



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:16 AM UTC

PDB ID : 2EA7 / pdb\_00002ea7  
Title : Crystal Structure of Adzuki Bean 7S Globulin-1  
Authors : Fukuda, T.; Mikami, B.; Utsumi, S.  
Deposited on : 2007-01-30  
Resolution : 1.80 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](mailto: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)  
Xtrriage (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

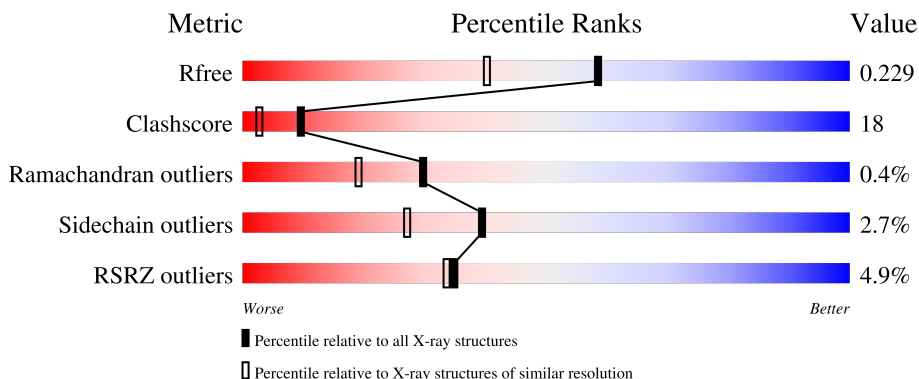
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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))
$R_{free}$	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	434	 7% 62% 24% • 10%
1	B	434	 3% 65% 21% • 12%
1	C	434	 3% 64% 22% • 13%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10203 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 7S globulin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	390	3187	2015	554	612	6	0	6	0
1	B	382	3127	1980	547	594	6	0	7	0
1	C	379	3116	1978	540	591	7	0	11	0

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Ca 1	0	0
2	B	2	Total 2	Ca 2	0	0
2	C	1	Total 1	Ca 1	0	0

- Molecule 3 is ACETIC ACID (CCD ID: ACY) (formula: C<sub>2</sub>H<sub>4</sub>O<sub>2</sub>).



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

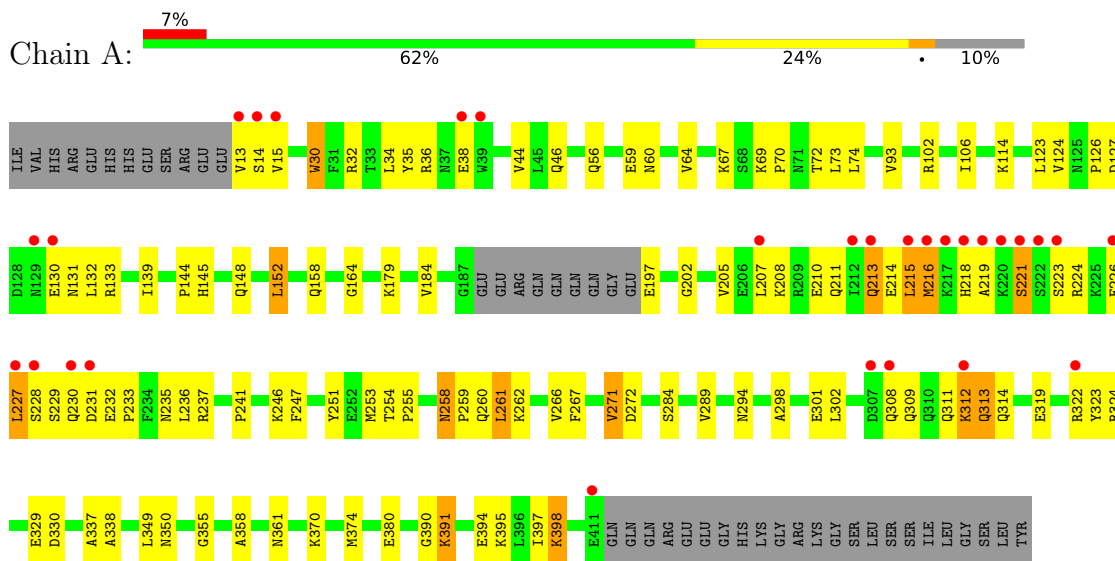
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	214	Total O 214 214	0	0
4	B	247	Total O 247 247	0	0
4	C	296	Total O 296 296	0	0

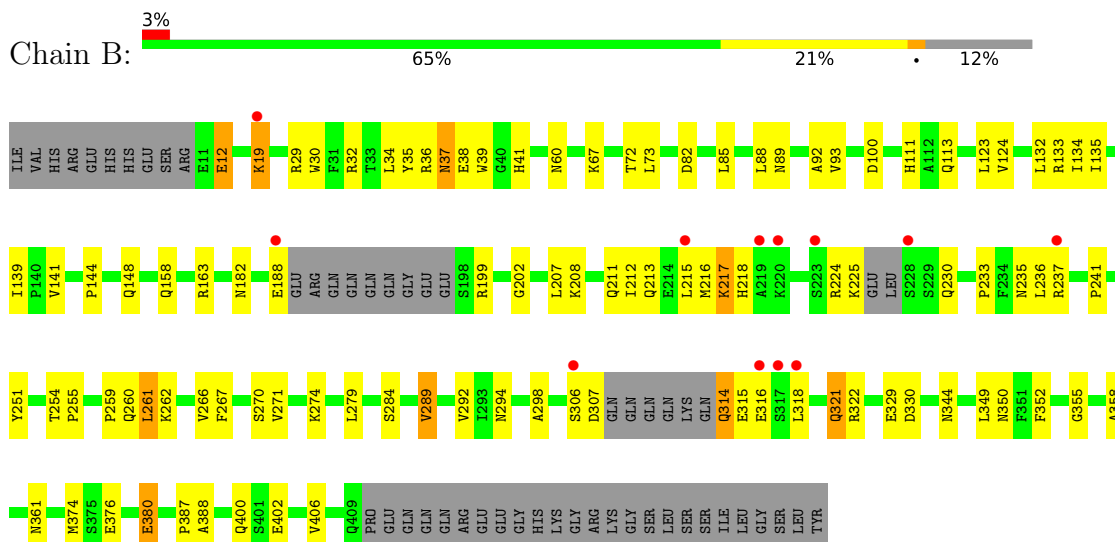
### 3 Residue-property plots [i](#)

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: 7S globulin-1



- Molecule 1: 7S globulin-1



- Molecule 1: 7S globulin-1





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.60Å 48.55Å 119.77Å 90.00° 97.12° 90.00°	Depositor
Resolution (Å)	14.98 – 1.80 14.98 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.4 (14.98-1.80) 97.3 (14.98-1.80)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.44 (at 1.81Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.193 , 0.228 0.195 , 0.229	Depositor DCC
$R_{free}$ test set	10508 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.4	Xtrriage
Anisotropy	0.537	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 49.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10203	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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: CA, ACY

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	0.33	0/3276	0.87	7/4422 (0.2%)
1	B	0.31	0/3217	0.87	5/4338 (0.1%)
1	C	0.36	0/3224	0.88	10/4349 (0.2%)
All	All	0.33	0/9717	0.87	22/13109 (0.2%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	358	ALA	N-CA-C	10.42	122.72	111.36
1	A	358	ALA	N-CA-C	8.66	121.87	111.82
1	C	358	ALA	N-CA-C	7.73	121.97	112.23
1	C	30	TRP	N-CA-C	6.43	120.83	112.92
1	C	141	VAL	N-CA-C	6.26	117.19	111.81
1	B	289	VAL	N-CA-C	6.14	117.14	108.36
1	A	289	VAL	N-CA-C	6.01	116.96	108.36
1	C	289	VAL	N-CA-C	5.97	116.53	108.17
1	A	258	ASN	CA-C-N	5.84	125.05	118.97
1	A	258	ASN	C-N-CA	5.84	125.05	118.97
1	C	280	LEU	N-CA-C	5.58	117.59	109.84
1	B	30	TRP	N-CA-C	5.42	119.59	112.92
1	C	349	LEU	N-CA-C	5.32	117.48	109.23
1	A	271	VAL	N-CA-C	5.30	115.53	108.11
1	A	184	VAL	N-CA-C	5.23	116.70	111.00
1	C	143	ASN	N-CA-C	-5.20	99.17	109.10
1	B	279	LEU	N-CA-C	-5.19	100.63	108.67
1	C	125	ASN	N-CA-C	-5.15	98.35	109.01
1	C	137	LEU	N-CA-C	-5.14	100.86	109.24
1	C	75	LEU	N-CA-C	5.10	116.93	109.84
1	B	141	VAL	N-CA-C	5.10	116.19	111.81

*Continued on next page...*

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	30	TRP	N-CA-C	5.01	119.34	112.88

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	3187	0	3123	149	0
1	B	3127	0	3074	98	0
1	C	3116	0	3060	109	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
2	C	1	0	0	0	0
3	A	4	0	3	1	0
3	B	4	0	3	1	0
3	C	4	0	3	0	0
4	A	214	0	0	7	0
4	B	247	0	0	5	0
4	C	296	0	0	10	0
All	All	10203	0	9266	334	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 18.

All (334) 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:19:LYS:HE2	1:B:19:LYS:H	0.99	1.12
1:C:322:ARG:HB3	1:C:324:ARG:HH22	1.19	1.05
1:C:322:ARG:HB3	1:C:324:ARG:NH2	1.75	1.00
1:B:306:SER:HB2	1:B:321:GLN:HE22	1.28	0.98
1:C:35[B]:TYR:OH	1:C:202:GLY:HA3	1.65	0.96
1:B:19:LYS:HE2	1:B:19:LYS:N	1.81	0.95
1:A:322[A]:ARG:HD2	1:A:324:ARG:HG3	1.49	0.94

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:19:LYS:H	1:B:19:LYS:CE	1.81	0.93
1:A:223:SER:HB2	1:A:226:GLU:HG2	1.51	0.93
1:C:135:ILE:CD1	1:C:292:VAL:HG21	2.00	0.92
1:A:311:GLN:HG2	1:A:314:GLN:HE21	1.36	0.90
1:B:89[B]:ASN:HD21	1:B:294:ASN:ND2	1.69	0.90
1:A:322[A]:ARG:HH21	1:C:165:PHE:HA	1.39	0.87
1:C:208:LYS:HB2	1:C:211:GLN:HE21	1.39	0.87
1:B:32:ARG:HH22	1:C:316:GLU:HB2	1.39	0.86
1:B:89[B]:ASN:HD21	1:B:294:ASN:HD21	1.27	0.81
1:C:318:LEU:HD13	1:C:318:LEU:H	1.45	0.81
1:A:226:GLU:HB3	1:A:233:PRO:O	1.79	0.81
1:C:208:LYS:H	1:C:211:GLN:NE2	1.79	0.81
1:A:235:ASN:HD21	1:A:237:ARG:HB2	1.46	0.80
1:A:301:GLU:HG2	1:A:324:ARG:HG2	1.65	0.79
1:B:217:LYS:HG2	1:B:218:HIS:ND1	1.97	0.78
1:A:308:GLN:HG3	1:A:319:GLU:OE2	1.82	0.78
1:B:93:VAL:HB	1:B:124[A]:VAL:CG1	2.14	0.78
1:B:199:ARG:HA	4:C:745:HOH:O	1.82	0.77
1:C:380:GLU:CD	1:C:380:GLU:H	1.94	0.74
1:C:71:ASN:HD21	1:C:209:ARG:HH11	1.34	0.74
1:C:208:LYS:H	1:C:211:GLN:HE21	1.35	0.74
1:C:19:LYS:H	1:C:19:LYS:HD2	1.53	0.73
1:B:89[B]:ASN:ND2	1:B:294:ASN:HD21	1.85	0.73
1:C:135:ILE:HD13	1:C:292:VAL:HG21	1.70	0.73
1:A:302:LEU:N	1:A:322[A]:ARG:NH1	2.38	0.72
1:A:322[A]:ARG:CD	1:A:324:ARG:HE	2.05	0.69
1:C:324:ARG:NH2	4:C:657:HOH:O	2.25	0.69
1:C:29:ARG:HH11	1:C:29:ARG:HG2	1.58	0.69
1:C:93:VAL:HG22	1:C:106:ILE:HD13	1.74	0.68
1:B:89[B]:ASN:ND2	1:B:133:ARG:NH1	2.43	0.66
1:C:13:VAL:HA	1:C:322:ARG:NH2	2.10	0.66
1:B:35:TYR:OH	1:B:202:GLY:HA3	1.96	0.66
1:A:235:ASN:ND2	1:A:237:ARG:H	1.93	0.65
1:A:164:GLY:O	1:B:322:ARG:HD3	1.96	0.65
1:A:301:GLU:HB3	1:A:322[A]:ARG:CZ	2.25	0.65
1:C:24:TYR:O	1:C:51:ARG:NH2	2.30	0.65
1:C:301:GLU:HG2	1:C:324:ARG:CD	2.25	0.65
1:B:380:GLU:H	1:B:380:GLU:CD	2.02	0.65
1:A:241:PRO:HG3	1:A:251:TYR:CE2	2.32	0.64
1:B:254:THR:HB	1:B:255:PRO:HD2	1.79	0.64
1:A:74:LEU:HB3	1:A:123:LEU:HD23	1.80	0.64

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322[A]:ARG:NH2	1:C:165:PHE:HA	2.12	0.63
1:B:306:SER:CB	1:B:321:GLN:HE22	2.06	0.63
1:C:236:LEU:HA	1:C:253:MET:HE3	1.81	0.63
1:C:301:GLU:HG2	1:C:324:ARG:HD3	1.80	0.63
1:B:224:ARG:N	1:B:224:ARG:HD2	2.13	0.63
1:A:322[A]:ARG:HD2	1:A:324:ARG:HE	1.62	0.62
1:A:309:GLN:HE22	1:A:311:GLN:C	2.06	0.62
1:A:322[A]:ARG:HD3	1:A:323:TYR:N	2.15	0.62
1:A:322[A]:ARG:HD2	1:A:324:ARG:CG	2.28	0.62
1:A:215:LEU:HD12	1:A:216:MET:N	2.14	0.62
1:C:53:LYS:HD3	4:C:731:HOH:O	1.99	0.62
1:A:322[A]:ARG:CD	1:A:324:ARG:NE	2.63	0.61
1:A:60[B]:ASN:ND2	1:A:139:ILE:HG23	2.15	0.61
1:A:322[A]:ARG:HD2	1:A:324:ARG:NE	2.16	0.61
1:C:230:GLN:OE1	1:C:259:PRO:HB2	2.01	0.61
1:B:92:ALA:HB1	1:B:123:LEU:HD11	1.82	0.61
1:B:37:ASN:C	1:B:37:ASN:HD22	2.07	0.61
1:C:133:ARG:NH2	1:C:294:ASN:ND2	2.49	0.61
1:B:37:ASN:ND2	1:B:39:TRP:H	2.00	0.60
1:A:322[A]:ARG:HE	1:A:324:ARG:HH21	1.48	0.60
1:A:197:GLU:HG2	1:B:388:ALA:HA	1.83	0.60
1:B:36:ARG:HG3	1:B:41:HIS:HB3	1.82	0.60
1:A:210:GLU:CD	1:A:210:GLU:H	2.10	0.60
1:A:226:GLU:HB2	4:A:658:HOH:O	2.01	0.60
1:A:391:LYS:HB3	1:A:391:LYS:NZ	2.17	0.60
1:A:14:SER:O	1:A:322[A]:ARG:HB3	2.02	0.60
1:A:197:GLU:HG3	1:B:387:PRO:O	2.01	0.59
1:A:390:GLY:O	1:A:394:GLU:HG3	2.03	0.59
1:C:209:ARG:CZ	1:C:213:GLN:NE2	2.65	0.59
1:C:133:ARG:HH22	1:C:294:ASN:HD22	1.50	0.59
1:A:301:GLU:C	1:A:322[A]:ARG:HH12	2.10	0.59
1:A:32:ARG:HG3	1:B:315:GLU:HG2	1.85	0.58
1:C:318:LEU:H	1:C:318:LEU:CD1	2.16	0.58
1:C:318:LEU:HD22	1:C:318:LEU:O	2.03	0.58
1:A:32:ARG:CG	1:B:315:GLU:HG2	2.33	0.58
1:A:35:TYR:OH	1:A:202:GLY:HA3	2.03	0.58
1:B:93:VAL:HB	1:B:124[A]:VAL:HG12	1.84	0.58
1:B:135:ILE:HD13	1:B:292:VAL:HG11	1.85	0.58
1:B:306:SER:HB2	1:B:321:GLN:NE2	2.10	0.58
1:A:106:ILE:HB	1:A:221:SER:HA	1.85	0.58
1:A:395:LYS:O	1:A:398:LYS:HD3	2.03	0.58

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:139:ILE:HD12	1:B:139:ILE:N	2.19	0.58
1:C:199:ARG:HA	4:C:668:HOH:O	2.03	0.57
1:A:301:GLU:C	1:A:322[A]:ARG:NH1	2.62	0.57
1:A:322[A]:ARG:HG2	1:A:324:ARG:CZ	2.35	0.57
1:A:284:SER:HB3	1:A:361:ASN:HD21	1.69	0.57
1:B:307:ASP:O	1:B:316:GLU:HB2	2.04	0.57
1:C:209:ARG:HG2	4:C:748:HOH:O	2.04	0.57
1:A:302:LEU:N	1:A:322[A]:ARG:HH12	2.02	0.57
1:B:224:ARG:HA	4:B:681:HOH:O	2.04	0.57
1:C:167:LYS:O	1:C:171:GLU:HG3	2.04	0.57
1:C:237[B]:ARG:NH2	1:C:272:ASP:OD2	2.35	0.57
1:A:230:GLN:HA	1:A:260:GLN:HG3	1.86	0.57
1:B:402:GLU:HB3	1:B:406:VAL:HG12	1.87	0.57
1:C:241:PRO:HG3	1:C:251:TYR:CE2	2.39	0.57
1:A:179:LYS:HE2	4:A:654:HOH:O	2.04	0.56
1:A:208:LYS:NZ	1:A:208:LYS:HB3	2.20	0.56
1:A:301:GLU:HB3	1:A:322[A]:ARG:NH1	2.19	0.56
1:A:133:ARG:HH12	1:A:294:ASN:HD22	1.53	0.56
1:A:133:ARG:HH12	1:A:294:ASN:ND2	2.02	0.56
1:A:322[A]:ARG:HH21	1:C:165:PHE:CA	2.15	0.56
1:B:93:VAL:HB	1:B:124[A]:VAL:HG13	1.89	0.55
1:C:139:ILE:N	1:C:139:ILE:HD12	2.22	0.55
1:A:370:LYS:HD2	4:C:665:HOH:O	2.07	0.55
1:B:93:VAL:O	1:B:123:LEU:HD12	2.07	0.55
1:B:241:PRO:HG3	1:B:251:TYR:CE2	2.42	0.54
1:C:159[A]:GLN:NE2	1:C:163:ARG:HB2	2.23	0.54
1:C:394:GLU:O	1:C:398:LYS:HG2	2.07	0.54
1:A:374:MET:HG2	1:C:152:LEU:HD21	1.89	0.54
1:A:322[A]:ARG:NH2	1:C:164:GLY:O	2.41	0.54
1:A:309:GLN:NE2	1:A:311:GLN:O	2.41	0.54
1:B:111:HIS:HD2	4:B:615:HOH:O	1.91	0.54
1:C:19:LYS:HD2	1:C:19:LYS:N	2.23	0.54
1:C:93:VAL:HG22	1:C:106:ILE:CD1	2.38	0.54
1:B:208:LYS:H	1:B:211:GLN:NE2	2.05	0.54
1:A:261:LEU:HG	1:A:266:VAL:O	2.07	0.53
1:C:30:TRP:CH2	1:C:51:ARG:HD3	2.43	0.53
1:A:322[A]:ARG:NE	1:A:324:ARG:HE	2.07	0.53
1:B:230:GLN:HA	1:B:260:GLN:HG3	1.90	0.53
1:B:236:LEU:HD11	1:B:270:SER:HB2	1.91	0.53
1:A:235:ASN:ND2	1:A:237:ARG:HB2	2.20	0.53
1:C:135:ILE:HD11	1:C:292:VAL:HG21	1.85	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:133:ARG:HH22	1:C:294:ASN:ND2	2.05	0.53
1:C:254:THR:HB	1:C:255:PRO:HD2	1.90	0.53
1:C:229:SER:HB3	1:C:232:GLU:HB2	1.89	0.53
1:C:19:LYS:H	1:C:19:LYS:CD	2.13	0.53
1:A:322[A]:ARG:NE	1:C:164:GLY:O	2.42	0.53
1:B:284:SER:HB3	1:B:361:ASN:HD21	1.74	0.53
1:A:230:GLN:HE21	1:A:260:GLN:HA	1.74	0.52
1:B:182:ASN:ND2	1:B:188:GLU:HG2	2.24	0.52
1:A:73:LEU:HD13	1:A:124:VAL:HG22	1.91	0.52
1:A:210:GLU:O	1:A:214:GLU:HG3	2.08	0.52
1:A:44:VAL:HG22	1:A:64:VAL:HG22	1.91	0.52
1:C:217:LYS:HE3	1:C:218:HIS:CE1	2.45	0.52
1:A:215:LEU:HD23	1:B:380:GLU:HG2	1.93	0.51
1:B:208:LYS:H	1:B:211:GLN:HE21	1.58	0.51
1:A:36:ARG:HH11	1:A:36:ARG:HG3	1.75	0.51
1:A:309:GLN:NE2	1:A:314:GLN:HB2	2.25	0.51
1:B:148[A]:GLN:OE1	1:C:305:LEU:HB2	2.11	0.51
1:A:227:LEU:O	1:A:227:LEU:HD12	2.11	0.51
1:A:59:GLU:OE1	1:A:145:HIS:HE1	1.93	0.51
1:C:69:LYS:HA	1:C:131[A]:ASN:HD22	1.75	0.50
1:B:34:LEU:HD22	1:C:316:GLU:OE1	2.11	0.50
1:B:314:GLN:NE2	1:B:314:GLN:N	2.60	0.50
1:A:72:THR:O	1:A:124:VAL:HG13	2.12	0.50
1:A:380[A]:GLU:HG2	4:A:635:HOH:O	2.11	0.49
1:C:133:ARG:NH2	1:C:294:ASN:HD22	2.08	0.49
1:A:232:GLU:HG3	1:A:233:PRO:HD2	1.94	0.49
1:A:322[A]:ARG:HH21	1:C:164:GLY:C	2.20	0.49
1:B:67:LYS:HA	1:B:132:LEU:O	2.12	0.49
1:A:60[B]:ASN:HD21	1:A:139:ILE:HG23	1.76	0.49
1:C:208:LYS:HB2	1:C:211:GLN:NE2	2.19	0.49
1:B:89[B]:ASN:CG	1:B:294:ASN:HD21	2.19	0.49
1:B:294:ASN:C	1:B:294:ASN:HD22	2.20	0.49
1:C:322:ARG:CB	1:C:324:ARG:HH22	2.07	0.49
1:A:34:LEU:HG	1:A:44:VAL:HG23	1.94	0.49
1:C:229:SER:CB	1:C:232:GLU:HB2	2.42	0.49
1:C:380:GLU:CD	1:C:380:GLU:N	2.68	0.49
1:B:89[B]:ASN:ND2	1:B:294:ASN:ND2	2.46	0.49
1:B:163[A]:ARG:NH2	1:C:322:ARG:NH1	2.60	0.49
1:C:402:GLU:HB2	1:C:406:VAL:HG12	1.95	0.49
1:A:309:GLN:HE22	1:A:311:GLN:CA	2.26	0.49
1:B:267:PHE:C	1:B:267:PHE:CD2	2.90	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:135:ILE:HD12	1:C:292:VAL:HG11	1.94	0.48
1:C:60[B]:ASN:OD1	1:C:144:PRO:HB2	2.12	0.48
1:C:71:ASN:HD21	1:C:209:ARG:NH1	2.06	0.48
1:B:37:ASN:C	1:B:37:ASN:ND2	2.71	0.48
1:A:294:ASN:CB	1:A:350:ASN:HD22	2.27	0.48
1:A:302:LEU:C	1:A:322[A]:ARG:NH1	2.72	0.48
1:A:60[B]:ASN:HD21	1:A:139:ILE:CG2	2.27	0.48
1:A:148:GLN:NE2	1:B:318:LEU:HD22	2.28	0.48
1:A:216:MET:HE2	1:A:219:ALA:HB3	1.93	0.48
1:A:73:LEU:HB3	1:A:207:LEU:HD11	1.95	0.48
1:B:36:ARG:HG2	1:B:37:ASN:N	2.29	0.48
1:C:110:GLY:HA3	1:C:237[A]:ARG:NH1	2.29	0.48
1:A:271:VAL:O	1:A:350:ASN:HA	2.13	0.48
1:C:151:PHE:CE2	1:C:203:VAL:HB	2.49	0.48
1:C:13:VAL:O	1:C:13:VAL:HG13	2.14	0.48
1:C:267:PHE:C	1:C:267:PHE:CD2	2.92	0.48
1:C:109:GLN:NE2	4:C:733:HOH:O	2.47	0.47
1:A:207:LEU:HD12	1:A:207:LEU:N	2.28	0.47
1:A:230:GLN:NE2	1:A:260:GLN:HG2	2.29	0.47
1:B:163[A]:ARG:NH2	1:C:322:ARG:HH12	2.12	0.47
1:A:34:LEU:HD11	1:A:44:VAL:CG2	2.44	0.47
1:A:67:LYS:HA	1:A:132:LEU:O	2.15	0.47
1:B:213:GLN:HA	1:B:213:GLN:HE21	1.79	0.47
1:A:255:PRO:HB3	1:A:262:LYS:HA	1.95	0.47
1:A:309:GLN:CD	1:A:311:GLN:H	2.22	0.47
1:B:274:LYS:HE3	4:B:678:HOH:O	2.14	0.47
1:A:298:ALA:HB2	1:A:349:LEU:HD22	1.97	0.47
1:C:318:LEU:HD22	1:C:318:LEU:C	2.40	0.46
1:A:93:VAL:CG2	1:A:216:MET:HE3	2.46	0.46
1:C:231:ASP:HB2	4:C:755:HOH:O	2.14	0.46
1:A:294:ASN:HB3	1:A:350:ASN:HD22	1.80	0.46
1:A:311:GLN:O	1:A:314:GLN:HB2	2.14	0.46
1:B:289:VAL:HG11	3:B:461:ACY:H2	1.97	0.46
1:C:15:VAL:HG12	1:C:322:ARG:HB2	1.97	0.46
1:A:32:ARG:HB2	1:A:46[A]:GLN:NE2	2.30	0.46
1:A:210:GLU:CD	1:A:210:GLU:N	2.72	0.46
1:B:215:LEU:HD21	1:C:380:GLU:HG2	1.96	0.46
1:C:249:ARG:HD2	1:C:251:TYR:OH	2.15	0.46
1:C:294:ASN:HB3	1:C:350:ASN:HD22	1.80	0.46
1:B:60:ASN:ND2	1:B:144:PRO:HB2	2.31	0.46
1:C:284:SER:HB3	1:C:361:ASN:HD21	1.81	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:213:GLN:HA	1:B:213:GLN:NE2	2.31	0.45
1:A:56:GLN:NE2	4:A:574:HOH:O	2.49	0.45
1:A:127:ASP:OD2	1:A:130:GLU:HB2	2.16	0.45
1:C:29:ARG:HG2	1:C:29:ARG:NH1	2.29	0.45
1:A:152:LEU:HD11	1:B:374:MET:HG2	1.99	0.45
1:B:123:LEU:HD21	1:B:134:ILE:CD1	2.45	0.45
1:A:13:VAL:C	1:A:15:VAL:H	2.24	0.45
1:A:106:ILE:HD11	1:A:216:MET:HE1	1.97	0.45
1:A:114:LYS:HD3	1:A:230:GLN:HE22	1.82	0.45
1:B:225:LYS:HD2	1:B:225:LYS:N	2.32	0.45
1:B:329:GLU:O	1:B:330:ASP:HB2	2.17	0.45
1:B:230:GLN:HG2	1:B:259:PRO:HB2	1.98	0.45
1:B:261:LEU:HG	1:B:266:VAL:O	2.16	0.45
1:C:71:ASN:ND2	1:C:209:ARG:HH11	2.10	0.45
1:A:70:PRO:HD3	1:A:131:ASN:ND2	2.32	0.45
1:B:12:GLU:N	1:B:12:GLU:OE1	2.50	0.45
1:B:271:VAL:O	1:B:350:ASN:HA	2.17	0.45
1:C:107:LEU:HA	4:C:650:HOH:O	2.17	0.45
1:A:34:LEU:HD11	1:A:44:VAL:HG21	1.99	0.44
1:A:309:GLN:NE2	1:A:311:GLN:H	2.15	0.44
1:A:32:ARG:HB2	1:A:46[A]:GLN:HE22	1.82	0.44
1:A:309:GLN:HE22	1:A:311:GLN:N	2.15	0.44
1:C:158:GLN:NE2	1:C:158:GLN:C	2.76	0.44
1:C:200:GLU:HG3	1:C:205:VAL:HG11	2.00	0.44
1:A:302:LEU:O	1:A:322[A]:ARG:NH1	2.51	0.44
1:B:182:ASN:HD21	1:B:188:GLU:HG2	1.82	0.44
1:C:208:LYS:N	1:C:211:GLN:HE21	2.11	0.44
1:A:311:GLN:O	1:A:312:LYS:C	2.60	0.44
1:C:322:ARG:HD3	1:C:324:ARG:HH12	1.83	0.44
1:A:311:GLN:CG	1:A:314:GLN:HG3	2.47	0.44
3:A:460:ACY:H3	4:A:485:HOH:O	2.18	0.44
1:A:232:GLU:HG2	4:A:657:HOH:O	2.18	0.43
1:A:246:LYS:HE3	1:A:247:PHE:CE2	2.53	0.43
1:B:207:LEU:HD12	1:B:212:ILE:HD13	2.00	0.43
1:C:225:LYS:O	1:C:225:LYS:HG2	2.19	0.43
1:A:267:PHE:C	1:A:267:PHE:CD2	2.96	0.43
1:A:380[A]:GLU:OE1	1:C:211:GLN:OE1	2.36	0.43
1:A:38:GLU:N	1:A:38:GLU:CD	2.76	0.43
1:B:344:ASN:C	1:B:344:ASN:HD22	2.25	0.43
1:C:113[B]:GLN:NE2	1:C:231:ASP:O	2.48	0.43
1:A:127:ASP:OD2	1:A:130:GLU:N	2.51	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:VAL:HA	1:A:355:GLY:O	2.18	0.43
1:B:212:ILE:O	1:B:216:MET:HG2	2.19	0.43
1:C:35[B]:TYR:CD2	1:C:203:VAL:HG22	2.54	0.43
1:B:217:LYS:HD3	1:B:217:LYS:N	2.33	0.43
1:A:36:ARG:HG3	1:A:36:ARG:NH1	2.33	0.43
1:B:89[B]:ASN:HD21	1:B:133:ARG:NH1	2.15	0.43
1:B:100:ASP:OD1	1:B:100:ASP:N	2.52	0.43
1:C:13:VAL:O	1:C:13:VAL:HG22	2.18	0.43
1:A:229:SER:C	1:A:231:ASP:H	2.27	0.42
1:A:216:MET:C	1:A:218:HIS:H	2.27	0.42
1:A:205:VAL:HG23	1:A:207:LEU:HD11	2.01	0.42
1:A:374:MET:HE2	1:A:397:ILE:HD11	2.01	0.42
1:C:318:LEU:HD13	1:C:318:LEU:N	2.25	0.42
1:A:208:LYS:H	1:A:211:GLN:NE2	2.17	0.42
1:A:30:TRP:O	1:A:46[A]:GLN:HG2	2.19	0.42
1:B:217:LYS:HD3	1:B:217:LYS:H	1.84	0.42
1:B:255:PRO:CB	1:B:262:LYS:HA	2.50	0.42
1:C:111:HIS:HE1	4:C:673:HOH:O	2.03	0.42
1:B:400:GLN:OE1	1:B:402:GLU:HB2	2.20	0.42
1:C:294:ASN:CB	1:C:350:ASN:HD22	2.33	0.42
1:B:85:LEU:HD23	1:B:85:LEU:C	2.45	0.42
1:B:88:LEU:HD11	1:B:135:ILE:CG2	2.50	0.42
1:C:94:LEU:HD23	1:C:113[A]:GLN:OE1	2.19	0.42
1:A:102:ARG:HD3	1:B:376:GLU:O	2.20	0.42
1:A:311:GLN:HG3	1:A:314:GLN:HG3	2.02	0.42
1:C:86:VAL:HG21	1:C:352:PHE:CZ	2.55	0.42
1:A:311:GLN:HE21	1:A:313:GLN:HG2	1.84	0.42
1:A:391:LYS:HB3	1:A:391:LYS:HZ2	1.83	0.42
1:A:218:HIS:HA	4:A:628:HOH:O	2.20	0.41
1:A:337:ALA:O	1:A:338:ALA:HB3	2.20	0.41
1:B:113:GLN:HB2	1:B:233:PRO:HB3	2.01	0.41
1:B:344:ASN:C	1:B:344:ASN:ND2	2.77	0.41
1:A:229:SER:HB2	1:A:232:GLU:CB	2.50	0.41
1:C:337:ALA:O	1:C:338:ALA:HB3	2.20	0.41
1:B:73:LEU:HD13	1:B:124[B]:VAL:HG22	2.02	0.41
1:B:294:ASN:ND2	1:B:294:ASN:C	2.78	0.41
1:A:205:VAL:HG23	1:A:207:LEU:CD1	2.50	0.41
1:A:213:GLN:OE1	1:A:213:GLN:N	2.54	0.41
1:A:258:ASN:CG	1:A:259:PRO:HD2	2.44	0.41
1:A:329:GLU:O	1:A:330:ASP:HB2	2.21	0.41
1:A:69:LYS:HE2	1:A:69:LYS:HB3	1.83	0.41

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:237:ARG:HH12	1:A:272:ASP:CG	2.27	0.41
1:A:374:MET:HE2	1:A:374:MET:HB3	1.98	0.41
1:C:89[B]:ASN:HD22	1:C:133:ARG:HH21	1.68	0.41
1:C:209:ARG:HD2	1:C:209:ARG:HA	1.88	0.41
1:C:236:LEU:HD11	1:C:270:SER:HB2	2.02	0.41
1:B:38:GLU:HG2	4:B:637:HOH:O	2.20	0.41
1:A:246:LYS:HE3	1:A:247:PHE:CZ	2.56	0.41
1:C:106:ILE:HD11	1:C:216[A]:MET:HG3	2.03	0.41
1:A:124:VAL:O	1:A:126:PRO:HD3	2.20	0.41
1:A:133:ARG:NH1	1:A:294:ASN:ND2	2.68	0.41
1:A:254:THR:HB	1:A:255:PRO:HD2	2.02	0.41
1:B:29:ARG:NH2	4:B:630:HOH:O	2.54	0.41
1:B:135:ILE:HD11	1:B:352:PHE:CD2	2.56	0.40
1:C:67:LYS:HA	1:C:132:LEU:O	2.21	0.40
1:C:159[A]:GLN:HE21	1:C:163:ARG:HG2	1.86	0.40
1:A:395:LYS:O	1:A:398:LYS:CD	2.69	0.40
1:B:298:ALA:HB2	1:B:349:LEU:HD22	2.02	0.40
1:C:69:LYS:HA	1:C:131[A]:ASN:ND2	2.36	0.40
1:C:247:PHE:CZ	1:C:407:ASP:HB2	2.57	0.40
1:A:179:LYS:HD3	1:A:179:LYS:HA	1.90	0.40
1:A:236:LEU:HA	1:A:253:MET:SD	2.61	0.40
1:A:312:LYS:C	1:A:314:GLN:H	2.29	0.40
1:B:72:THR:O	1:B:124[A]:VAL:HG23	2.21	0.40
1:B:225:LYS:HD2	1:B:225:LYS:H	1.86	0.40
1:A:70:PRO:HB3	1:A:127:ASP:O	2.21	0.40
1:A:93:VAL:HG22	1:A:216:MET:HE3	2.04	0.40
1:A:398:LYS:O	1:A:398:LYS:HG2	2.21	0.40
1:B:29:ARG:HB3	1:B:29:ARG:HH21	1.86	0.40
1:B:266:VAL:HA	1:B:355:GLY:O	2.22	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	392/434 (90%)	370 (94%)	17 (4%)	5 (1%)	9	3
1	B	381/434 (88%)	370 (97%)	11 (3%)	0	100	100
1	C	382/434 (88%)	367 (96%)	15 (4%)	0	100	100
All	All	1155/1302 (89%)	1107 (96%)	43 (4%)	5 (0%)	30	19

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	ARG
1	A	228	SER
1	A	312	LYS
1	A	221	SER
1	A	313	GLN

### 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	358/391 (92%)	349 (98%)	9 (2%)	42	30
1	B	351/391 (90%)	341 (97%)	10 (3%)	38	26
1	C	352/391 (90%)	341 (97%)	11 (3%)	35	23
All	All	1061/1173 (90%)	1031 (97%)	30 (3%)	39	26

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	152	LEU
1	A	158	GLN
1	A	213	GLN
1	A	215	LEU
1	A	216	MET
1	A	227	LEU
1	A	261	LEU
1	A	391	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	398	LYS
1	B	12	GLU
1	B	19	LYS
1	B	37	ASN
1	B	82	ASP
1	B	158	GLN
1	B	217	LYS
1	B	261	LEU
1	B	314	GLN
1	B	321	GLN
1	B	380	GLU
1	C	19	LYS
1	C	158	GLN
1	C	159[A]	GLN
1	C	159[B]	GLN
1	C	232	GLU
1	C	261	LEU
1	C	271	VAL
1	C	274[A]	LYS
1	C	274[B]	LYS
1	C	318	LEU
1	C	380	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	HIS
1	A	50	GLN
1	A	56	GLN
1	A	89	ASN
1	A	109	GLN
1	A	129	ASN
1	A	131	ASN
1	A	145	HIS
1	A	158	GLN
1	A	211	GLN
1	A	230	GLN
1	A	235	ASN
1	A	238	ASN
1	A	294	ASN
1	A	311	GLN
1	A	314	GLN

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	350	ASN
1	A	357	ASN
1	A	360	ASN
1	A	361	ASN
1	B	37	ASN
1	B	54	GLN
1	B	60	ASN
1	B	109	GLN
1	B	131	ASN
1	B	158	GLN
1	B	159	GLN
1	B	182	ASN
1	B	211	GLN
1	B	213	GLN
1	B	230	GLN
1	B	235	ASN
1	B	238	ASN
1	B	294	ASN
1	B	314	GLN
1	B	321	GLN
1	B	344	ASN
1	B	357	ASN
1	B	360	ASN
1	B	361	ASN
1	B	409	GLN
1	C	46	GLN
1	C	54	GLN
1	C	56	GLN
1	C	71	ASN
1	C	109	GLN
1	C	158	GLN
1	C	211	GLN
1	C	213	GLN
1	C	218	HIS
1	C	235	ASN
1	C	238	ASN
1	C	294	ASN
1	C	321	GLN
1	C	344	ASN
1	C	350	ASN
1	C	357	ASN
1	C	360	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	361	ASN
1	C	409	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 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	ACY	A	460	-	3,3,3	0.51	0	3,3,3	0.80	0
3	ACY	B	461	-	3,3,3	0.56	0	3,3,3	0.86	0
3	ACY	C	462	-	3,3,3	0.55	0	3,3,3	0.85	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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	460	ACY	1	0
3	B	461	ACY	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, 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	390/434 (89%)	0.26	29 (7%) 20 19	16, 31, 75, 102	6 (1%)
1	B	382/434 (88%)	0.09	12 (3%) 51 51	18, 30, 69, 95	7 (1%)
1	C	379/434 (87%)	-0.12	15 (3%) 42 41	13, 24, 55, 86	11 (2%)
All	All	1151/1302 (88%)	0.08	56 (4%) 35 33	13, 29, 67, 102	24 (2%)

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	227	LEU	5.7
1	A	215	LEU	4.0
1	A	216	MET	3.9
1	A	226	GLU	3.9
1	A	212	ILE	3.7
1	A	228	SER	3.6
1	C	410	PRO	3.6
1	A	223	SER	3.4
1	B	317	SER	3.4
1	C	318	LEU	3.2
1	A	14	SER	3.2
1	C	317	SER	3.1
1	C	13	VAL	3.1
1	A	13	VAL	3.0
1	A	322[A]	ARG	3.0
1	A	221	SER	2.9
1	B	215	LEU	2.9
1	A	15	VAL	2.9
1	C	408	ALA	2.8
1	A	222	SER	2.8
1	B	219	ALA	2.8
1	C	156	GLU	2.7
1	A	207	LEU	2.7

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	219	ALA	2.6
1	C	307	ASP	2.6
1	C	223	SER	2.6
1	A	312	LYS	2.6
1	B	228	SER	2.6
1	B	318	LEU	2.5
1	A	307	ASP	2.5
1	A	130	GLU	2.4
1	A	220	LYS	2.4
1	C	199	ARG	2.4
1	A	129	ASN	2.4
1	A	411	GLU	2.3
1	A	218	HIS	2.3
1	C	316	GLU	2.2
1	A	231	ASP	2.2
1	C	231	ASP	2.2
1	A	217	LYS	2.2
1	A	38	GLU	2.2
1	C	319	GLU	2.2
1	A	39	TRP	2.2
1	C	238	ASN	2.2
1	B	188	GLU	2.2
1	A	308	GLN	2.2
1	B	220	LYS	2.2
1	B	316	GLU	2.2
1	A	230	GLN	2.2
1	B	306	SER	2.1
1	B	19	LYS	2.1
1	C	256	GLU	2.1
1	C	222	SER	2.1
1	B	223	SER	2.0
1	A	213	GLN	2.0
1	B	237[A]	ARG	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, 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	B-factors(Å <sup>2</sup> )	Q<0.9
3	ACY	A	460	4/4	0.60	0.22	46,47,47,48	0
2	CA	B	453	1/1	0.85	0.13	65,65,65,65	0
3	ACY	C	462	4/4	0.85	0.10	39,40,40,41	0
3	ACY	B	461	4/4	0.89	0.10	52,53,53,53	0
2	CA	C	451	1/1	0.94	0.18	47,47,47,47	0
2	CA	B	452	1/1	0.94	0.16	54,54,54,54	0
2	CA	A	450	1/1	0.96	0.17	42,42,42,42	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.