Full wwPDB X-ray Structure Validation Report (i)

Dec 17, 2023 – 08:23 am GMT

PDB ID	:	4AQ8
Title	:	CRYSTAL STRUCTURE OF MOUSE CADHERIN-23 EC1-2 AND PROTOCADHERIN-15 EC1- 2 FORM II
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Deposited on	:	2012-04-13
Resolution	:	2.63 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 (1)) were used in the production of this report:

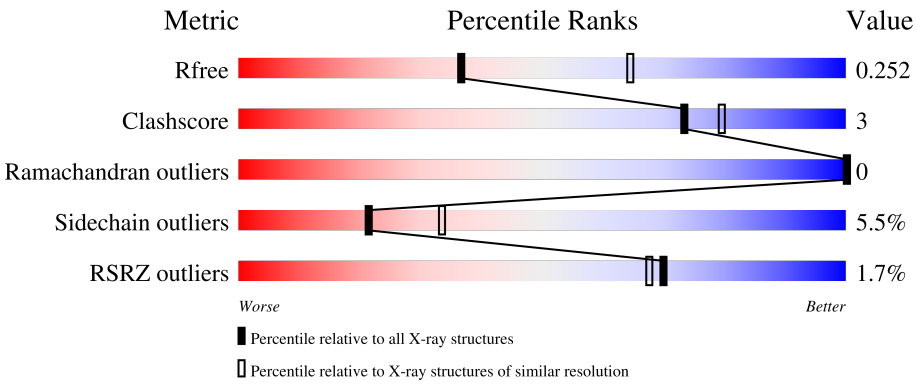
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.63 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	1426 (2.66-2.62)
Clashscore	141614	1472 (2.66-2.62)
Ramachandran outliers	138981	1446 (2.66-2.62)
Sidechain outliers	138945	1446 (2.66-2.62)
RSRZ outliers	127900	1408 (2.66-2.62)

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	214	2% 87% 10% •
1	B	214	% 86% 10% • •
2	C	242	2% 85% 11% • •
2	D	242	2% 89% 8% •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7517 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 CADHERIN-23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	208	1636	1039	270	325	2	0	1	0
1	B	208	1626	1033	267	324	2	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP Q99PF4
A	207	LEU	-	expression tag	UNP Q99PF4
A	208	GLU	-	expression tag	UNP Q99PF4
A	209	HIS	-	expression tag	UNP Q99PF4
A	210	HIS	-	expression tag	UNP Q99PF4
A	211	HIS	-	expression tag	UNP Q99PF4
A	212	HIS	-	expression tag	UNP Q99PF4
A	213	HIS	-	expression tag	UNP Q99PF4
A	214	HIS	-	expression tag	UNP Q99PF4
B	1	MET	-	expression tag	UNP Q99PF4
B	207	LEU	-	expression tag	UNP Q99PF4
B	208	GLU	-	expression tag	UNP Q99PF4
B	209	HIS	-	expression tag	UNP Q99PF4
B	210	HIS	-	expression tag	UNP Q99PF4
B	211	HIS	-	expression tag	UNP Q99PF4
B	212	HIS	-	expression tag	UNP Q99PF4
B	213	HIS	-	expression tag	UNP Q99PF4
B	214	HIS	-	expression tag	UNP Q99PF4

- Molecule 2 is a protein called PROTOCADHERIN-15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	237	1885	1177	324	378	6	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	236	1876	1172	322	376	6	0	0	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	MET	-	expression tag	UNP Q99PJ1
C	234	LEU	-	expression tag	UNP Q99PJ1
C	235	GLU	-	expression tag	UNP Q99PJ1
C	236	HIS	-	expression tag	UNP Q99PJ1
C	237	HIS	-	expression tag	UNP Q99PJ1
C	238	HIS	-	expression tag	UNP Q99PJ1
C	239	HIS	-	expression tag	UNP Q99PJ1
C	240	HIS	-	expression tag	UNP Q99PJ1
C	241	HIS	-	expression tag	UNP Q99PJ1
C	8	TYR	PHE	SEE REMARK 999	UNP Q99PJ1
C	10	ASP	ASN	SEE REMARK 999	UNP Q99PJ1
D	0	MET	-	expression tag	UNP Q99PJ1
D	234	LEU	-	expression tag	UNP Q99PJ1
D	235	GLU	-	expression tag	UNP Q99PJ1
D	236	HIS	-	expression tag	UNP Q99PJ1
D	237	HIS	-	expression tag	UNP Q99PJ1
D	238	HIS	-	expression tag	UNP Q99PJ1
D	239	HIS	-	expression tag	UNP Q99PJ1
D	240	HIS	-	expression tag	UNP Q99PJ1
D	241	HIS	-	expression tag	UNP Q99PJ1
D	8	TYR	PHE	SEE REMARK 999	UNP Q99PJ1
D	10	ASP	ASN	SEE REMARK 999	UNP Q99PJ1

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
3	A	4	4	4	0	0
3	B	4	4	4	0	0
3	C	3	3	3	0	0
3	D	3	3	3	0	0

- Molecule 4 is water.

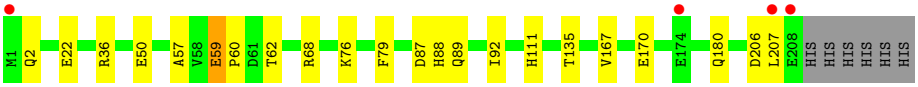
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	132	132	132	0	0
			Total	O		
4	B	118	118	118	0	0
			Total	O		
4	C	140	140	140	0	0
			Total	O		
4	D	90	90	90	0	0

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: CADHERIN-23

Chain A:

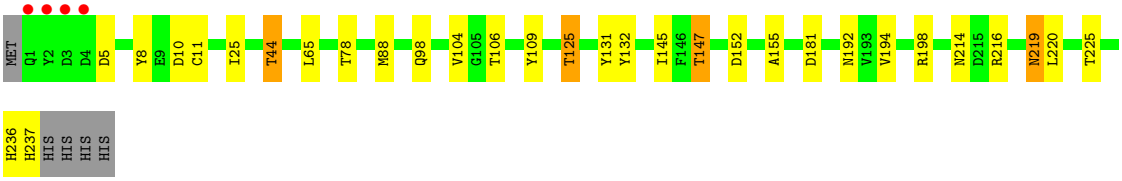


- Molecule 1: CADHERIN-23

Chain B:

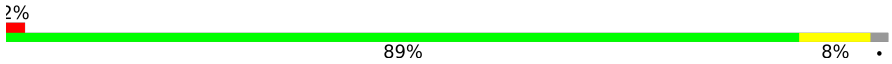
- Molecule 2: PROTOCADHERIN-15

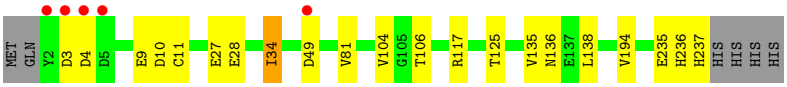
Chain C:



- Molecule 2: PROTOCADHERIN-15

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	158.75Å 57.03Å 156.16Å 90.00° 98.92° 90.00°	Depositor
Resolution (Å)	38.57 – 2.63 38.57 – 2.63	Depositor EDS
% Data completeness (in resolution range)	99.2 (38.57-2.63) 99.2 (38.57-2.63)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.21 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.189 , 0.243 0.200 , 0.252	Depositor DCC
R_{free} test set	2113 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	43.0	Xtriage
Anisotropy	0.094	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 34.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7517	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.24% 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: CA

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	0.50	0/1675	0.63	0/2294
1	B	0.48	0/1664	0.63	0/2279
2	C	0.51	0/1922	0.65	0/2623
2	D	0.44	0/1913	0.60	0/2611
All	All	0.48	0/7174	0.63	0/9807

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	D	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	236	HIS	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1636	0	1579	9	0
1	B	1626	0	1573	11	0
2	C	1885	0	1830	16	0
2	D	1876	0	1819	11	0
3	A	4	0	0	0	0
3	B	4	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
4	A	132	0	0	0	0
4	B	118	0	0	1	0
4	C	140	0	0	1	0
4	D	90	0	0	2	0
All	All	7517	0	6801	45	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 3.

All (45) 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:87:ASP:O	1:A:88:HIS:ND1	2.15	0.79
2:D:104:VAL:HG12	2:D:106:THR:HG23	1.70	0.73
1:B:25:PRO:O	1:B:28:SER:OG	2.08	0.70
2:C:104:VAL:HG12	2:C:106:THR:HG23	1.74	0.69
2:D:27:GLU:HG2	2:D:28:GLU:HG3	1.82	0.61
2:C:10:ASP:O	2:C:11:CYS:HB2	2.01	0.60
1:A:59:GLU:HG2	1:A:62:THR:OG1	2.04	0.57
1:A:92:ILE:C	1:A:92:ILE:HD12	2.26	0.56
2:D:34:ILE:HG23	4:D:2017:HOH:O	2.07	0.54
2:D:10:ASP:O	2:D:11:CYS:HB2	2.08	0.54
2:D:136:ASN:HA	2:D:235:GLU:HB3	1.91	0.52
1:B:1:MET:HE3	1:B:2:GLN:O	2.09	0.51
2:D:135:VAL:HG13	2:D:135:VAL:O	2.10	0.51
1:B:146:LEU:HD21	2:D:106:THR:HG21	1.93	0.51
2:D:104:VAL:CG1	2:D:106:THR:HG23	2.41	0.49
1:A:57:ALA:HB2	1:A:68:ARG:HD2	1.95	0.49
2:C:104:VAL:CG1	2:C:106:THR:HG23	2.42	0.48
2:C:147:THR:HA	2:C:192:ASN:ND2	2.29	0.48
1:B:206:ASP:O	1:B:207:LEU:HD22	2.14	0.48
2:C:152:ASP:HA	4:C:2096:HOH:O	2.14	0.48
1:A:111:HIS:HE1	1:A:135:THR:OG1	1.96	0.48
2:C:214:ASN:HB3	2:C:225:THR:HG22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:172:ASP:OD2	1:B:175:VAL:HG23	2.14	0.46
2:C:145:ILE:C	2:C:145:ILE:HD12	2.35	0.46
2:C:44:THR:CG2	2:C:44:THR:O	2.65	0.45
2:C:44:THR:O	2:C:44:THR:HG23	2.17	0.45
1:B:110:PHE:CZ	1:B:185:ALA:HB2	2.51	0.45
2:C:236:HIS:O	2:C:237:HIS:HB2	2.15	0.45
1:B:38:MET:HA	1:B:38:MET:CE	2.47	0.45
1:B:113:GLN:NE2	4:B:2079:HOH:O	2.50	0.44
2:C:8:TYR:CE2	2:C:104:VAL:HG11	2.52	0.44
2:C:214:ASN:CB	2:C:225:THR:HG22	2.48	0.43
1:A:87:ASP:O	1:A:88:HIS:CG	2.70	0.43
2:C:131:TYR:C	2:C:132:TYR:CD1	2.92	0.43
2:C:125:THR:O	2:C:155:ALA:HA	2.19	0.42
2:D:136:ASN:OD1	2:D:138:LEU:HD13	2.19	0.42
1:B:15:ASP:O	2:D:117:ARG:NH1	2.49	0.42
2:C:98:GLN:HE21	2:C:109:TYR:HE1	1.66	0.42
2:C:219:ASN:C	2:C:219:ASN:HD22	2.23	0.42
2:D:125:THR:HG22	4:D:2049:HOH:O	2.19	0.42
1:A:59:GLU:HA	1:A:60:PRO:HD3	1.90	0.41
1:A:76:LYS:HE3	1:A:79:PHE:CD1	2.56	0.41
1:B:58:VAL:HG22	1:B:65:VAL:HG22	2.03	0.41
1:A:59:GLU:CG	1:A:62:THR:OG1	2.68	0.40
1:B:92:ILE:C	1:B:92:ILE:HD12	2.42	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	207/214 (97%)	202 (98%)	5 (2%)	0	100	100
1	B	206/214 (96%)	200 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	235/242 (97%)	226 (96%)	9 (4%)	0	100	100
2	D	234/242 (97%)	226 (97%)	8 (3%)	0	100	100
All	All	882/912 (97%)	854 (97%)	28 (3%)	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	186/191 (97%)	175 (94%)	11 (6%)	19	30
1	B	185/191 (97%)	174 (94%)	11 (6%)	19	30
2	C	214/219 (98%)	200 (94%)	14 (6%)	17	26
2	D	213/219 (97%)	205 (96%)	8 (4%)	33	50
All	All	798/820 (97%)	754 (94%)	44 (6%)	21	33

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLN
1	A	22	GLU
1	A	36	ARG
1	A	50	GLU
1	A	59	GLU
1	A	89	GLN
1	A	167	VAL
1	A	170	GLU
1	A	180	GLN
1	A	206	ASP
1	A	207	LEU
1	B	2	GLN
1	B	6	LEU
1	B	12	HIS

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Mol	Chain	Res	Type
1	B	28	SER
1	B	73	ARG
1	B	92	ILE
1	B	145	VAL
1	B	174	GLU
1	B	177	GLN
1	B	197	LEU
1	B	208	GLU
2	C	5	ASP
2	C	25	ILE
2	C	44	THR
2	C	65	LEU
2	C	78	THR
2	C	88	MET
2	C	125	THR
2	C	147	THR
2	C	181	ASP
2	C	194	VAL
2	C	198	ARG
2	C	216	ARG
2	C	219	ASN
2	C	220	LEU
2	D	3	ASP
2	D	4	ASP
2	D	9	GLU
2	D	34	ILE
2	D	49	ASP
2	D	81	VAL
2	D	194	VAL
2	D	237	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	ASN
1	A	111	HIS
1	A	169	GLN
1	B	2	GLN
1	B	113	GLN
1	B	133	ASN
2	C	31	ASN
2	C	171	GLN

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Mol	Chain	Res	Type
2	C	192	ASN
2	C	219	ASN
2	C	237	HIS
2	D	31	ASN
2	D	98	GLN
2	D	171	GLN
2	D	221	ASN
2	D	236	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 14 ligands modelled in this entry, 14 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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	208/214 (97%)	-0.24	4 (1%)	66	64	21, 34, 66, 97	0
1	B	208/214 (97%)	-0.38	2 (0%)	82	81	20, 36, 80, 117	0
2	C	237/242 (97%)	-0.33	4 (1%)	70	67	20, 36, 62, 102	0
2	D	236/242 (97%)	-0.21	5 (2%)	63	60	27, 47, 81, 119	0
All	All	889/912 (97%)	-0.29	15 (1%)	70	67	20, 39, 76, 119	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	MET	8.1
2	D	2	TYR	7.9
2	D	3	ASP	6.8
2	C	3	ASP	4.7
2	D	4	ASP	3.8
2	C	1	GLN	3.7
1	A	207	LEU	3.4
1	A	174	GLU	3.3
2	C	2	TYR	2.9
1	B	174	GLU	2.5
2	C	4	ASP	2.3
2	D	49	ASP	2.3
1	A	208	GLU	2.3
2	D	5	ASP	2.1
1	B	1	MET	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
3	CA	A	1210	1/1	0.98	0.09	32,32,32,32	0
3	CA	B	1211	1/1	0.98	0.12	23,23,23,23	0
3	CA	C	1239	1/1	0.98	0.08	33,33,33,33	0
3	CA	D	1238	1/1	0.98	0.10	46,46,46,46	0
3	CA	D	1239	1/1	0.98	0.09	34,34,34,34	0
3	CA	A	1209	1/1	0.99	0.14	33,33,33,33	0
3	CA	B	1212	1/1	0.99	0.11	24,24,24,24	0
3	CA	C	1238	1/1	0.99	0.09	25,25,25,25	0
3	CA	A	1211	1/1	0.99	0.14	29,29,29,29	0
3	CA	C	1240	1/1	0.99	0.09	27,27,27,27	0
3	CA	B	1209	1/1	0.99	0.10	40,40,40,40	0
3	CA	B	1210	1/1	0.99	0.10	26,26,26,26	0
3	CA	D	1240	1/1	0.99	0.08	35,35,35,35	0
3	CA	A	1212	1/1	1.00	0.10	20,20,20,20	0

6.5 Other polymers (i)

There are no such residues in this entry.