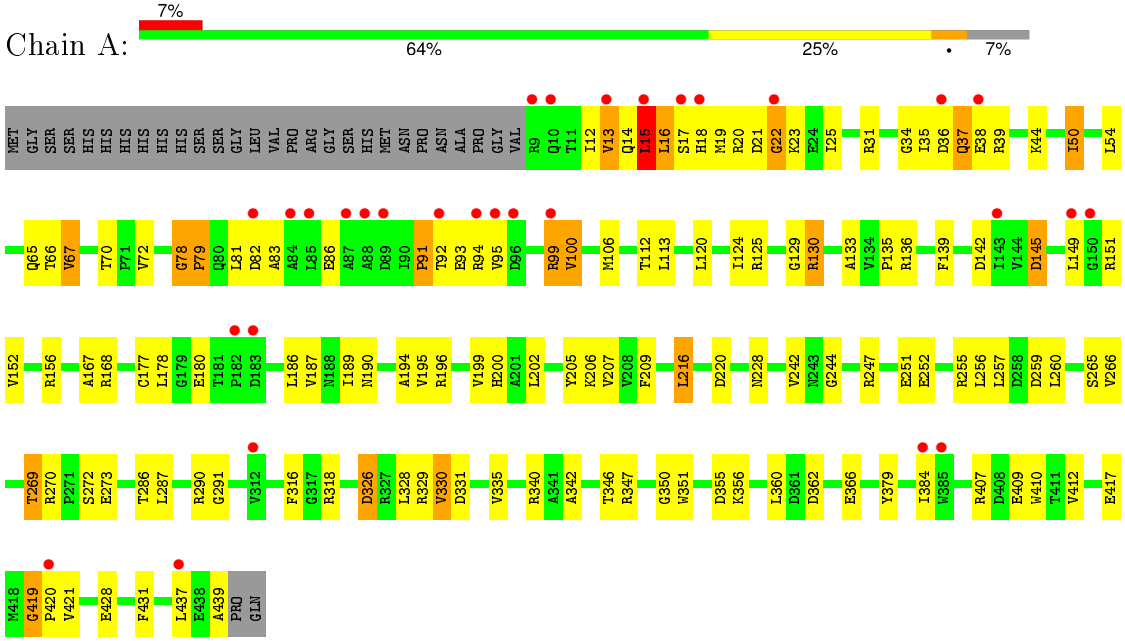
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	4	Total O 4 4	0	0
4	B	5	Total O 5 5	0	0
4	X	2	Total O 2 2	0	0
4	Y	7	Total O 7 7	0	0

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 errors 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.

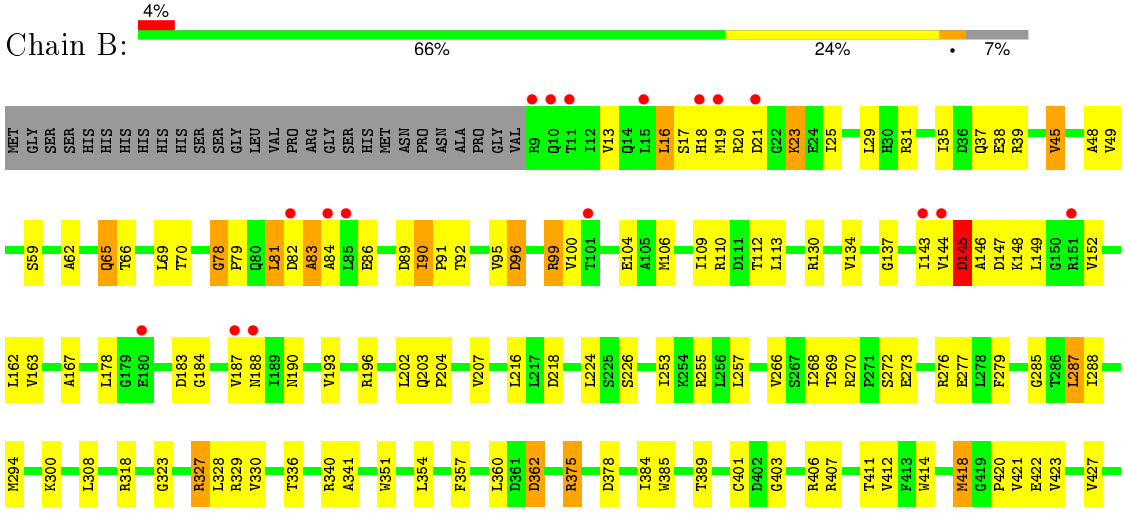
- Molecule 1: N-acetylglutamate kinase / N-acetylglutamate synthase

Chain A:



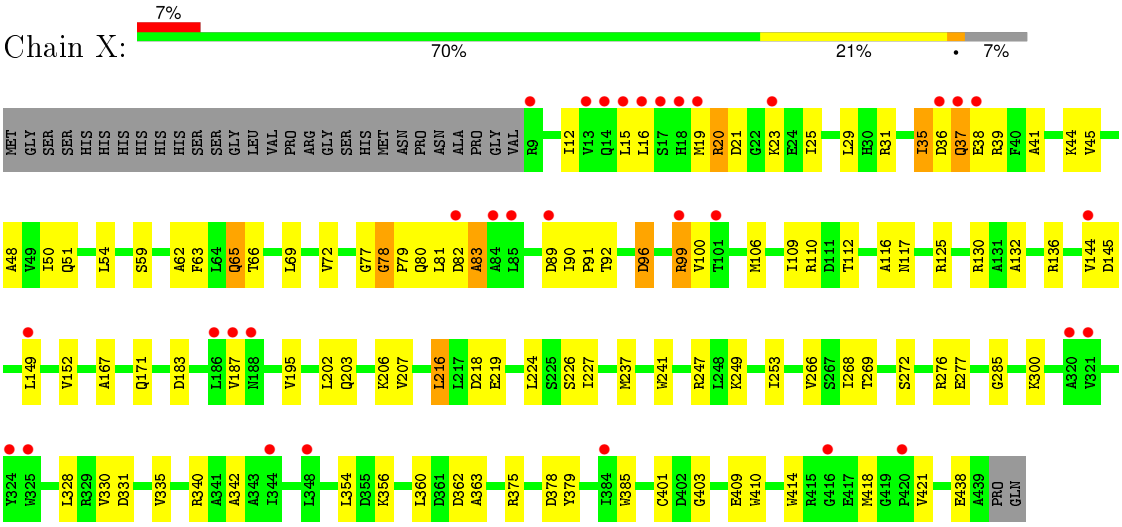
- Molecule 1: N-acetylglutamate kinase / N-acetylglutamate synthase

Chain B:



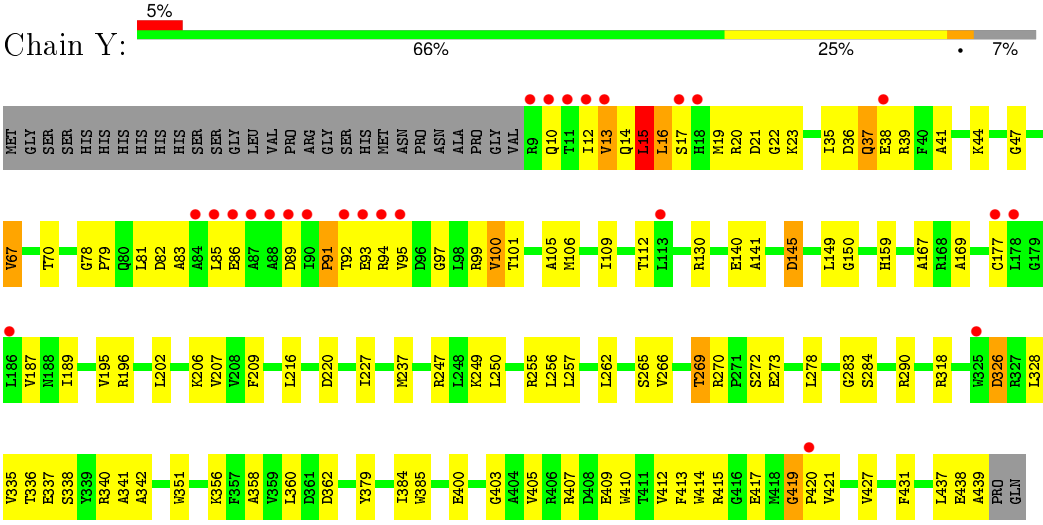
• Molecule 1: N-acetylglutamate kinase / N-acetylglutamate synthase

Chain X:



• Molecule 1: N-acetylglutamate kinase / N-acetylglutamate synthase

Chain Y:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	165.83Å 110.82Å 117.20Å 90.00° 91.02° 90.00°	Depositor
Resolution (Å)	39.30 – 2.80 49.66 – 2.79	Depositor EDS
% Data completeness (in resolution range)	89.8 (39.30-2.80) 84.6 (49.66-2.79)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.05 (at 2.77Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.196 , 0.265 0.202 , 0.267	Depositor DCC
R_{free} test set	1989 reflections (4.64%)	DCC
Wilson B-factor (Å^2)	77.0	Xtriage
Anisotropy	0.552	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 46.2	EDS
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 47668 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	13338	wwPDB-VP
Average B, all atoms (Å^2)	102.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: PEG

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	0.46	0/3369	0.68	1/4576 (0.0%)
1	B	0.48	0/3369	0.68	1/4576 (0.0%)
1	X	0.44	0/3369	0.66	0/4576
1	Y	0.46	0/3369	0.66	1/4576 (0.0%)
All	All	0.46	0/13476	0.67	3/18304 (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	1
1	Y	0	1
All	All	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	34	GLY	N-CA-C	-5.54	99.25	113.10
1	Y	15	LEU	CA-CB-CG	5.33	127.56	115.30
1	B	81	LEU	CA-CB-CG	5.18	127.20	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	15	LEU	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	Y	15	LEU	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	3311	0	3302	93	0
1	B	3311	0	3302	81	0
1	X	3311	0	3302	63	0
1	Y	3311	0	3302	84	0
2	A	12	0	12	2	0
2	B	12	0	12	1	0
2	X	12	0	12	1	0
2	Y	12	0	12	2	0
3	A	7	0	10	3	0
3	B	7	0	10	1	0
3	X	7	0	10	0	0
3	Y	7	0	10	0	0
4	A	4	0	0	3	0
4	B	5	0	0	4	0
4	X	2	0	0	0	0
4	Y	7	0	0	3	0
All	All	13338	0	13296	303	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 11.

All (303) 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:329:ARG:NH2	4:B:605:HOH:O	1.85	1.07
1:Y:249:LYS:NZ	4:Y:606:HOH:O	1.93	0.99
1:Y:65:GLN:HG2	1:Y:130:ARG:H	1.40	0.87
1:Y:12:ILE:HG21	1:Y:67:VAL:HA	1.57	0.86
1:A:65:GLN:HG2	1:A:130:ARG:H	1.39	0.84
1:A:38:GLU:HG2	1:A:167:ALA:HB2	1.64	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:GLN:HB3	4:A:604:HOH:O	1.83	0.78
1:X:300:LYS:NZ	1:X:328:LEU:O	2.18	0.76
1:A:207:VAL:HB	1:A:266:VAL:HG22	1.67	0.76
1:B:300:LYS:NZ	1:B:328:LEU:O	2.18	0.75
1:Y:409:GLU:HG2	1:Y:410:TRP:CD1	2.22	0.75
1:B:38:GLU:HG2	1:B:167:ALA:HB2	1.69	0.74
1:B:145:ASP:HB2	1:B:149:LEU:HB2	1.71	0.72
1:A:142:ASP:OD1	1:A:156:ARG:NH2	2.23	0.71
1:B:70:THR:HG21	1:B:167:ALA:HA	1.73	0.71
1:X:136:ARG:NH2	1:Y:180:GLU:OE2	2.23	0.70
1:B:59:SER:HB3	1:Y:14:GLN:HG2	1.72	0.69
1:A:14:GLN:HG2	1:X:59:SER:HB3	1.73	0.69
1:A:228:ASN:ND2	1:A:291:GLY:HA3	2.06	0.69
1:X:39:ARG:NH1	1:X:203:GLN:O	2.26	0.69
1:A:409:GLU:HG2	1:A:410:TRP:CD1	2.29	0.68
1:B:218:ASP:HB3	1:B:224:LEU:HD13	1.75	0.68
1:A:37:GLN:OE1	1:A:168:ARG:NH1	2.27	0.68
1:A:437:LEU:HD22	3:A:502:PEG:H12	1.77	0.66
1:A:21:ASP:O	1:A:23:LYS:N	2.27	0.66
1:Y:318:ARG:HD2	1:Y:439:ALA:HB3	1.77	0.66
1:B:148:LYS:HG2	1:B:149:LEU:HD23	1.77	0.66
1:Y:257:LEU:HD21	1:Y:266:VAL:HG23	1.78	0.65
1:Y:206:LYS:NZ	1:Y:265:SER:OG	2.27	0.65
1:Y:38:GLU:HG2	1:Y:167:ALA:HB2	1.77	0.65
1:X:38:GLU:HG2	1:X:167:ALA:HB2	1.80	0.64
1:B:106:MET:HE2	1:B:106:MET:HA	1.80	0.63
1:X:19:MET:O	1:X:21:ASP:N	2.32	0.63
1:A:50:ILE:HG22	1:A:54:LEU:HD13	1.81	0.63
1:A:44:LYS:HB2	1:A:195:VAL:HG21	1.81	0.63
1:Y:21:ASP:O	1:Y:23:LYS:N	2.32	0.63
1:Y:15:LEU:HB3	1:Y:16:LEU:HD23	1.81	0.62
1:Y:262:LEU:HG	1:Y:290:ARG:HH21	1.64	0.62
1:B:39:ARG:NH1	1:B:203:GLN:O	2.32	0.62
1:Y:421:VAL:HG13	4:Y:604:HOH:O	1.99	0.61
1:B:340:ARG:HG2	1:B:360:LEU:HD12	1.84	0.60
1:A:151:ARG:HG3	1:A:187:VAL:HG23	1.83	0.60
1:A:20:ARG:HE	1:X:276:ARG:HE	1.50	0.60
1:Y:409:GLU:HG2	1:Y:410:TRP:HD1	1.64	0.60
1:A:265:SER:HB2	1:A:287:LEU:HD11	1.84	0.60
1:X:110:ARG:NH1	1:Y:180:GLU:OE1	2.35	0.60
1:X:409:GLU:HG2	1:X:410:TRP:HD1	1.67	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:419:GLY:O	1:Y:421:VAL:N	2.32	0.60
1:A:242:VAL:HG12	1:A:247:ARG:HG3	1.84	0.59
1:B:375:ARG:HB2	1:B:375:ARG:HH11	1.67	0.59
1:X:409:GLU:HG2	1:X:410:TRP:CD1	2.37	0.59
1:B:19:MET:O	1:B:21:ASP:N	2.34	0.58
1:X:39:ARG:HD2	1:X:202:LEU:O	2.04	0.58
1:A:16:LEU:HA	1:A:19:MET:HG3	1.84	0.58
1:A:35:ILE:C	1:A:37:GLN:H	2.08	0.58
1:B:39:ARG:HD2	1:B:202:LEU:O	2.03	0.57
1:Y:278:LEU:O	2:Y:501:ARG:N	2.38	0.57
1:A:318:ARG:HD2	1:A:439:ALA:HB3	1.87	0.57
1:B:329:ARG:CZ	4:B:605:HOH:O	2.42	0.56
1:Y:35:ILE:HG22	1:Y:37:GLN:H	1.70	0.56
1:Y:400:GLU:O	1:Y:415:ARG:NH1	2.38	0.56
1:Y:145:ASP:HB2	1:Y:149:LEU:HB2	1.86	0.56
1:A:38:GLU:HB3	1:A:72:VAL:HG23	1.88	0.56
1:A:419:GLY:O	1:A:421:VAL:N	2.33	0.56
1:B:276:ARG:NH2	1:Y:20:ARG:O	2.37	0.55
1:A:38:GLU:OE2	1:A:70:THR:OG1	2.20	0.55
1:X:340:ARG:HB3	1:X:363:ALA:HB2	1.89	0.55
1:Y:140:GLU:OE1	1:Y:159:HIS:NE2	2.40	0.55
1:B:99:ARG:O	1:B:152:VAL:HG21	2.07	0.55
1:Y:177:CYS:HB3	1:Y:189:ILE:O	2.06	0.55
1:Y:85:LEU:HD12	1:Y:112:THR:HG23	1.89	0.55
1:A:38:GLU:CG	1:A:167:ALA:HB2	2.36	0.54
1:A:14:GLN:HG3	1:A:18:HIS:NE2	2.22	0.54
1:B:62:ALA:O	1:B:66:THR:HG23	2.07	0.54
1:B:65:GLN:HA	1:B:69:LEU:O	2.08	0.54
1:A:257:LEU:HD21	1:A:266:VAL:HG23	1.90	0.53
1:A:19:MET:HG2	1:X:19:MET:HG3	1.89	0.53
1:A:31:ARG:HD3	1:A:205:TYR:OH	2.08	0.53
1:B:406:ARG:HD2	1:B:411:THR:OG1	2.08	0.53
1:A:351:TRP:HB3	1:A:384:ILE:HD13	1.91	0.53
1:X:237:MET:SD	1:X:247:ARG:HG2	2.49	0.53
1:Y:207:VAL:HB	1:Y:266:VAL:HG22	1.90	0.53
1:B:25:ILE:HG23	1:B:279:PHE:HB3	1.91	0.53
1:Y:145:ASP:OD1	1:Y:150:GLY:N	2.41	0.53
1:A:340:ARG:HG2	1:A:360:LEU:HD12	1.90	0.53
1:B:269:THR:HG21	1:B:277:GLU:HB2	1.91	0.53
1:Y:269:THR:CG2	1:Y:273:GLU:HB2	2.39	0.53
1:B:196:ARG:HH11	1:B:255:ARG:HD2	1.75	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:113:LEU:HD12	1:B:178:LEU:HD21	1.90	0.52
1:X:331:ASP:OD2	1:X:379:TYR:OH	2.16	0.52
1:Y:196:ARG:HH11	1:Y:255:ARG:HD2	1.74	0.52
1:B:323:GLY:C	1:B:327:ARG:HH21	2.13	0.52
1:Y:412:VAL:HG23	1:Y:431:PHE:CE1	2.44	0.52
1:A:362:ASP:O	1:A:366:GLU:HG3	2.10	0.52
1:X:249:LYS:O	1:X:253:ILE:HG13	2.10	0.52
1:A:81:LEU:HB3	1:A:112:THR:HG21	1.91	0.52
1:Y:405:VAL:HG21	1:Y:427:VAL:HG11	1.91	0.52
1:Y:81:LEU:HB3	1:Y:112:THR:HG21	1.92	0.51
1:X:96:ASP:HB2	1:X:100:VAL:HG13	1.93	0.51
1:A:16:LEU:HD12	1:A:17:SER:H	1.76	0.51
1:B:65:GLN:OE1	1:B:130:ARG:HB2	2.10	0.51
1:X:35:ILE:O	1:X:37:GLN:N	2.39	0.51
1:X:44:LYS:HD2	1:X:195:VAL:HG21	1.91	0.51
1:X:340:ARG:HG2	1:X:360:LEU:HD12	1.93	0.51
1:Y:328:LEU:HG	1:Y:330:VAL:HG23	1.93	0.51
1:B:190:ASN:HB3	1:B:193:VAL:HG22	1.93	0.50
1:X:403:GLY:HA3	1:X:414:TRP:CZ2	2.46	0.50
1:B:17:SER:HB2	1:B:18:HIS:CD2	2.45	0.50
1:X:41:ALA:HA	1:X:206:LYS:O	2.11	0.50
1:A:120:LEU:O	1:A:124:ILE:HG13	2.11	0.50
1:B:38:GLU:CG	1:B:167:ALA:HB2	2.40	0.50
1:A:244:GLY:HA2	1:A:247:ARG:HD3	1.93	0.50
1:X:269:THR:HG21	1:X:277:GLU:HB2	1.93	0.50
1:Y:81:LEU:O	1:Y:86:GLU:HB2	2.12	0.50
1:A:328:LEU:HG	1:A:330:VAL:HG23	1.93	0.50
1:Y:331:ASP:OD2	1:Y:379:TYR:OH	2.18	0.50
1:A:20:ARG:HB2	1:X:20:ARG:CG	2.42	0.49
1:B:269:THR:HG22	1:B:285:GLY:HA3	1.94	0.49
1:X:65:GLN:HA	1:X:69:LEU:O	2.11	0.49
1:X:81:LEU:HD12	1:X:82:ASP:N	2.27	0.49
1:A:35:ILE:O	1:A:37:GLN:N	2.32	0.49
1:X:354:LEU:HB3	1:X:385:TRP:HB3	1.95	0.49
1:A:136:ARG:HH21	1:B:137:GLY:HA2	1.76	0.49
1:X:99:ARG:O	1:X:152:VAL:HG21	2.13	0.49
1:B:38:GLU:HG3	1:B:163:VAL:HG12	1.94	0.49
1:Y:340:ARG:HG2	1:Y:360:LEU:HD12	1.95	0.49
1:B:362:ASP:N	1:B:362:ASP:OD2	2.41	0.48
1:A:22:GLY:HA2	1:A:25:ILE:HD12	1.95	0.48
1:B:13:VAL:O	1:B:16:LEU:HD11	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:78:GLY:O	1:X:82:ASP:HB3	2.14	0.48
1:B:354:LEU:HB3	1:B:385:TRP:HB3	1.96	0.48
1:A:269:THR:HG22	1:A:270:ARG:H	1.77	0.48
1:B:270:ARG:HG2	1:B:273:GLU:HG2	1.95	0.48
1:X:81:LEU:HD22	1:X:109:ILE:HG12	1.96	0.48
1:A:133:ALA:C	1:A:135:PRO:HD3	2.34	0.48
1:B:147:ASP:OD1	1:B:147:ASP:N	2.46	0.48
1:X:125:ARG:HD3	1:Y:169:ALA:HB2	1.96	0.48
1:B:19:MET:C	1:B:21:ASP:H	2.17	0.48
1:A:228:ASN:HD21	1:A:291:GLY:HA3	1.79	0.47
1:Y:269:THR:HG22	1:Y:270:ARG:H	1.78	0.47
1:A:86:GLU:HG2	1:A:91:PRO:HG2	1.95	0.47
1:A:99:ARG:O	1:A:152:VAL:HG21	2.14	0.47
1:A:196:ARG:NH1	1:A:252:GLU:OE1	2.46	0.47
1:A:347:ARG:NH1	1:A:350:GLY:O	2.47	0.47
1:X:269:THR:HG22	1:X:285:GLY:HA3	1.96	0.47
1:B:357:PHE:H	3:B:502:PEG:H21	1.78	0.47
1:A:331:ASP:OD2	1:A:379:TYR:OH	2.26	0.47
1:Y:421:VAL:N	4:Y:604:HOH:O	2.48	0.47
1:Y:14:GLN:NE2	1:Y:17:SER:HB2	2.30	0.47
1:A:145:ASP:CG	1:A:149:LEU:HB2	2.35	0.47
1:A:81:LEU:HD12	1:A:82:ASP:N	2.30	0.47
1:Y:362:ASP:N	1:Y:362:ASP:OD2	2.47	0.47
1:B:134:VAL:HG13	1:B:162:LEU:HD13	1.97	0.47
1:Y:97:GLY:H	1:Y:149:LEU:HD21	1.80	0.47
1:A:186:LEU:HB3	1:B:184:GLY:HA3	1.95	0.47
1:B:257:LEU:HD21	1:B:266:VAL:HG23	1.97	0.47
1:A:37:GLN:HB3	1:A:38:GLU:H	1.47	0.46
1:B:81:LEU:HD22	1:B:109:ILE:HG12	1.97	0.46
1:B:86:GLU:HG2	1:B:91:PRO:HG2	1.97	0.46
1:Y:141:ALA:O	1:Y:181:THR:HA	2.15	0.46
1:A:412:VAL:HG23	1:A:431:PHE:CE1	2.51	0.46
1:Y:16:LEU:HA	1:Y:19:MET:HG3	1.97	0.46
1:A:200:HIS:ND1	1:A:259:ASP:OD2	2.47	0.46
1:Y:36:ASP:O	1:Y:37:GLN:HB2	2.16	0.46
1:A:196:ARG:NH1	1:A:255:ARG:HD2	2.30	0.46
1:Y:39:ARG:HD2	1:Y:202:LEU:O	2.16	0.46
1:B:96:ASP:HB2	1:B:100:VAL:HG13	1.98	0.46
1:Y:105:ALA:O	1:Y:109:ILE:HG13	2.16	0.46
1:B:354:LEU:HB3	1:B:385:TRP:CB	2.47	0.45
1:X:90:ILE:N	1:X:91:PRO:HD3	2.31	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:403:GLY:HA3	1:Y:414:TRP:CZ2	2.51	0.45
1:Y:237:MET:O	1:Y:247:ARG:NH1	2.49	0.45
1:Y:38:GLU:OE2	1:Y:70:THR:OG1	2.30	0.45
1:Y:89:ASP:HB3	1:Y:91:PRO:HD3	1.98	0.45
1:A:94:ARG:O	1:A:100:VAL:HG13	2.16	0.45
1:A:346:THR:HG23	1:A:355:ASP:HB2	1.97	0.45
1:Y:336:THR:HG22	1:Y:341:ALA:O	2.16	0.45
1:Y:38:GLU:CG	1:Y:167:ALA:HB2	2.44	0.45
1:X:81:LEU:C	1:X:83:ALA:H	2.20	0.45
1:B:308:LEU:HD23	1:B:308:LEU:HA	1.76	0.45
1:X:207:VAL:HB	1:X:266:VAL:HG22	1.99	0.45
1:B:38:GLU:HA	1:B:38:GLU:OE2	2.15	0.45
1:A:50:ILE:O	1:A:54:LEU:HB2	2.15	0.45
1:X:106:MET:HE2	1:X:106:MET:HA	1.98	0.45
1:Y:227:ILE:HD13	1:Y:250:LEU:HD21	1.98	0.45
1:A:130:ARG:CG	1:A:130:ARG:HH11	2.30	0.45
1:B:81:LEU:C	1:B:83:ALA:H	2.20	0.45
1:Y:196:ARG:HA	1:Y:256:LEU:HD21	1.99	0.45
1:A:113:LEU:HD12	1:A:178:LEU:HD21	1.99	0.45
1:A:136:ARG:NH2	1:B:137:GLY:HA2	2.31	0.45
1:A:125:ARG:HA	1:A:129:GLY:O	2.17	0.45
1:X:132:ALA:HB2	1:X:171:GLN:OE1	2.17	0.44
1:B:106:MET:CE	1:B:188:ASN:HB2	2.47	0.44
1:B:351:TRP:HB3	1:B:384:ILE:HD13	1.99	0.44
1:X:51:GLN:HB2	1:X:80:GLN:NE2	2.32	0.44
1:Y:326:ASP:OD1	1:Y:326:ASP:N	2.50	0.44
1:X:12:ILE:HG23	1:X:15:LEU:HB3	1.99	0.44
1:B:422:GLU:HB2	4:B:603:HOH:O	2.17	0.44
1:A:38:GLU:HB2	4:A:604:HOH:O	2.17	0.44
1:Y:44:LYS:HD3	1:Y:209:PHE:CE1	2.52	0.44
1:X:216:LEU:HD22	1:X:268:ILE:HD12	1.99	0.44
1:A:199:VAL:HG13	1:A:260:LEU:HD21	1.99	0.44
1:A:409:GLU:HG2	1:A:410:TRP:HD1	1.79	0.44
1:Y:269:THR:HG21	1:Y:273:GLU:HB2	1.99	0.44
1:X:12:ILE:HG23	1:X:15:LEU:HD23	2.00	0.44
1:A:20:ARG:O	1:X:276:ARG:NH2	2.49	0.44
1:B:276:ARG:HE	1:Y:20:ARG:HA	1.83	0.44
1:B:318:ARG:HD2	1:B:439:ALA:HB3	1.99	0.44
1:A:44:LYS:HD3	1:A:209:PHE:CE1	2.53	0.44
1:Y:41:ALA:HA	1:Y:206:LYS:O	2.18	0.43
1:B:354:LEU:HD21	1:B:357:PHE:HB2	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:207:VAL:HB	1:B:266:VAL:HG22	1.99	0.43
1:X:438:GLU:HG2	1:X:438:GLU:H	1.57	0.43
1:A:335:VAL:HG13	1:A:342:ALA:HB2	2.00	0.43
1:A:287:LEU:HB2	2:A:501:ARG:NE	2.33	0.43
1:A:180:GLU:OE1	1:B:110:ARG:NH1	2.51	0.43
1:X:356:LYS:HA	1:X:356:LYS:HD3	1.76	0.43
1:A:35:ILE:C	1:A:37:GLN:N	2.71	0.43
1:A:196:ARG:HA	1:A:256:LEU:HD21	1.99	0.43
1:B:412:VAL:HG11	1:B:427:VAL:HG22	1.98	0.43
1:B:418:MET:HG3	1:B:423:VAL:CG1	2.49	0.43
1:X:206:LYS:HE2	2:X:501:ARG:OXT	2.19	0.43
1:A:269:THR:CG2	1:A:273:GLU:HB2	2.48	0.43
1:A:177:CYS:HB3	1:A:189:ILE:O	2.18	0.43
1:A:316:PHE:HE1	3:A:502:PEG:H21	1.83	0.43
1:Y:12:ILE:O	1:Y:16:LEU:HD21	2.18	0.43
1:B:389:THR:HG21	1:B:407:ARG:O	2.19	0.43
1:Y:97:GLY:HA3	1:Y:149:LEU:HD21	2.01	0.42
1:Y:181:THR:HG23	1:Y:185:THR:O	2.19	0.42
1:B:287:LEU:HG	1:B:288:ILE:N	2.34	0.42
1:A:35:ILE:HG22	1:A:37:GLN:N	2.34	0.42
1:B:143:ILE:O	1:B:145:ASP:N	2.52	0.42
1:A:39:ARG:HD2	1:A:202:LEU:O	2.19	0.42
1:A:410:TRP:HH2	3:A:502:PEG:H11	1.83	0.42
1:Y:412:VAL:HG23	1:Y:431:PHE:CZ	2.55	0.42
1:X:65:GLN:HE22	1:X:130:ARG:HD3	1.85	0.42
1:A:12:ILE:HG21	1:A:67:VAL:HA	2.01	0.42
1:A:290:ARG:HD3	4:A:602:HOH:O	2.20	0.42
1:B:285:GLY:O	2:B:501:ARG:NH2	2.53	0.42
1:Y:351:TRP:HB3	1:Y:384:ILE:HD13	2.02	0.42
1:A:14:GLN:NE2	1:A:17:SER:HB2	2.35	0.42
1:Y:47:GLY:O	1:Y:50:ILE:HG13	2.19	0.42
1:B:86:GLU:O	1:B:91:PRO:HG2	2.20	0.42
1:A:216:LEU:HA	1:A:216:LEU:HD12	1.91	0.42
1:B:19:MET:SD	1:Y:19:MET:HG2	2.58	0.42
1:X:38:GLU:CG	1:X:167:ALA:HB2	2.46	0.42
1:A:326:ASP:N	1:A:326:ASP:OD1	2.52	0.42
1:A:15:LEU:HB3	1:A:16:LEU:HD23	2.02	0.41
1:Y:336:THR:O	1:Y:338:SER:N	2.53	0.41
1:B:403:GLY:HA3	1:B:414:TRP:CZ2	2.55	0.41
1:B:90:ILE:N	1:B:91:PRO:HD3	2.35	0.41
1:Y:101:THR:O	1:Y:101:THR:OG1	2.34	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:GLU:OE1	1:B:70:THR:HG22	2.20	0.41
1:X:38:GLU:HB3	1:X:72:VAL:CG2	2.51	0.41
1:Y:196:ARG:NH1	1:Y:255:ARG:HD2	2.35	0.41
1:B:81:LEU:HD12	1:B:82:ASP:N	2.36	0.41
1:Y:341:ALA:HA	1:Y:358:ALA:O	2.21	0.41
1:A:216:LEU:HB2	1:A:286:THR:HG21	2.02	0.41
1:X:48:ALA:HA	1:X:79:PRO:HG2	2.02	0.41
1:X:25:ILE:H	1:X:25:ILE:HG12	1.75	0.41
1:A:15:LEU:HD22	1:X:63:PHE:HE1	1.85	0.41
1:B:78:GLY:O	1:B:82:ASP:HB3	2.20	0.41
1:X:218:ASP:HB3	1:X:224:LEU:HD13	2.02	0.41
1:Y:89:ASP:C	1:Y:91:PRO:HD3	2.41	0.41
1:X:219:GLU:HB2	1:X:241:TRP:CE2	2.56	0.41
1:A:78:GLY:HA3	1:A:79:PRO:HD3	1.89	0.41
1:B:294:MET:SD	1:B:375:ARG:HD2	2.60	0.41
1:B:104:GLU:HG2	1:B:104:GLU:H	1.64	0.41
1:Y:269:THR:HG22	1:Y:273:GLU:HB2	2.02	0.41
1:X:65:GLN:CD	1:X:130:ARG:H	2.24	0.41
1:X:50:ILE:HD12	1:X:116:ALA:HB1	2.02	0.41
1:B:253:ILE:HD11	1:B:268:ILE:HD11	2.03	0.41
1:A:407:ARG:NH2	1:A:428:GLU:OE1	2.53	0.41
1:Y:10:GLN:O	1:Y:13:VAL:HG23	2.20	0.41
1:B:38:GLU:OE2	1:B:70:THR:HB	2.21	0.41
1:Y:38:GLU:OE2	1:Y:38:GLU:HA	2.21	0.41
1:A:206:LYS:HZ3	2:A:501:ARG:C	2.23	0.41
1:Y:81:LEU:HD12	1:Y:82:ASP:N	2.36	0.41
1:Y:403:GLY:HA3	1:Y:414:TRP:CH2	2.55	0.41
1:X:224:LEU:HD23	1:X:227:ILE:HD11	2.03	0.41
1:B:23:LYS:N	4:B:601:HOH:O	2.53	0.41
1:Y:385:TRP:CE2	1:Y:413:PHE:HB2	2.56	0.41
1:A:356:LYS:HA	1:A:356:LYS:HD3	1.81	0.41
1:B:48:ALA:HA	1:B:79:PRO:HG2	2.03	0.41
1:Y:140:GLU:HB2	1:Y:159:HIS:CD2	2.55	0.41
1:X:50:ILE:O	1:X:54:LEU:HB2	2.21	0.41
1:B:45:VAL:HG23	1:B:49:VAL:HB	2.03	0.41
1:B:336:THR:HG22	1:B:341:ALA:O	2.20	0.41
1:B:39:ARG:O	1:B:204:PRO:HA	2.21	0.40
1:A:20:ARG:HA	1:X:276:ARG:HE	1.86	0.40
1:A:139:PHE:CZ	1:A:194:ALA:HB1	2.56	0.40
1:Y:356:LYS:HE3	1:Y:437:LEU:HD13	2.03	0.40
1:X:19:MET:C	1:X:21:ASP:H	2.23	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:283:GLY:HA3	2:Y:501:ARG:NH1	2.36	0.40
1:X:77:GLY:O	1:X:81:LEU:HG	2.21	0.40
1:A:251:GLU:HG2	1:A:255:ARG:NH2	2.36	0.40
1:B:253:ILE:HG21	1:B:288:ILE:HD12	2.04	0.40
1:Y:335:VAL:HG13	1:Y:342:ALA:HB2	2.02	0.40
1:Y:44:LYS:HB2	1:Y:195:VAL:HG21	2.03	0.40
1:X:219:GLU:HB2	1:X:241:TRP:CD2	2.56	0.40
1:X:62:ALA:O	1:X:66:THR:HG23	2.21	0.40
1:Y:94:ARG:O	1:Y:100:VAL:HG13	2.21	0.40
1:X:335:VAL:HG22	1:X:342:ALA:HB1	2.03	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	429/461 (93%)	376 (88%)	36 (8%)	17 (4%)	4	12
1	B	429/461 (93%)	382 (89%)	33 (8%)	14 (3%)	5	16
1	X	429/461 (93%)	383 (89%)	34 (8%)	12 (3%)	6	21
1	Y	429/461 (93%)	381 (89%)	30 (7%)	18 (4%)	3	11
All	All	1716/1844 (93%)	1522 (89%)	133 (8%)	61 (4%)	4	14

All (61) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	15	LEU
1	A	22	GLY
1	A	37	GLN
1	A	145	ASP
1	A	417	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	420	PRO
1	B	20	ARG
1	B	96	ASP
1	B	144	VAL
1	B	145	ASP
1	X	20	ARG
1	X	37	GLN
1	X	144	VAL
1	X	145	ASP
1	Y	15	LEU
1	Y	22	GLY
1	Y	37	GLN
1	Y	417	GLU
1	Y	420	PRO
1	A	36	ASP
1	A	78	GLY
1	A	83	ALA
1	A	92	THR
1	A	93	GLU
1	A	419	GLY
1	B	23	LYS
1	B	78	GLY
1	B	84	ALA
1	X	23	LYS
1	X	78	GLY
1	X	96	ASP
1	Y	83	ALA
1	Y	93	GLU
1	Y	145	ASP
1	B	31	ARG
1	B	37	GLN
1	B	83	ALA
1	X	83	ALA
1	Y	92	THR
1	Y	330	VAL
1	Y	337	GLU
1	A	330	VAL
1	B	146	ALA
1	X	31	ARG
1	X	92	THR
1	X	330	VAL
1	Y	13	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Y	78	GLY
1	Y	419	GLY
1	A	91	PRO
1	A	329	ARG
1	B	92	THR
1	B	330	VAL
1	Y	91	PRO
1	Y	284	SER
1	X	36	ASP
1	Y	329	ARG
1	B	420	PRO
1	Y	79	PRO
1	A	13	VAL
1	A	79	PRO

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	342/367 (93%)	326 (95%)	16 (5%)	32	67
1	B	342/367 (93%)	317 (93%)	25 (7%)	17	44
1	X	342/367 (93%)	321 (94%)	21 (6%)	23	55
1	Y	342/367 (93%)	326 (95%)	16 (5%)	32	67
All	All	1368/1468 (93%)	1290 (94%)	78 (6%)	25	58

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	VAL
1	A	16	LEU
1	A	50	ILE
1	A	66	THR
1	A	67	VAL
1	A	95	VAL
1	A	99	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	100	VAL
1	A	106	MET
1	A	130	ARG
1	A	190	ASN
1	A	216	LEU
1	A	220	ASP
1	A	269	THR
1	A	272	SER
1	A	326	ASP
1	B	16	LEU
1	B	29	LEU
1	B	35	ILE
1	B	45	VAL
1	B	65	GLN
1	B	89	ASP
1	B	90	ILE
1	B	95	VAL
1	B	99	ARG
1	B	112	THR
1	B	145	ASP
1	B	183	ASP
1	B	187	VAL
1	B	216	LEU
1	B	226	SER
1	B	272	SER
1	B	287	LEU
1	B	327	ARG
1	B	362	ASP
1	B	375	ARG
1	B	378	ASP
1	B	401	CYS
1	B	418	MET
1	B	421	VAL
1	B	438	GLU
1	X	16	LEU
1	X	29	LEU
1	X	35	ILE
1	X	45	VAL
1	X	65	GLN
1	X	89	ASP
1	X	99	ARG
1	X	112	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	X	117	ASN
1	X	149	LEU
1	X	183	ASP
1	X	187	VAL
1	X	216	LEU
1	X	226	SER
1	X	272	SER
1	X	362	ASP
1	X	375	ARG
1	X	378	ASP
1	X	401	CYS
1	X	418	MET
1	X	421	VAL
1	Y	16	LEU
1	Y	50	ILE
1	Y	66	THR
1	Y	67	VAL
1	Y	95	VAL
1	Y	99	ARG
1	Y	100	VAL
1	Y	106	MET
1	Y	187	VAL
1	Y	216	LEU
1	Y	220	ASP
1	Y	269	THR
1	Y	272	SER
1	Y	326	ASP
1	Y	407	ARG
1	Y	438	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	228	ASN

5.3.3 RNA

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

8 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	ARG	A	501	-	5,11,11	0.43	0	3,13,13	0.46	0
3	PEG	A	502	-	6,6,6	0.48	0	5,5,5	1.52	0
2	ARG	B	501	-	5,11,11	0.39	0	3,13,13	0.61	0
3	PEG	B	502	-	6,6,6	0.46	0	5,5,5	1.52	0
2	ARG	X	501	-	5,11,11	0.33	0	3,13,13	0.40	0
3	PEG	X	502	-	6,6,6	0.66	0	5,5,5	1.24	0
2	ARG	Y	501	-	5,11,11	0.44	0	3,13,13	0.46	0
3	PEG	Y	502	-	6,6,6	0.51	0	5,5,5	1.31	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	ARG	A	501	-	-	0/5/11/11	0/0/0/0
3	PEG	A	502	-	-	0/4/4/4	0/0/0/0
2	ARG	B	501	-	-	0/5/11/11	0/0/0/0
3	PEG	B	502	-	-	0/4/4/4	0/0/0/0
2	ARG	X	501	-	-	0/5/11/11	0/0/0/0
3	PEG	X	502	-	-	0/4/4/4	0/0/0/0
2	ARG	Y	501	-	-	0/5/11/11	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PEG	Y	502	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	ARG	2	0
3	A	502	PEG	3	0
2	B	501	ARG	1	0
3	B	502	PEG	1	0
2	X	501	ARG	1	0
2	Y	501	ARG	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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^{th} 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	431/461 (93%)	0.37	30 (6%)	19	11	59, 96, 163, 205	0
1	B	431/461 (93%)	0.11	18 (4%)	40	28	43, 84, 154, 193	0
1	X	431/461 (93%)	0.29	32 (7%)	17	9	68, 102, 167, 199	0
1	Y	431/461 (93%)	0.21	25 (5%)	26	16	57, 98, 174, 214	0
All	All	1724/1844 (93%)	0.24	105 (6%)	25	15	43, 96, 166, 214	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Y	18	HIS	9.4
1	B	18	HIS	9.3
1	A	87	ALA	9.1
1	Y	85	LEU	6.5
1	X	144	VAL	6.5
1	X	18	HIS	6.2
1	Y	88	ALA	6.0
1	Y	420	PRO	6.0
1	A	18	HIS	5.8
1	Y	9	ARG	5.5
1	Y	17	SER	5.1
1	Y	10	GLN	5.0
1	X	420	PRO	4.7
1	Y	87	ALA	4.7
1	A	84	ALA	4.6
1	X	17	SER	4.6
1	X	14	GLN	4.6
1	Y	94	ARG	4.5
1	A	22	GLY	4.4
1	B	84	ALA	4.4
1	Y	12	ILE	4.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	Y	89	ASP	4.2
1	A	10	GLN	4.2
1	B	9	ARG	4.2
1	X	82	ASP	4.2
1	B	144	VAL	4.1
1	A	17	SER	4.0
1	A	149	LEU	4.0
1	Y	90	ILE	3.9
1	A	88	ALA	3.8
1	A	143	ILE	3.7
1	A	9	ARG	3.7
1	X	149	LEU	3.7
1	A	82	ASP	3.6
1	B	101	THR	3.6
1	A	96	ASP	3.5
1	B	21	ASP	3.5
1	Y	178	LEU	3.4
1	Y	92	THR	3.4
1	A	85	LEU	3.4
1	B	143	ILE	3.4
1	X	344	ILE	3.3
1	X	324	TYR	3.3
1	B	180	GLU	3.3
1	B	15	LEU	3.3
1	X	85	LEU	3.2
1	X	16	LEU	3.2
1	B	82	ASP	3.2
1	Y	95	VAL	3.2
1	A	36	ASP	3.2
1	A	420	PRO	3.1
1	B	85	LEU	3.1
1	X	186	LEU	3.1
1	X	89	ASP	3.0
1	Y	13	VAL	3.0
1	A	94	ARG	3.0
1	Y	38	GLU	2.9
1	Y	84	ALA	2.9
1	Y	177	CYS	2.9
1	A	89	ASP	2.8
1	B	11	THR	2.8
1	A	13	VAL	2.8
1	X	99	ARG	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	X	348	LEU	2.7
1	X	187	VAL	2.7
1	A	99	ARG	2.6
1	A	312	VAL	2.6
1	A	182	PRO	2.6
1	A	15	LEU	2.6
1	X	416	GLY	2.6
1	Y	11	THR	2.6
1	X	321	VAL	2.6
1	X	38	GLU	2.6
1	Y	86	GLU	2.5
1	X	15	LEU	2.5
1	A	150	GLY	2.5
1	A	38	GLU	2.5
1	B	19	MET	2.4
1	B	10	GLN	2.4
1	A	95	VAL	2.4
1	Y	93	GLU	2.4
1	X	320	ALA	2.4
1	X	36	ASP	2.4
1	A	384	ILE	2.4
1	B	188	ASN	2.3
1	X	101	THR	2.3
1	A	437	LEU	2.3
1	A	385	TRP	2.3
1	B	187	VAL	2.2
1	A	92	THR	2.2
1	X	37	GLN	2.2
1	Y	325	TRP	2.2
1	X	84	ALA	2.2
1	X	384	ILE	2.2
1	X	23	LYS	2.2
1	X	188	ASN	2.1
1	X	9	ARG	2.1
1	X	13	VAL	2.1
1	A	183	ASP	2.1
1	B	437	LEU	2.1
1	B	151	ARG	2.0
1	X	19	MET	2.0
1	X	325	TRP	2.0
1	Y	186	LEU	2.0
1	Y	113	LEU	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 carbohydrates 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. 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^{th} 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^2)	Q<0.9
3	PEG	X	502	7/7	0.88	0.45	5.05	55,81,109,119	0
3	PEG	Y	502	7/7	0.91	0.40	2.30	66,85,107,113	0
2	ARG	B	501	12/12	0.93	0.23	1.78	53,67,86,103	0
3	PEG	A	502	7/7	0.88	0.32	0.98	53,70,86,92	0
2	ARG	X	501	12/12	0.93	0.19	0.04	61,70,87,89	0
2	ARG	A	501	12/12	0.93	0.18	-0.27	47,62,84,85	0
2	ARG	Y	501	12/12	0.94	0.16	-0.37	50,62,79,88	0
3	PEG	B	502	7/7	0.88	0.16	-0.77	55,95,101,111	0

6.5 Other polymers (i)

There are no such residues in this entry.