Full wwPDB X-ray Structure Validation Report (i)

Dec 3, 2023 – 08:07 am GMT

PDB ID	:	1HFK
Title	:	Asparaginase from Erwinia chrysanthemi, hexagonal form with weak sulfate
Authors	:	Lubkowski, J.; Palm, G.J.; Kozak, M.; Jaskolski, M.; Wlodawer, A.
Deposited on	:	2000-12-05
Resolution	:	2.17 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	NOT EXECUTED
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	NOT EXECUTED
Percentile statistics	:	NOT EXECUTED
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.17 Å.

There are no overall percentile quality scores available for this entry.

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	327	.% 65% 28% • 5%
1	C	327	.% 70% 24% 5%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5139 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.

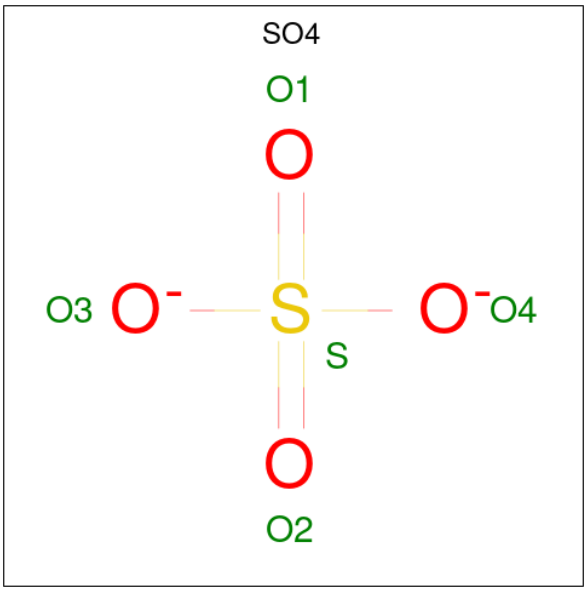
- Molecule 1 is a protein called L-ASPARAGINE AMIDOHYDROLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	310	2353	1479	414	451	9	0	0	0
1	C	310	2353	1479	414	451	9	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	156	ILE	LEU	variant	UNP P06608
A	178	ARG	LYS	variant	UNP P06608
A	267	LEU	MET	variant	UNP P06608
A	274	MET	ILE	variant	UNP P06608
C	156	ILE	LEU	variant	UNP P06608
C	178	ARG	LYS	variant	UNP P06608
C	267	LEU	MET	variant	UNP P06608
C	274	MET	ILE	variant	UNP P06608

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 3 is water.

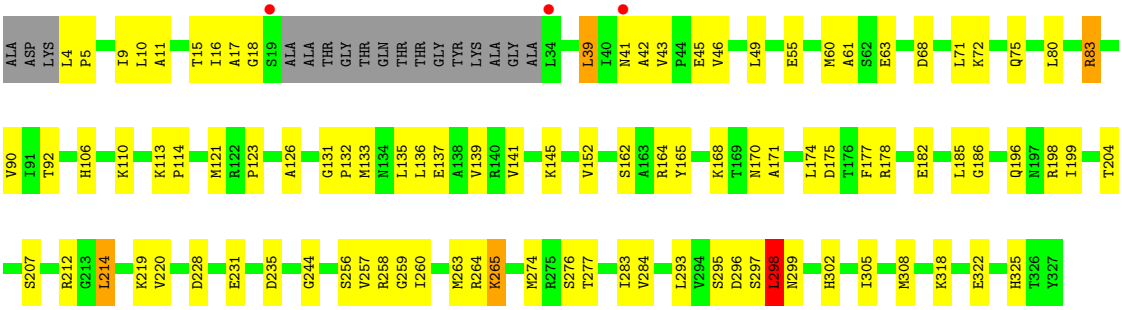
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	207	Total O 207 207	0	0
3	C	216	Total O 216 216	0	0

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.

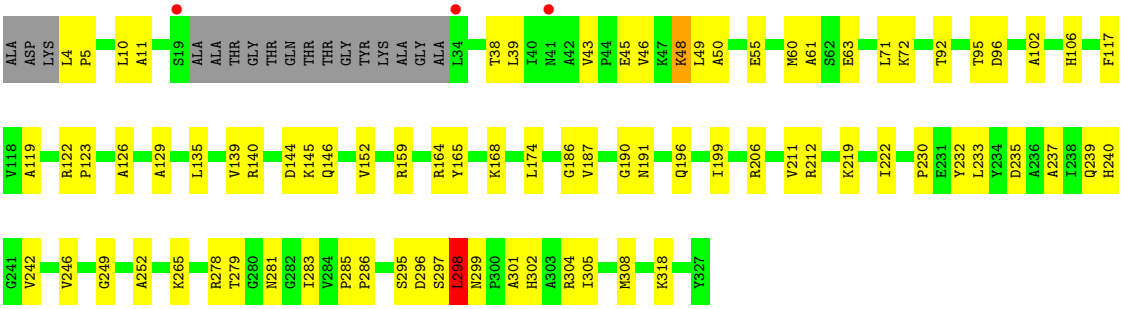
• Molecule 1: L-ASPARAGINE AMIDOHYDROLASE

Chain A:



• Molecule 1: L-ASPARAGINE AMIDOHYDROLASE

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α, β, γ	90.72Å 90.72Å 339.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 2.17 9.99 – 2.17	Depositor EDS
% Data completeness (in resolution range)	82.6 (10.00-2.17) 82.6 (9.99-2.17)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	2.82 (at 2.17Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.199 , 0.252 0.197 , 0.251	Depositor DCC
R_{free} test set	1167 reflections (3.03%)	wwPDB-VP
Wilson B-factor (Å^2)	15.3	Xtriage
Anisotropy	0.474	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 57.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	5139	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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, 0.333 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: SO4

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	0.49	0/2387	0.74	2/3235 (0.1%)
1	C	0.50	0/2387	0.74	1/3235 (0.0%)
All	All	0.50	0/4774	0.74	3/6470 (0.0%)

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	C	298	LEU	CA-CB-CG	5.51	127.97	115.30
1	A	298	LEU	CA-CB-CG	5.47	127.88	115.30
1	A	284	VAL	N-CA-C	-5.36	96.52	111.00

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	2353	0	2397	71	0
1	C	2353	0	2397	57	0
2	A	5	0	0	0	0
2	C	5	0	0	0	0
3	A	207	0	0	11	0
3	C	216	0	0	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5139	0	4794	124	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 13.

All (124) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:THR:HG23	1:A:39:LEU:HB2	1.45	0.96
1:C:123:PRO:HG2	1:C:126:ALA:HB2	1.64	0.79
1:A:123:PRO:HG2	1:A:126:ALA:HB2	1.66	0.77
1:A:15:THR:HG22	1:A:17:ALA:H	1.53	0.73
1:A:256:SER:HB2	3:C:2019:HOH:O	1.91	0.71
1:A:43:VAL:HG21	1:A:135:LEU:HD23	1.73	0.70
1:C:235:ASP:OD1	1:C:265:LYS:HE3	1.92	0.69
1:A:318:LYS:HE2	3:A:2196:HOH:O	1.91	0.68
1:A:16:ILE:O	1:A:131:GLY:HA3	1.95	0.66
1:A:80:LEU:O	1:A:83:ARG:HG3	1.96	0.66
1:A:264:ARG:HH11	1:A:264:ARG:HG3	1.60	0.65
1:C:43:VAL:HG21	1:C:135:LEU:HD23	1.79	0.64
1:C:230:PRO:HG2	1:C:233:LEU:HD12	1.80	0.63
1:C:10:LEU:HD23	1:C:55:GLU:HB3	1.81	0.62
1:A:185:LEU:HD21	1:A:199:ILE:HG23	1.82	0.61
1:A:257:VAL:HG22	3:C:2019:HOH:O	2.00	0.61
1:A:106:HIS:HA	1:A:152:VAL:HG23	1.83	0.60
1:A:61:ALA:HB1	1:A:63:GLU:OE1	2.02	0.59
1:C:165:TYR:CE2	1:C:199:ILE:HG22	2.38	0.59
1:A:45:GLU:H	1:A:45:GLU:CD	2.07	0.58
1:C:5:PRO:O	1:C:50:ALA:HB1	2.02	0.58
1:A:186:GLY:HA2	1:A:196:GLN:HG3	1.85	0.58
1:C:222:ILE:HA	1:C:246:VAL:O	2.05	0.56
1:C:106:HIS:HA	1:C:152:VAL:HG23	1.89	0.55
1:A:185:LEU:HD21	1:A:199:ILE:CG2	2.36	0.55
1:A:276:SER:HA	1:A:295:SER:OG	2.07	0.55
1:C:4:LEU:HB3	1:C:50:ALA:HA	1.88	0.55
1:C:230:PRO:HB2	1:C:232:TYR:CD2	2.42	0.55
1:A:17:ALA:HB1	1:A:132:PRO:HG3	1.89	0.54
1:C:295:SER:O	1:C:298:LEU:HD23	2.07	0.54
1:A:106:HIS:HA	1:A:152:VAL:CG2	2.38	0.54
1:A:10:LEU:HD23	1:A:55:GLU:HB3	1.88	0.54
1:A:71:LEU:O	1:A:75:GLN:HG3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:318:LYS:HE3	3:C:2196:HOH:O	2.07	0.54
1:A:164:ARG:CZ	1:A:298:LEU:HD22	2.38	0.54
1:C:39:LEU:HD21	1:C:135:LEU:HD22	1.89	0.53
1:A:256:SER:O	1:A:260:ILE:HG13	2.07	0.53
1:C:237:ALA:O	1:C:242:VAL:HG22	2.08	0.53
1:A:145:LYS:HD3	3:A:2069:HOH:O	2.07	0.53
1:A:274:MET:HE2	1:A:293:LEU:HB2	1.91	0.53
1:A:162:SER:OG	1:A:199:ILE:HD13	2.09	0.53
1:A:15:THR:CG2	1:A:17:ALA:O	2.57	0.52
1:A:15:THR:HG21	1:A:17:ALA:O	2.10	0.52
1:A:235:ASP:OD1	1:A:265:LYS:HE3	2.09	0.52
1:C:212:ARG:HD3	3:C:2010:HOH:O	2.09	0.52
1:C:240:HIS:HB3	3:C:2154:HOH:O	2.09	0.52
1:C:283:ILE:HD13	1:C:297:SER:HB3	1.92	0.51
1:A:259:GLY:O	1:A:263:MET:HG3	2.09	0.51
1:C:61:ALA:HB1	1:C:63:GLU:OE1	2.11	0.51
1:A:175:ASP:OD2	1:A:178:ARG:NH2	2.44	0.50
1:A:168:LYS:O	1:C:279:THR:HG22	2.12	0.50
1:C:122:ARG:NE	1:C:174:LEU:HD21	2.26	0.50
1:C:129:ALA:HB1	3:C:2064:HOH:O	2.11	0.49
1:C:304:ARG:O	1:C:308:MET:HG3	2.12	0.49
1:C:11:ALA:HA	1:C:92:THR:OG1	2.12	0.49
1:C:72:LYS:HE3	3:C:2020:HOH:O	2.12	0.49
1:A:43:VAL:CG2	1:A:135:LEU:HD23	2.42	0.49
1:A:18:GLY:HA3	1:A:42:ALA:HB2	1.95	0.49
1:C:106:HIS:HA	1:C:152:VAL:CG2	2.43	0.49
1:A:43:VAL:HG12	3:A:2007:HOH:O	2.12	0.48
1:A:198:ARG:NH2	3:A:2112:HOH:O	2.44	0.48
1:A:165:TYR:CD1	1:A:182:GLU:HG2	2.49	0.48
1:A:295:SER:O	1:A:296:ASP:HB3	2.14	0.47
1:C:45:GLU:H	1:C:45:GLU:CD	2.17	0.47
1:A:212:ARG:HA	3:A:2128:HOH:O	2.14	0.47
1:C:49:LEU:HD11	1:C:140:ARG:NH1	2.29	0.47
1:A:322:GLU:HA	3:A:2199:HOH:O	2.15	0.47
1:A:4:LEU:HD11	3:A:2010:HOH:O	2.14	0.47
1:A:110:LYS:HE2	1:A:207:SER:O	2.14	0.47
1:C:102:ALA:HA	1:C:117:PHE:CE1	2.50	0.46
1:C:206:ARG:HD2	3:C:2129:HOH:O	2.16	0.46
1:A:219:LYS:HG3	3:A:2130:HOH:O	2.16	0.46
1:A:9:ILE:HA	1:A:90:VAL:O	2.15	0.46
1:A:121:MET:HB2	1:A:174:LEU:HD23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:PHE:C	1:A:178:ARG:HG3	2.37	0.46
1:C:159:ARG:HD2	1:C:187:VAL:HG12	1.98	0.46
1:A:231:GLU:OE2	1:A:265:LYS:NZ	2.46	0.45
3:A:2147:HOH:O	1:C:219:LYS:HE3	2.15	0.45
1:C:122:ARG:CD	1:C:174:LEU:HD21	2.46	0.45
1:A:220:VAL:HA	1:A:244:GLY:O	2.17	0.45
1:A:41:ASN:HB2	3:A:2005:HOH:O	2.17	0.45
1:A:228:ASP:HB2	1:C:304:ARG:NH2	2.32	0.45
1:A:15:THR:HG23	1:A:39:LEU:CB	2.32	0.44
1:A:133:MET:O	1:A:137:GLU:HG3	2.17	0.44
1:A:137:GLU:O	1:A:141:VAL:HG23	2.18	0.44
1:A:257:VAL:HG23	1:A:258:ARG:N	2.33	0.44
1:A:264:ARG:HG3	1:A:264:ARG:NH1	2.28	0.44
1:A:299:ASN:OD1	1:A:302:HIS:ND1	2.47	0.44
1:C:144:ASP:OD1	1:C:146:GLN:HB2	2.17	0.44
1:A:5:PRO:HD2	1:A:49:LEU:O	2.18	0.44
1:A:170:ASN:HA	1:C:281:ASN:O	2.17	0.44
1:C:299:ASN:OD1	1:C:302:HIS:ND1	2.46	0.44
1:A:11:ALA:HA	1:A:92:THR:OG1	2.18	0.44
1:C:46:VAL:HG13	1:C:139:VAL:HG11	1.98	0.44
1:A:283:ILE:HD13	1:A:297:SER:HB3	1.99	0.44
1:C:60:MET:HG2	3:C:2001:HOH:O	2.18	0.44
1:A:49:LEU:HD21	1:A:136:LEU:HD11	1.99	0.43
1:C:239:GLN:NE2	3:C:2153:HOH:O	2.52	0.43
1:A:318:LYS:HE3	1:A:318:LYS:HB3	1.82	0.43
1:C:38:THR:HA	3:C:2002:HOH:O	2.18	0.43
1:C:95:THR:HG22	1:C:119:ALA:HB1	1.99	0.43
1:A:165:TYR:CE1	1:A:182:GLU:HG2	2.53	0.43
1:A:305:ILE:HA	1:A:308:MET:HE2	2.00	0.43
1:C:145:LYS:HD3	1:C:145:LYS:HA	1.85	0.42
1:C:186:GLY:HA2	1:C:196:GLN:HG3	2.00	0.42
1:C:45:GLU:O	1:C:48:LYS:HB2	2.19	0.42
1:C:71:LEU:HD11	1:C:211:VAL:HB	2.00	0.42
1:A:113:LYS:HA	1:A:114:PRO:HD3	1.93	0.42
1:C:96:ASP:OD1	1:C:168:LYS:NZ	2.52	0.42
1:A:171:ALA:HB1	1:C:252:ALA:HA	2.01	0.42
1:C:285:PRO:HA	1:C:286:PRO:HD3	1.91	0.42
1:A:46:VAL:HG13	1:A:139:VAL:HG21	2.02	0.41
1:A:68:ASP:O	1:A:72:LYS:HG2	2.20	0.41
1:C:165:TYR:HE2	1:C:199:ILE:HG22	1.84	0.41
1:A:276:SER:OG	1:A:277:THR:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:43:VAL:HG23	1:C:43:VAL:O	2.19	0.41
1:C:164:ARG:NH2	1:C:298:LEU:HD22	2.36	0.41
1:C:190:GLY:O	1:C:191:ASN:HB2	2.20	0.41
1:A:325:HIS:HA	3:A:2183:HOH:O	2.20	0.41
1:A:214:LEU:HD23	1:A:214:LEU:HA	1.87	0.41
1:C:301:ALA:O	1:C:305:ILE:HD13	2.21	0.41
1:C:39:LEU:CD2	1:C:135:LEU:HD22	2.50	0.40
1:C:249:GLY:O	1:C:278:ARG:HG2	2.22	0.40
1:C:295:SER:O	1:C:296:ASP:HB3	2.21	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	306/327 (94%)	293 (96%)	12 (4%)	1 (0%)	41 43
1	C	306/327 (94%)	293 (96%)	13 (4%)	0	100 100
All	All	612/654 (94%)	586 (96%)	25 (4%)	1 (0%)	47 52

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	204	THR

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	255/264 (97%)	249 (98%)	6 (2%)	49	59
1	C	255/264 (97%)	253 (99%)	2 (1%)	81	89
All	All	510/528 (97%)	502 (98%)	8 (2%)	62	74

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	LEU
1	A	60	MET
1	A	83	ARG
1	A	214	LEU
1	A	265	LYS
1	A	298	LEU
1	C	48	LYS
1	C	298	LEU

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

Mol	Chain	Res	Type
1	A	51	ASN
1	A	157	ASN
1	A	191	ASN
1	A	227	GLN
1	C	157	ASN
1	C	180	ASN
1	C	191	ASN
1	C	227	GLN
1	C	239	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)

Mogul was not executed - this section is therefore empty.

5.5 Carbohydrates (i)

Mogul was not executed - this section is therefore empty.

5.6 Ligand geometry (i)

Mogul was not executed - this section is therefore empty.

5.7 Other polymers (i)

Mogul was not executed - this section is therefore empty.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	310/327 (94%)	-0.55	3 (0%)	82	82	12, 20, 43, 58	0
1	C	310/327 (94%)	-0.63	3 (0%)	82	82	7, 18, 39, 50	0
All	All	620/654 (94%)	-0.59	6 (0%)	82	82	7, 19, 42, 58	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	34	LEU	4.0
1	A	19	SER	3.6
1	A	41	ASN	3.4
1	C	34	LEU	3.3
1	C	41	ASN	2.8
1	C	19	SER	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	SO4	A	400	5/5	0.88	0.20	52,52,53,54	0
2	SO4	C	400	5/5	0.90	0.19	59,59,61,61	0

6.5 Other polymers (i)

There are no such residues in this entry.