



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 18, 2022 – 02:03 PM EDT

PDB ID : 7SPN
Title : Crystal structure of IS11, a thermophilic esterase
Authors : Stogios, P.J.; Evdokimova, E.; Khusnutdinova, A.; Yakunin, A.F.; Savchenko, A.
Deposited on : 2021-11-02
Resolution : 2.92 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at <http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.29
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
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) : 2.29

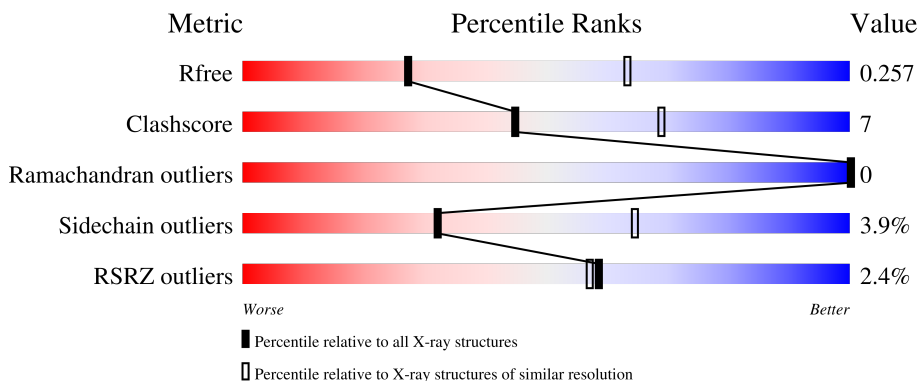
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.92 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}	130704	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	456	
1	B	456	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 7013 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 IS11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	456	3497	2242	616	630	9	0	0	0
1	B	455	3493	2240	615	629	9	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP A0A7C2VFT1
A	293	ASP	GLY	conflict	UNP A0A7C2VFT1
A	363	ALA	THR	conflict	UNP A0A7C2VFT1
A	386	VAL	ILE	conflict	UNP A0A7C2VFT1
A	411	LEU	VAL	conflict	UNP A0A7C2VFT1
B	0	GLY	-	expression tag	UNP A0A7C2VFT1
B	293	ASP	GLY	conflict	UNP A0A7C2VFT1
B	363	ALA	THR	conflict	UNP A0A7C2VFT1
B	386	VAL	ILE	conflict	UNP A0A7C2VFT1
B	411	LEU	VAL	conflict	UNP A0A7C2VFT1

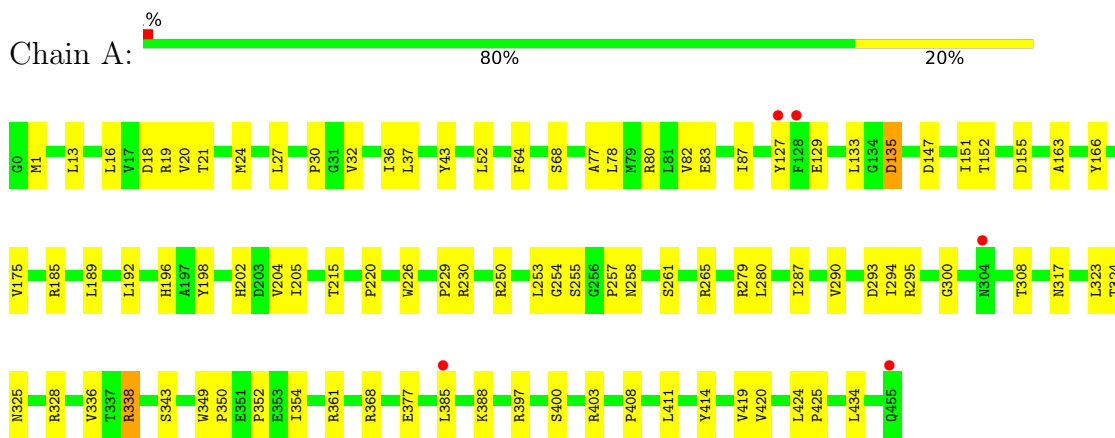
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	11	Total	O	0	0
			11	11		
2	B	12	Total	O	0	0
			12	12		

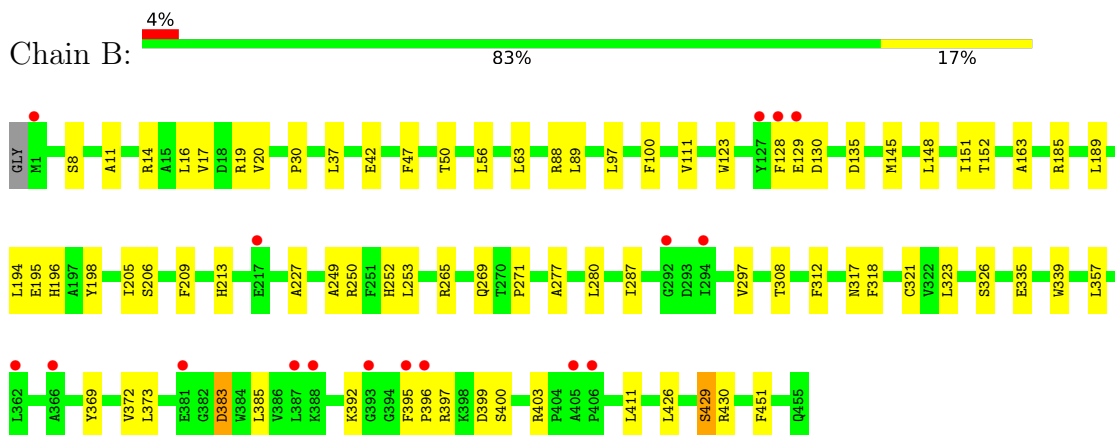
3 Residue-property plots [i](#)

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: IS11



- Molecule 1: IS11



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.22Å 103.36Å 94.86Å 90.00° 103.48° 90.00°	Depositor
Resolution (Å)	45.09 – 2.92 46.12 – 2.91	Depositor EDS
% Data completeness (in resolution range)	89.7 (45.09-2.92) 89.2 (46.12-2.91)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.91Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.197 , 0.258 0.197 , 0.257	Depositor DCC
R_{free} test set	1996 reflections (9.83%)	wwPDB-VP
Wilson B-factor (Å ²)	64.2	Xtrriage
Anisotropy	0.290	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , -6.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.038 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7013	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.02% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.26	0/3592	0.51	0/4896
1	B	0.25	0/3588	0.50	0/4891
All	All	0.26	0/7180	0.51	0/9787

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	3497	0	3468	50	0
1	B	3493	0	3465	45	0
2	A	11	0	0	0	0
2	B	12	0	0	0	0
All	All	7013	0	6933	91	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 7.

All (91) 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:133:LEU:O	1:A:230:ARG:NH1	2.22	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:ILE:HG22	1:A:152:THR:HG23	1.77	0.65
1:A:352:PRO:HB2	1:A:414:TYR:HB2	1.77	0.65
1:A:202:HIS:HB2	1:B:227:ALA:HB2	1.78	0.65
1:B:383:ASP:OD1	1:B:383:ASP:N	2.29	0.65
1:B:185:ARG:HA	1:B:189:LEU:HB2	1.79	0.65
1:A:16:LEU:HD11	1:A:336:VAL:HG13	1.81	0.62
1:B:395:PHE:CD1	1:B:396:PRO:HA	2.34	0.62
1:A:83:GLU:OE2	1:A:261:SER:OG	2.15	0.62
1:A:253:LEU:HD13	1:A:317:ASN:HA	1.83	0.61
1:B:252:HIS:HA	1:B:265:ARG:HD2	1.83	0.60
1:A:290:VAL:HB	1:A:294:ILE:HG22	1.83	0.59
1:A:1:MET:SD	1:A:1:MET:N	2.75	0.59
1:A:377:GLU:HB3	1:A:388:LYS:HB2	1.86	0.58
1:B:277:ALA:HB1	1:B:430:ARG:HD2	1.84	0.57
1:B:397:ARG:O	1:B:400:SER:OG	2.20	0.57
1:B:88:ARG:HD3	1:B:89:LEU:N	2.20	0.56
1:A:32:VAL:HG22	1:A:324:THR:HG22	1.88	0.56
1:A:338:ARG:NH2	1:A:349:TRP:CE2	2.74	0.56
1:A:13:LEU:HD11	1:A:43:TYR:HB3	1.87	0.55
1:B:271:PRO:HB3	1:B:280:LEU:HB3	1.90	0.53
1:A:411:LEU:HD13	1:A:419:VAL:HG21	1.90	0.53
1:A:87:ILE:HD11	1:A:175:VAL:HG21	1.89	0.53
1:B:269:GLN:HG2	1:B:297:VAL:HG11	1.89	0.53
1:A:308:THR:HG22	1:A:323:LEU:HA	1.90	0.53
1:B:249:ALA:O	1:B:253:LEU:HG	2.09	0.52
1:A:37:LEU:HD21	1:A:250:ARG:HD3	1.92	0.52
1:A:354:ILE:HD11	1:A:420:VAL:HG12	1.92	0.52
1:B:17:VAL:HG12	1:B:47:PHE:CZ	2.45	0.52
1:A:349:TRP:CD2	1:A:350:PRO:HD2	2.45	0.51
1:A:20:VAL:O	1:A:24:MET:HG3	2.10	0.51
1:B:151:ILE:HG22	1:B:152:THR:HG23	1.91	0.51
1:A:293:ASP:N	1:A:293:ASP:OD1	2.43	0.51
1:B:395:PHE:HD2	1:B:403:ARG:HH21	1.57	0.51
1:B:129:GLU:HG2	1:B:130:ASP:H	1.76	0.51
1:A:30:PRO:HB2	1:A:325:ASN:HD21	1.76	0.50
1:A:185:ARG:HA	1:A:189:LEU:HB2	1.93	0.50
1:B:253:LEU:HD13	1:B:317:ASN:HA	1.94	0.49
1:B:308:THR:HG22	1:B:323:LEU:HA	1.93	0.49
1:A:205:ILE:HG23	1:B:209:PHE:CE1	2.48	0.48
1:B:42:GLU:OE2	1:B:250:ARG:NH1	2.43	0.47
1:B:372:VAL:HG12	1:B:373:LEU:HD23	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:ILE:HG13	1:B:205:ILE:HD12	1.96	0.47
1:A:226:TRP:CE3	1:B:205:ILE:HG21	2.50	0.47
1:B:11:ALA:HA	1:B:14:ARG:HG2	1.96	0.46
1:A:280:LEU:HB2	1:A:287:ILE:HB	1.97	0.46
1:B:88:ARG:HD3	1:B:89:LEU:H	1.79	0.46
1:A:18:ASP:HA	1:A:21:THR:HG22	1.98	0.46
1:B:111:VAL:HG21	1:B:123:TRP:HH2	1.81	0.46
1:A:27:LEU:HD21	1:A:424:LEU:HD22	1.99	0.45
1:A:68:SER:HB2	1:A:300:GLY:O	2.17	0.45
1:A:127:TYR:OH	1:A:129:GLU:OE2	2.27	0.45
1:B:50:THR:HG23	1:B:56:LEU:O	2.16	0.45
1:A:198:TYR:HD2	1:A:204:VAL:HG12	1.82	0.45
1:B:14:ARG:HA	1:B:14:ARG:HD2	1.79	0.45
1:B:16:LEU:O	1:B:20:VAL:HG23	2.17	0.45
1:B:369:TYR:HB3	1:B:451:PHE:HB3	1.99	0.45
1:B:16:LEU:HD23	1:B:339:TRP:CE3	2.52	0.44
1:B:253:LEU:HD21	1:B:312:PHE:HB2	1.99	0.44
1:A:349:TRP:CD1	1:A:350:PRO:C	2.90	0.44
1:A:192:LEU:HD23	1:A:257:PRO:HG2	2.00	0.44
1:B:385:LEU:O	1:B:411:LEU:N	2.51	0.44
1:B:111:VAL:HG21	1:B:123:TRP:CH2	2.52	0.43
1:B:145:MET:HE3	1:B:163:ALA:HB1	2.00	0.43
1:A:77:ALA:O	1:A:80:ARG:HB3	2.19	0.43
1:A:198:TYR:CD2	1:A:204:VAL:HG12	2.53	0.43
1:B:195:GLU:HG3	1:B:196:HIS:ND1	2.33	0.43
1:A:16:LEU:O	1:A:20:VAL:HG23	2.18	0.43
1:A:254:GLY:HA2	1:A:265:ARG:NH1	2.33	0.43
1:A:78:LEU:O	1:A:82:VAL:HG23	2.19	0.43
1:A:163:ALA:HA	1:A:166:TYR:CD2	2.54	0.42
1:A:229:PRO:HG3	1:A:397:ARG:HH11	1.83	0.42
1:A:64:PHE:HB2	1:A:323:LEU:HD22	2.00	0.42
1:A:385:LEU:O	1:A:411:LEU:N	2.43	0.42
1:B:63:LEU:HD21	1:B:196:HIS:HB3	2.02	0.42
1:B:97:LEU:HB3	1:B:100:PHE:HB2	2.02	0.42
1:B:426:LEU:O	1:B:429:SER:OG	2.38	0.42
1:A:196:HIS:HA	1:A:198:TYR:CZ	2.55	0.41
1:B:196:HIS:HA	1:B:198:TYR:CE2	2.55	0.41
1:B:280:LEU:HB2	1:B:287:ILE:HB	2.02	0.41
1:A:52:LEU:HD23	1:A:52:LEU:HA	1.86	0.41
1:B:37:LEU:O	1:B:318:PHE:HA	2.21	0.41
1:A:135:ASP:OD1	1:A:135:ASP:N	2.52	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:ARG:HG2	1:A:425:PRO:CB	2.51	0.41
1:A:215:THR:HA	1:A:220:PRO:HA	2.02	0.41
1:A:388:LYS:HG2	1:A:408:PRO:HB3	2.03	0.40
1:B:17:VAL:HG12	1:B:47:PHE:HZ	1.84	0.40
1:B:30:PRO:HG2	1:B:213:HIS:ND1	2.36	0.40
1:B:128:PHE:HE2	1:B:373:LEU:HD11	1.87	0.40
1:A:36:ILE:HB	1:A:43:TYR:HB2	2.04	0.40
1:B:148:LEU:HD23	1:B:148:LEU:HA	1.86	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	454/456 (100%)	438 (96%)	16 (4%)	0	100	100
1	B	453/456 (99%)	432 (95%)	21 (5%)	0	100	100
All	All	907/912 (100%)	870 (96%)	37 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	358/358 (100%)	343 (96%)	15 (4%)	30	62

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	358/358 (100%)	345 (96%)	13 (4%)	35	67
All	All	716/716 (100%)	688 (96%)	28 (4%)	32	64

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	ARG
1	A	135	ASP
1	A	147	ASP
1	A	155	ASP
1	A	255	SER
1	A	258	ASN
1	A	279	ARG
1	A	295	ARG
1	A	338	ARG
1	A	343	SER
1	A	361	ARG
1	A	368	ARG
1	A	400	SER
1	A	403	ARG
1	A	434	LEU
1	B	8	SER
1	B	19	ARG
1	B	135	ASP
1	B	194	LEU
1	B	206	SER
1	B	321	CYS
1	B	326	SER
1	B	335	GLU
1	B	357	LEU
1	B	383	ASP
1	B	392	LYS
1	B	399	ASP
1	B	429	SER

Sometimes 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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	456/456 (100%)	-0.22	5 (1%) 80 81	40, 60, 91, 160	0
1	B	455/456 (99%)	-0.12	17 (3%) 41 38	44, 68, 117, 180	0
All	All	911/912 (99%)	-0.17	22 (2%) 59 57	40, 63, 108, 180	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	396	PRO	5.3
1	B	129	GLU	4.7
1	B	217	GLU	4.4
1	A	127	TYR	3.7
1	B	388	LYS	3.6
1	B	128	PHE	3.4
1	B	405	ALA	3.1
1	A	385	LEU	2.8
1	B	393	GLY	2.8
1	A	128	PHE	2.7
1	B	366	ALA	2.7
1	B	395	PHE	2.6
1	B	1	MET	2.6
1	B	362	LEU	2.6
1	B	381	GLU	2.5
1	B	294	ILE	2.2
1	A	455	GLN	2.2
1	B	387	LEU	2.2
1	B	406	PRO	2.2
1	B	127	TYR	2.2
1	A	304	ASN	2.1
1	B	292	GLY	2.1

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.