



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 1, 2017 – 06:36 AM EDT

PDB ID : 1ONX
Title : Crystal structure of isoaspartyl dipeptidase from escherichia coli complexed with aspartate
Authors : Thoden, J.B.; Marti-Arbona, R.; Raushel, F.M.; Holden, H.M.
Deposited on : unknown
Resolution : 2.10 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

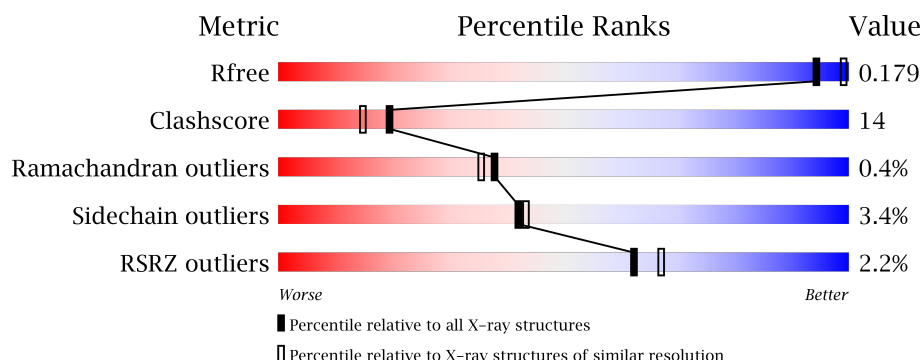
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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 $\leq 5\%$. 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	390	<div> <div>2%</div> <div>59%</div> <div>35%</div> <div>5%</div> </div>
1	B	390	<div> <div>3%</div> <div>67%</div> <div>29%</div> <div>.</div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ASP	A	450	-	-	-	X

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.

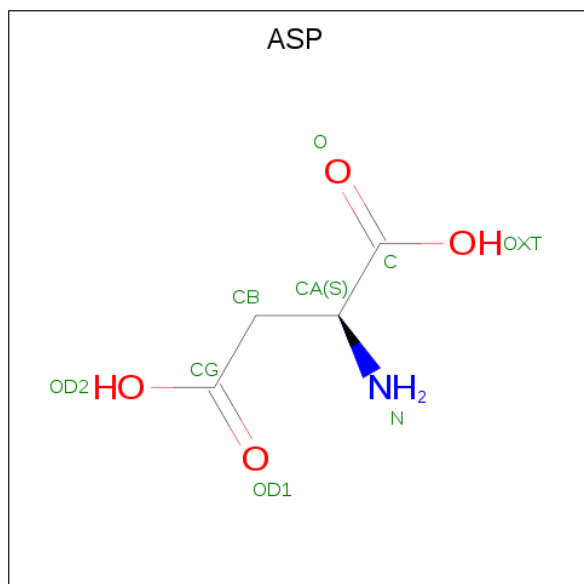
- Molecule 1 is a protein called Isoaspartyl dipeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	389	Total 2887	C 1817	N 495	O 563	S 12	0	1	0
1	B	389	Total 2887	C 1817	N 495	O 563	S 12	0	1	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Zn 2 2	0	0
2	A	2	Total Zn 2 2	0	0

- Molecule 3 is ASPARTIC ACID (three-letter code: ASP) (formula: $\text{C}_4\text{H}_7\text{NO}_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			9	4	1	4		
3	B	1	Total	C	N	O	0	0
			9	4	1	4		

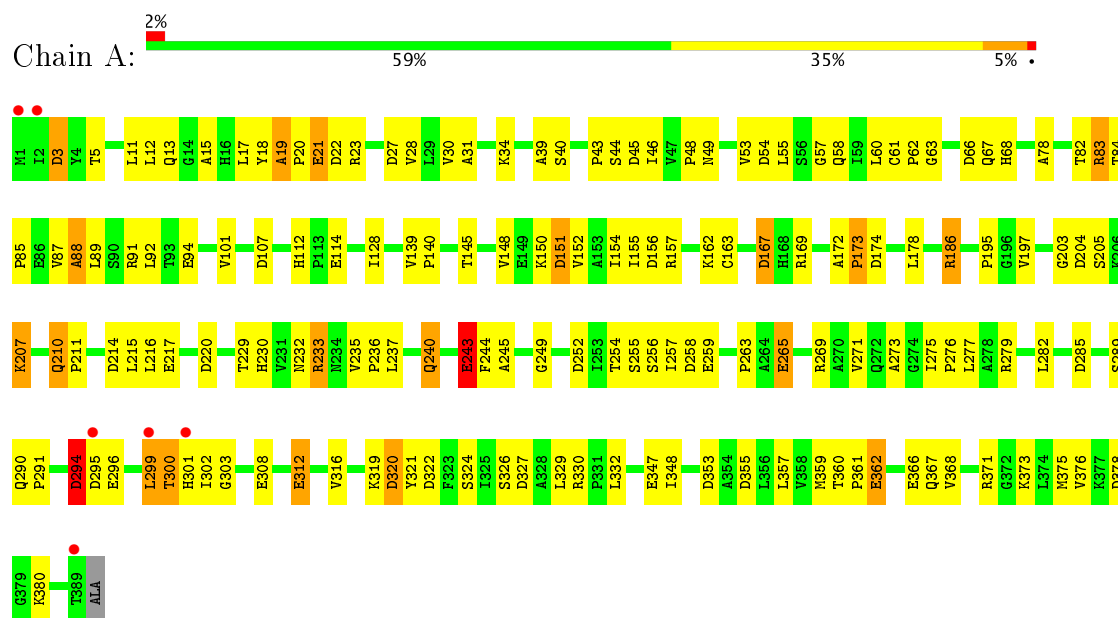
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	129	Total	O	0	0
			129	129		
4	B	128	Total	O	0	0
			128	128		

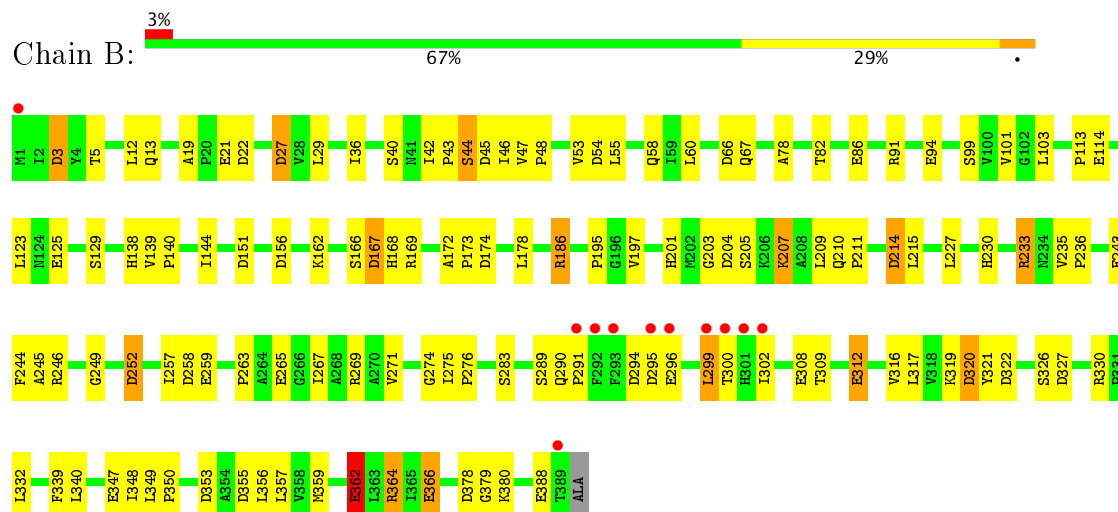
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Isoaspartyl dipeptidase



• Molecule 1: Isoaspartyl dipeptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α , β , γ	119.10Å 119.10Å 138.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.10 40.39 – 2.04	Depositor EDS
% Data completeness (in resolution range)	94.5 (30.00-2.10) 90.3 (40.39-2.04)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.05Å)	Xtriage
Refinement program	TNT 5E	Depositor
R, R_{free}	0.177 , 0.246 0.178 , 0.179	Depositor DCC
R_{free} test set	5583 reflections (11.25%)	DCC
Wilson B-factor (Å ²)	22.3	Xtriage
Anisotropy	0.157	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 103.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6053	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, KCX

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	0.97	12/2928 (0.4%)	1.44	43/3984 (1.1%)
1	B	0.99	15/2928 (0.5%)	1.44	44/3984 (1.1%)
All	All	0.98	27/5856 (0.5%)	1.44	87/7968 (1.1%)

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	362	GLU	CD-OE2	8.29	1.34	1.25
1	A	312	GLU	CD-OE2	7.76	1.34	1.25
1	B	259	GLU	CD-OE2	7.53	1.33	1.25
1	B	296	GLU	CD-OE2	7.22	1.33	1.25
1	A	296	GLU	CD-OE2	7.12	1.33	1.25
1	B	347	GLU	CD-OE2	7.05	1.33	1.25
1	B	362	GLU	CD-OE2	6.89	1.33	1.25
1	A	243	GLU	CD-OE2	6.86	1.33	1.25
1	A	114	GLU	CD-OE2	6.83	1.33	1.25
1	B	366	GLU	CD-OE2	6.56	1.32	1.25
1	B	312	GLU	CD-OE2	6.54	1.32	1.25
1	A	94	GLU	CD-OE2	6.46	1.32	1.25
1	A	21	GLU	CD-OE2	6.40	1.32	1.25
1	B	21	GLU	CD-OE2	6.28	1.32	1.25
1	A	217	GLU	CD-OE2	6.26	1.32	1.25
1	B	86	GLU	CD-OE2	6.18	1.32	1.25
1	B	388	GLU	CD-OE2	6.15	1.32	1.25
1	B	243	GLU	CD-OE2	6.15	1.32	1.25
1	A	347	GLU	CD-OE2	5.90	1.32	1.25
1	B	125	GLU	CD-OE2	5.60	1.31	1.25
1	B	86	GLU	CD-OE1	-5.58	1.19	1.25
1	A	308	GLU	CD-OE2	5.51	1.31	1.25
1	B	114	GLU	CD-OE1	-5.49	1.19	1.25
1	B	265	GLU	CD-OE2	5.43	1.31	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	265	GLU	CD-OE2	5.26	1.31	1.25
1	A	259	GLU	CD-OE2	5.25	1.31	1.25
1	B	94	GLU	CD-OE2	5.10	1.31	1.25

All (87) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	364	ARG	NE-CZ-NH1	10.80	125.70	120.30
1	A	151	ASP	CB-CG-OD2	-10.62	108.74	118.30
1	A	151	ASP	CB-CG-OD1	10.13	127.41	118.30
1	A	233	ARG	NE-CZ-NH2	-10.03	115.29	120.30
1	A	353	ASP	CB-CG-OD2	-9.44	109.80	118.30
1	B	151	ASP	CB-CG-OD2	-9.20	110.02	118.30
1	B	66	ASP	CB-CG-OD2	-9.19	110.03	118.30
1	A	233	ARG	NE-CZ-NH1	9.07	124.83	120.30
1	B	364	ARG	NE-CZ-NH2	-8.91	115.84	120.30
1	A	353	ASP	CB-CG-OD1	8.64	126.07	118.30
1	A	66	ASP	CB-CG-OD2	-8.62	110.54	118.30
1	A	294	ASP	CB-CG-OD2	-8.57	110.58	118.30
1	A	156	ASP	CB-CG-OD2	-8.46	110.69	118.30
1	A	107	ASP	CB-CG-OD1	8.17	125.66	118.30
1	A	327	ASP	CB-CG-OD2	-8.03	111.08	118.30
1	B	295	ASP	CB-CG-OD2	-7.92	111.17	118.30
1	A	107	ASP	CB-CG-OD2	-7.89	111.20	118.30
1	A	258	ASP	CB-CG-OD2	-7.72	111.35	118.30
1	B	258	ASP	CB-CG-OD2	-7.62	111.44	118.30
1	A	83	ARG	NE-CZ-NH1	7.30	123.95	120.30
1	B	355	ASP	CB-CG-OD2	-7.30	111.73	118.30
1	B	156	ASP	CB-CG-OD2	-7.24	111.79	118.30
1	A	22	ASP	CB-CG-OD1	7.22	124.80	118.30
1	B	322	ASP	CB-CG-OD1	7.06	124.66	118.30
1	A	174	ASP	CB-CG-OD2	-7.05	111.95	118.30
1	A	54	ASP	CB-CG-OD2	-6.98	112.02	118.30
1	B	322	ASP	CB-CG-OD2	-6.97	112.03	118.30
1	B	353	ASP	CB-CG-OD2	-6.97	112.03	118.30
1	B	66	ASP	CB-CG-OD1	6.91	124.52	118.30
1	B	378	ASP	CB-CG-OD2	-6.83	112.16	118.30
1	A	66	ASP	CB-CG-OD1	6.82	124.44	118.30
1	B	3	ASP	CB-CG-OD2	-6.82	112.16	118.30
1	B	320	ASP	CB-CG-OD2	-6.79	112.19	118.30
1	A	378	ASP	CB-CG-OD2	-6.79	112.19	118.30
1	B	167	ASP	CB-CG-OD2	-6.78	112.20	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	320	ASP	CB-CG-OD1	6.73	124.36	118.30
1	B	252	ASP	CB-CG-OD2	-6.71	112.26	118.30
1	B	45	ASP	CB-CG-OD2	-6.67	112.30	118.30
1	A	294	ASP	CB-CG-OD1	6.66	124.29	118.30
1	B	22	ASP	CB-CG-OD1	6.58	124.22	118.30
1	A	88	ALA	N-CA-CB	6.51	119.21	110.10
1	B	252	ASP	CB-CG-OD1	6.50	124.15	118.30
1	A	320	ASP	CB-CG-OD2	-6.39	112.55	118.30
1	A	167	ASP	CB-CG-OD2	-6.27	112.66	118.30
1	B	330	ARG	NE-CZ-NH2	-6.23	117.18	120.30
1	B	91	ARG	NE-CZ-NH2	-6.22	117.19	120.30
1	B	27	ASP	CB-CG-OD2	-6.21	112.71	118.30
1	A	301	HIS	N-CA-CB	-6.20	99.44	110.60
1	A	167	ASP	CB-CG-OD1	6.08	123.77	118.30
1	B	45	ASP	CB-CG-OD1	6.07	123.76	118.30
1	B	295	ASP	CB-CG-OD1	6.03	123.73	118.30
1	B	174	ASP	CB-CG-OD2	-6.00	112.90	118.30
1	B	186	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	B	246	ARG	NE-CZ-NH1	5.93	123.27	120.30
1	A	22	ASP	CB-CG-OD2	-5.91	112.98	118.30
1	B	355	ASP	CB-CG-OD1	5.90	123.61	118.30
1	A	54	ASP	CB-CG-OD1	5.88	123.59	118.30
1	A	3	ASP	CB-CG-OD2	-5.86	113.03	118.30
1	A	330	ARG	NE-CZ-NH2	-5.82	117.39	120.30
1	B	54	ASP	CB-CG-OD2	-5.81	113.07	118.30
1	B	233	ARG	NE-CZ-NH1	5.80	123.20	120.30
1	A	186	ARG	NE-CZ-NH1	5.77	123.19	120.30
1	A	220	ASP	CB-CG-OD2	-5.71	113.16	118.30
1	A	156	ASP	CB-CG-OD1	5.70	123.42	118.30
1	A	320	ASP	CB-CA-C	-5.69	99.03	110.40
1	A	45	ASP	CB-CG-OD2	-5.66	113.21	118.30
1	A	252	ASP	CB-CG-OD1	5.64	123.38	118.30
1	B	258	ASP	CB-CG-OD1	5.53	123.28	118.30
1	A	204	ASP	CB-CG-OD2	-5.50	113.35	118.30
1	A	355	ASP	CB-CG-OD1	5.46	123.21	118.30
1	B	353	ASP	CB-CG-OD1	5.41	123.17	118.30
1	B	204	ASP	CB-CG-OD1	5.37	123.14	118.30
1	B	269	ARG	NE-CZ-NH2	-5.35	117.62	120.30
1	B	327	ASP	CB-CG-OD2	-5.30	113.53	118.30
1	A	23	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	B	294	ASP	CB-CG-OD1	5.22	123.00	118.30
1	A	327	ASP	CB-CG-OD1	5.22	123.00	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	19	ALA	N-CA-C	5.21	125.07	111.00
1	B	167	ASP	CB-CG-OD1	5.21	122.99	118.30
1	A	220	ASP	CB-CG-OD1	5.20	122.98	118.30
1	B	214	ASP	CB-CG-OD2	-5.15	113.67	118.30
1	A	173	PRO	CB-CA-C	-5.12	99.19	112.00
1	B	151	ASP	CB-CG-OD1	5.08	122.87	118.30
1	B	214	ASP	CB-CG-OD1	5.08	122.87	118.30
1	B	19	ALA	N-CA-C	5.02	124.55	111.00
1	B	22	ASP	CB-CG-OD2	-5.01	113.79	118.30
1	A	330	ARG	NE-CZ-NH1	5.00	122.80	120.30

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	2887	0	2906	103	0
1	B	2887	0	2906	69	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	9	0	3	1	0
3	B	9	0	3	0	0
4	A	129	0	0	2	0
4	B	128	0	0	0	1
All	All	6053	0	5818	167	1

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 14.

All (167) 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:78:ALA:HB3	1:B:82:THR:HG21	1.58	0.85
1:A:43:PRO:HG2	1:A:46:ILE:HD13	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:SER:C	1:A:291:PRO:HD3	2.06	0.76
1:A:235:VAL:HB	1:A:236:PRO:HD3	1.71	0.72
1:A:289:SER:O	1:A:291:PRO:HD3	1.90	0.72
1:A:48:PRO:HG3	1:B:46:ILE:HG13	1.72	0.70
1:A:229:THR:HG23	1:A:230:HIS:CD2	2.27	0.70
1:B:299:LEU:HG	1:B:300:THR:N	2.08	0.68
1:B:289:SER:C	1:B:291:PRO:HD3	2.14	0.67
1:A:84:THR:HB	1:A:85:PRO:HD2	1.77	0.66
1:B:235:VAL:HB	1:B:236:PRO:HD3	1.77	0.66
1:A:48:PRO:HG3	1:B:46:ILE:CG1	2.24	0.66
1:B:289:SER:O	1:B:291:PRO:HD3	1.95	0.66
1:B:162:KCX:OQ2	1:B:201:HIS:HB2	1.97	0.65
1:A:257:ILE:O	1:A:263:PRO:HD3	1.99	0.63
1:A:290:GLN:O	1:A:302:ILE:HA	1.99	0.63
1:B:195:PRO:HG3	1:B:340:LEU:O	1.99	0.62
1:A:265:GLU:O	1:A:269:ARG:HG3	2.00	0.62
1:B:275:ILE:HG23	1:B:276:PRO:HD2	1.83	0.61
1:A:282:LEU:HB3	1:A:332:LEU:HD21	1.82	0.61
1:A:273:ALA:HB3	1:A:275:ILE:HD12	1.82	0.61
1:A:21:GLU:CD	1:A:21:GLU:H	2.04	0.61
1:A:319:LYS:HE2	1:A:320:ASP:OD1	2.02	0.60
1:B:168:HIS:CD2	1:B:169:ARG:HG3	2.37	0.60
1:B:205:SER:OG	1:B:207:LYS:HG2	2.01	0.60
1:A:294:ASP:CG	1:A:295:ASP:H	2.06	0.59
1:B:43:PRO:O	1:B:46:ILE:HG22	2.03	0.59
1:A:162:KCX:OQ1	3:A:450:ASP:OD2	2.21	0.59
1:A:245:ALA:HA	1:A:249:GLY:O	2.03	0.59
1:A:27:ASP:HB2	1:A:39:ALA:O	2.03	0.59
1:A:61:CYS:HB2	1:A:62:PRO:CD	2.33	0.58
1:B:203:GLY:O	1:B:233:ARG:HD3	2.04	0.58
1:B:319:LYS:HE2	1:B:320:ASP:OD1	2.03	0.57
1:A:282:LEU:HB3	1:A:332:LEU:CD2	2.34	0.57
1:A:205:SER:OG	1:A:207:LYS:HD2	2.04	0.57
1:A:58:GLN:HG2	1:A:366:GLU:OE1	2.04	0.57
1:A:128:ILE:O	1:A:371:ARG:NH2	2.30	0.56
1:B:113:PRO:HB2	1:B:144:ILE:CG1	2.35	0.56
1:A:15:ALA:HB2	1:A:55:LEU:CB	2.36	0.56
1:A:367:GLN:HA	1:A:376:VAL:O	2.05	0.56
1:B:230:HIS:O	1:B:233:ARG:HG2	2.06	0.56
1:A:167:ASP:OD1	1:A:169:ARG:HB2	2.05	0.55
1:A:299:LEU:HG	1:A:300:THR:N	2.20	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:KCX:HG2	1:A:163:CYS:N	2.20	0.55
1:A:233:ARG:HG2	1:A:237:LEU:HD23	1.88	0.55
1:A:48:PRO:HG3	1:B:46:ILE:CD1	2.38	0.54
1:A:151:ASP:HA	1:A:155:ILE:HD12	1.90	0.54
1:B:113:PRO:HB2	1:B:144:ILE:HG13	1.90	0.54
1:B:319:LYS:HG2	1:B:320:ASP:OD1	2.07	0.53
1:A:63:GLY:HA2	1:A:357:LEU:HG	1.91	0.53
1:A:249:GLY:O	1:A:279:ARG:HD2	2.08	0.53
1:A:215:LEU:C	1:A:215:LEU:HD23	2.29	0.53
1:A:150:LYS:O	1:A:154:ILE:HG12	2.09	0.52
1:A:78:ALA:HB2	1:A:299:LEU:HD22	1.91	0.52
1:B:290:GLN:O	1:B:302:ILE:HA	2.08	0.52
1:A:195:PRO:HB2	1:A:197:VAL:HG13	1.90	0.52
1:B:3:ASP:OD1	1:B:5:THR:HG23	2.10	0.52
1:A:48:PRO:HG3	1:B:46:ILE:HD11	1.91	0.51
1:B:27:ASP:HB2	1:B:42:ILE:HG13	1.92	0.51
1:B:195:PRO:HB2	1:B:197:VAL:HG13	1.93	0.51
1:B:53:VAL:HG12	1:B:55:LEU:HD21	1.93	0.51
1:A:232:ASN:ND2	1:A:257:ILE:HB	2.26	0.50
1:B:139:VAL:HA	1:B:140:PRO:C	2.31	0.50
1:A:255:SER:HA	1:A:263:PRO:HG3	1.93	0.50
1:A:145:THR:HG23	1:A:155:ILE:HD11	1.93	0.49
1:B:210:GLN:HA	1:B:210:GLN:OE1	2.12	0.49
1:B:99:SER:HA	1:B:129:SER:O	2.13	0.49
1:A:15:ALA:HB2	1:A:55:LEU:HB2	1.93	0.49
1:B:317:LEU:O	1:B:321:TYR:HB2	2.12	0.49
1:A:30:VAL:HG12	1:A:31:ALA:N	2.28	0.48
1:A:15:ALA:HB2	1:A:55:LEU:HB3	1.95	0.48
1:B:348:ILE:HG12	1:B:356:LEU:CD2	2.43	0.48
1:A:244:PHE:CE2	1:A:249:GLY:HA3	2.49	0.48
1:A:68:HIS:HD2	1:A:285:ASP:HA	1.79	0.48
1:B:60:LEU:HD12	1:B:357:LEU:O	2.13	0.48
1:A:148:VAL:O	1:A:152:VAL:HG23	2.13	0.48
1:A:43:PRO:O	1:A:46:ILE:HG22	2.13	0.48
1:B:210:GLN:N	1:B:211:PRO:CD	2.78	0.47
1:B:103:LEU:C	1:B:103:LEU:HD12	2.35	0.47
1:A:58:GLN:HB3	1:A:359:MET:O	2.15	0.47
1:B:379:GLY:O	1:B:380:LYS:HG3	2.15	0.47
1:B:257:ILE:O	1:B:263:PRO:HD3	2.15	0.47
1:A:373:LYS:O	1:A:375:MET:HG2	2.14	0.47
1:B:210:GLN:N	1:B:211:PRO:HD2	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:167:ASP:OD1	1:B:169:ARG:N	2.45	0.47
1:B:178:LEU:HB3	1:B:215:LEU:HD12	1.96	0.47
1:B:263:PRO:O	1:B:267:ILE:HG13	2.15	0.47
1:A:13:GLN:HA	1:A:27:ASP:OD1	2.16	0.46
1:A:376:VAL:HG13	1:A:380:LYS:C	2.35	0.46
1:A:210:GLN:N	1:A:211:PRO:CD	2.78	0.46
1:A:312:GLU:O	1:A:316:VAL:HG23	2.16	0.46
1:A:67:GLN:HA	1:A:101:VAL:HB	1.98	0.45
1:A:235:VAL:CB	1:A:236:PRO:HD3	2.43	0.45
1:B:252:ASP:OD1	1:B:283:SER:OG	2.33	0.45
1:B:215:LEU:HD23	1:B:215:LEU:C	2.37	0.45
1:A:203:GLY:O	1:A:233:ARG:HD3	2.17	0.45
1:B:29:LEU:CD2	1:B:36:ILE:HD11	2.47	0.45
1:A:139:VAL:HA	1:A:140:PRO:C	2.37	0.45
1:B:235:VAL:N	1:B:236:PRO:HD2	2.32	0.45
1:A:172:ALA:N	1:A:173:PRO:CD	2.80	0.44
1:A:62:PRO:N	1:A:348:ILE:HD11	2.32	0.44
1:A:83:ARG:HD3	4:A:403:HOH:O	2.18	0.44
1:A:290:GLN:N	1:A:291:PRO:HD3	2.30	0.44
1:A:240:GLN:O	1:A:243:GLU:HG3	2.18	0.44
1:A:30:VAL:HG13	1:A:34:LYS:O	2.17	0.44
1:A:30:VAL:CG1	1:A:31:ALA:N	2.81	0.44
1:B:245:ALA:HA	1:B:249:GLY:O	2.17	0.44
1:A:3:ASP:OD1	1:A:5:THR:OG1	2.30	0.44
1:B:67:GLN:HA	1:B:101:VAL:HB	2.00	0.44
1:A:216:LEU:HD23	1:A:216:LEU:HA	1.80	0.44
1:B:275:ILE:CG2	1:B:276:PRO:HD2	2.45	0.44
1:A:145:THR:CG2	1:A:155:ILE:HD11	2.48	0.43
1:A:11:LEU:HD12	1:A:28:VAL:O	2.18	0.43
1:A:178:LEU:HA	1:A:178:LEU:HD23	1.61	0.43
1:A:291:PRO:HB3	1:A:302:ILE:HD12	1.99	0.43
1:B:58:GLN:HG2	1:B:366:GLU:OE1	2.19	0.43
1:B:332:LEU:HD23	1:B:332:LEU:HA	1.80	0.43
1:A:88:ALA:O	1:A:91:ARG:HB2	2.18	0.43
1:B:244:PHE:CE2	1:B:249:GLY:HA3	2.54	0.43
1:A:275:ILE:HA	1:A:276:PRO:HD3	1.90	0.43
1:A:78:ALA:HB3	1:A:82:THR:HG21	1.99	0.43
1:B:210:GLN:NE2	1:B:214:ASP:OD1	2.50	0.43
1:A:289:SER:HA	1:A:303:GLY:O	2.19	0.43
1:A:357:LEU:CD2	1:A:368:VAL:HG22	2.48	0.43
1:A:112:HIS:CD2	1:A:112:HIS:N	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:HIS:CD2	1:A:285:ASP:HA	2.54	0.42
1:A:210:GLN:NE2	1:A:214:ASP:OD1	2.52	0.42
1:A:84:THR:HB	1:A:85:PRO:CD	2.47	0.42
1:B:359:MET:HA	1:B:364:ARG:O	2.19	0.42
1:A:299:LEU:HG	1:A:300:THR:H	1.84	0.42
1:B:362:GLU:H	1:B:362:GLU:CD	2.22	0.42
1:A:12:LEU:HD23	1:A:53:VAL:HB	2.01	0.42
1:B:167:ASP:OD1	1:B:169:ARG:HB2	2.19	0.42
1:A:360:THR:HB	1:A:361:PRO:HD2	2.00	0.42
1:A:87:VAL:HG11	1:A:92:LEU:HD11	2.01	0.42
1:A:46:ILE:HG13	1:B:48:PRO:HG3	2.01	0.42
1:A:255:SER:HB3	1:A:282:LEU:HD11	2.02	0.42
1:B:349:LEU:O	1:B:350:PRO:C	2.55	0.42
1:B:245:ALA:HB3	1:B:275:ILE:HD13	2.01	0.41
1:B:308:GLU:HG2	1:B:309:THR:N	2.34	0.41
1:B:235:VAL:N	1:B:236:PRO:CD	2.82	0.41
1:A:271:VAL:CG2	1:A:277:LEU:HD21	2.51	0.41
1:B:47:VAL:HB	1:B:48:PRO:HD2	2.02	0.41
1:B:271:VAL:O	1:B:274:GLY:N	2.33	0.41
1:A:18:TYR:C	1:A:20:PRO:HA	2.40	0.41
1:A:254:THR:HG22	1:A:256:SER:H	1.85	0.41
1:A:321:TYR:O	1:A:322:ASP:HB2	2.20	0.41
1:A:61:CYS:HB2	1:A:62:PRO:HD3	2.02	0.41
1:B:209:LEU:C	1:B:211:PRO:HD2	2.41	0.41
1:A:299:LEU:HD11	1:A:302:ILE:HB	2.03	0.41
1:A:68:HIS:O	1:A:285:ASP:HA	2.21	0.41
1:A:210:GLN:N	1:A:211:PRO:HD2	2.36	0.41
1:A:290:GLN:N	1:A:303:GLY:O	2.50	0.41
1:A:329:LEU:HA	1:A:329:LEU:HD23	1.88	0.41
1:B:312:GLU:O	1:B:316:VAL:HG23	2.20	0.41
1:A:61:CYS:C	1:A:348:ILE:HD11	2.41	0.41
1:B:166:SER:HB3	1:B:205:SER:HB3	2.03	0.41
1:A:57:GLY:HA3	4:A:502:HOH:O	2.21	0.40
1:B:123:LEU:HD23	1:B:123:LEU:HA	1.82	0.40
1:B:227:LEU:HB2	1:B:339:PHE:CZ	2.56	0.40
1:A:48:PRO:O	1:A:49:ASN:C	2.58	0.40
1:A:88:ALA:O	1:A:89:LEU:C	2.59	0.40
1:B:172:ALA:N	1:B:173:PRO:CD	2.85	0.40
1:A:157:ARG:HD2	1:A:157:ARG:HA	1.84	0.40
1:A:17:LEU:HD13	1:A:60:LEU:HD23	2.04	0.40
1:B:138:HIS:ND1	1:B:140:PRO:O	2.42	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:299:LEU:HG	1:B:300:THR:H	1.83	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:493:HOH:O	4:B:493:HOH:O[7_556]	2.13	0.07

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	387/390 (99%)	356 (92%)	29 (8%)	2 (0%)	32	28
1	B	387/390 (99%)	363 (94%)	23 (6%)	1 (0%)	44	44
All	All	774/780 (99%)	719 (93%)	52 (7%)	3 (0%)	38	35

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	294	ASP
1	A	19	ALA
1	B	44	SER

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	313/312 (100%)	301 (96%)	12 (4%)	38	38
1	B	313/312 (100%)	304 (97%)	9 (3%)	48	51
All	All	626/624 (100%)	605 (97%)	21 (3%)	42	43

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	SER
1	A	44	SER
1	A	186	ARG
1	A	207	LYS
1	A	210	GLN
1	A	240	GLN
1	A	243	GLU
1	A	299	LEU
1	A	300	THR
1	A	324	SER
1	A	326	SER
1	A	362	GLU
1	B	12	LEU
1	B	13	GLN
1	B	40	SER
1	B	44	SER
1	B	186	ARG
1	B	207	LYS
1	B	299	LEU
1	B	326	SER
1	B	362	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	ASN
1	A	68	HIS
1	A	112	HIS
1	A	210	GLN
1	A	230	HIS
1	A	290	GLN
1	A	315	GLN
1	A	367	GLN
1	B	13	GLN

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Mol	Chain	Res	Type
1	B	32	ASN
1	B	168	HIS
1	B	367	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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
1	KCX	A	162	1,2	8,11,12	0.93	1 (12%)	6,12,14	3.77	1 (16%)
1	KCX	B	162	1,2	8,11,12	0.67	0	6,12,14	4.47	2 (33%)

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
1	KCX	A	162	1,2	-	0/6/10/12	0/0/0/0
1	KCX	B	162	1,2	-	0/6/10/12	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	162	KCX	CA-C	2.24	1.53	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	162	KCX	CE-NZ-CX	-10.56	110.43	123.35
1	A	162	KCX	CE-NZ-CX	-9.02	112.31	123.35
1	B	162	KCX	O-C-CA	-2.20	118.94	125.02

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	162	KCX	2	0
1	B	162	KCX	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	ASP	A	450	2	1,8,8	0.23	0	1,10,10	0.40	0
3	ASP	B	550	2	1,8,8	0.16	0	1,10,10	0.16	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
3	ASP	A	450	2	-	0/2/8/8	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ASP	B	550	2	-	0/2/8/8	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	450	ASP	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 ⓘ

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, 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	388/390 (99%)	-0.36	6 (1%) 74 77	14, 29, 66, 97	0
1	B	388/390 (99%)	-0.22	11 (2%) 53 60	12, 28, 64, 100	0
All	All	776/780 (99%)	-0.29	17 (2%) 62 67	12, 28, 65, 100	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	292	PHE	6.1
1	B	295	ASP	5.7
1	B	301	HIS	4.2
1	B	299	LEU	3.9
1	A	1	MET	3.4
1	B	300	THR	3.2
1	A	389	THR	3.0
1	B	389	THR	3.0
1	A	299	LEU	2.7
1	B	291	PRO	2.6
1	B	1	MET	2.4
1	A	2	ILE	2.4
1	B	293	PHE	2.3
1	A	301	HIS	2.2
1	B	302	ILE	2.2
1	B	296	GLU	2.1
1	A	295	ASP	2.0

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

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, 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	LLDF	B-factors(\AA^2)	Q<0.9
1	KCX	B	162	12/13	0.93	0.15	-	8,30,45,52	0
1	KCX	A	162	12/13	0.96	0.11	-	17,32,53,71	0

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, 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	LLDF	B-factors(\AA^2)	Q<0.9
3	ASP	A	450	9/9	0.94	0.15	2.14	27,36,70,87	0
3	ASP	B	550	9/9	0.94	0.13	0.55	30,43,54,100	0
2	ZN	A	401	1/1	0.99	0.05	-	51,51,51,51	0
2	ZN	B	501	1/1	0.99	0.05	-	46,46,46,46	0
2	ZN	A	402	1/1	0.98	0.05	-	52,52,52,52	0
2	ZN	B	502	1/1	1.00	0.05	-	45,45,45,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.