Full wwPDB X-ray Structure Validation Report (i)

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PDB ID	:	3CJW
Title	:	Crystal structure of the human COUP-TFII ligand binding domain
Authors	:	Kruse, S.W.; Reynolds, R.; Vonrhein, C.; Xu, H.E.
Deposited on	:	2008-03-14
Resolution	:	1.48 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:

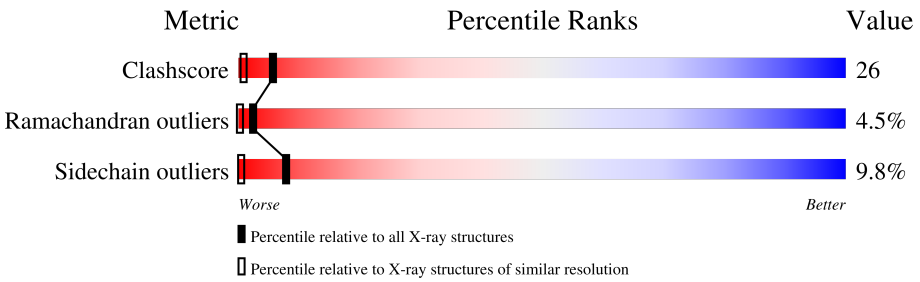
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 1.48 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))
Clashscore	141614	4955 (1.50-1.46)
Ramachandran outliers	138981	4846 (1.50-1.46)
Sidechain outliers	138945	4844 (1.50-1.46)

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%

Mol	Chain	Length	Quality of chain
1	A	244	50% 25% 7% • 15%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1636 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 COUP transcription factor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	207	1636	1050	274	301	11	0	1	0

There are 4 discrepancies between the modelled and reference sequences:

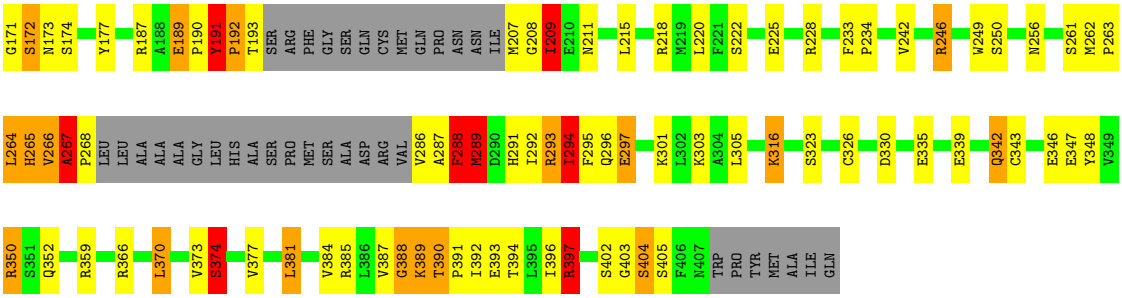
Chain	Residue	Modelled	Actual	Comment	Reference
A	171	GLY	-	expression tag	UNP P24468
A	172	SER	-	expression tag	UNP P24468
A	173	ASN	-	expression tag	UNP P24468
A	174	SER	-	expression tag	UNP P24468

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. 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. 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: COUP transcription factor 2

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	97.85Å 47.76Å 43.13Å 90.00° 100.87° 90.00°	Depositor
Resolution (Å)	6.00 – 1.48 48.05 – 1.48	Depositor EDS
% Data completeness (in resolution range)	7.7 (6.00-1.48) 99.3 (48.05-1.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.98 (at 1.48Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.168 , 0.238 0.252 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	24.3	Xtriage
Anisotropy	0.156	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 49.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	1636	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 9.92% 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)

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	1.70	19/1674 (1.1%)	1.50	28/2269 (1.2%)

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
1	A	0	8

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	294	ILE	CB-CG2	13.71	1.95	1.52
1	A	343	CYS	CB-SG	-11.54	1.62	1.82
1	A	339	GLU	CG-CD	-10.36	1.36	1.51
1	A	397	ARG	CD-NE	-8.91	1.31	1.46
1	A	343	CYS	CA-CB	8.40	1.72	1.53
1	A	288	PHE	CD1-CE1	8.16	1.55	1.39
1	A	295	PHE	CE2-CZ	-7.76	1.22	1.37
1	A	295	PHE	CB-CG	-7.42	1.38	1.51
1	A	342	GLN	CB-CG	-6.52	1.34	1.52
1	A	222	SER	CB-OG	-6.25	1.34	1.42
1	A	346	GLU	CG-CD	-6.11	1.42	1.51
1	A	250	SER	CB-OG	-5.83	1.34	1.42
1	A	189	GLU	CD-OE1	-5.42	1.19	1.25
1	A	335	GLU	CD-OE1	-5.37	1.19	1.25
1	A	346	GLU	CD-OE2	5.37	1.31	1.25
1	A	396	ILE	CA-CB	5.36	1.67	1.54
1	A	246	ARG	CZ-NH2	5.29	1.40	1.33
1	A	295	PHE	CA-C	5.10	1.66	1.52
1	A	374	SER	CB-OG	-5.06	1.35	1.42

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	343	CYS	CA-CB-SG	-12.15	92.14	114.00
1	A	305	LEU	CA-CB-CG	11.69	142.19	115.30
1	A	330	ASP	CB-CG-OD1	10.82	128.04	118.30
1	A	397	ARG	NE-CZ-NH2	-10.09	115.25	120.30
1	A	343	CYS	CB-CA-C	8.21	126.83	110.40
1	A	370	LEU	CB-CG-CD2	7.89	124.41	111.00
1	A	294	ILE	CB-CG1-CD1	-7.45	93.06	113.90
1	A	305	LEU	CB-CG-CD2	-7.04	99.03	111.00
1	A	350	ARG	NE-CZ-NH1	7.04	123.82	120.30
1	A	267	ALA	N-CA-C	-6.76	92.75	111.00
1	A	316	LYS	CD-CE-NZ	6.69	127.09	111.70
1	A	190	PRO	C-N-CA	-6.60	105.21	121.70
1	A	397	ARG	CG-CD-NE	-6.59	97.95	111.80
1	A	330	ASP	CB-CG-OD2	-6.48	112.47	118.30
1	A	366	ARG	NE-CZ-NH1	6.24	123.42	120.30
1	A	366	ARG	NE-CZ-NH2	-6.15	117.22	120.30
1	A	323	SER	N-CA-CB	5.93	119.40	110.50
1	A	294	ILE	CG1-CB-CG2	5.83	124.24	111.40
1	A	191	TYR	C-N-CD	5.77	140.52	128.40
1	A	339	GLU	OE1-CD-OE2	5.68	130.12	123.30
1	A	381	LEU	CA-CB-CG	5.43	127.80	115.30
1	A	359	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	A	397	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	A	264	LEU	N-CA-C	5.22	125.11	111.00
1	A	173	ASN	N-CA-CB	5.14	119.85	110.60
1	A	326[A]	CYS	CA-CB-SG	5.11	123.19	114.00
1	A	326[B]	CYS	CA-CB-SG	5.11	123.19	114.00
1	A	262	MET	CG-SD-CE	-5.00	92.19	100.20

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	172	SER	Peptide
1	A	265	HIS	Peptide
1	A	267	ALA	Peptide
1	A	288	PHE	Peptide
1	A	388	GLY	Peptide
1	A	397	ARG	Sidechain
1	A	402	SER	Peptide
1	A	404	SER	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	1648	84	0
All	All	1636	0	1648	84	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 26.

All (84) 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:294:ILE:CB	1:A:294:ILE:CG2	1.95	1.44
1:A:264:LEU:HD13	1:A:296:GLN:HG2	1.28	1.13
1:A:293:ARG:CZ	1:A:294:ILE:HG22	1.84	1.06
1:A:287:ALA:CB	1:A:292:ILE:HD11	1.89	1.03
1:A:293:ARG:HA	1:A:296:GLN:OE1	1.60	1.01
1:A:266:VAL:CG2	1:A:266:VAL:O	2.10	0.99
1:A:266:VAL:O	1:A:266:VAL:HG22	1.61	0.98
1:A:387:VAL:HG13	1:A:390:THR:HG23	1.45	0.98
1:A:293:ARG:NH1	1:A:294:ILE:CG2	2.27	0.97
1:A:264:LEU:CD1	1:A:265:HIS:HD2	1.81	0.94
1:A:287:ALA:HB1	1:A:292:ILE:HD11	1.48	0.92
1:A:225:GLU:OE1	1:A:228:ARG:NH2	2.04	0.89
1:A:387:VAL:O	1:A:390:THR:HG22	1.70	0.89
1:A:264:LEU:CD1	1:A:265:HIS:CD2	2.57	0.86
1:A:293:ARG:CZ	1:A:294:ILE:CG2	2.52	0.86
1:A:388:GLY:HA3	1:A:389:LYS:CB	2.06	0.85
1:A:208:GLY:O	1:A:209:ILE:O	1.95	0.85
1:A:289:MET:HG3	1:A:292:ILE:HB	1.60	0.84
1:A:264:LEU:HD11	1:A:265:HIS:CD2	2.13	0.83
1:A:293:ARG:NH1	1:A:294:ILE:HG23	1.97	0.77
1:A:264:LEU:HD12	1:A:265:HIS:HD2	1.50	0.75
1:A:289:MET:HE1	1:A:292:ILE:HG21	1.71	0.73
1:A:264:LEU:HD12	1:A:265:HIS:CD2	2.24	0.72
1:A:388:GLY:HA3	1:A:389:LYS:HB2	1.71	0.70
1:A:388:GLY:HA3	1:A:389:LYS:HB3	1.74	0.70
1:A:387:VAL:O	1:A:390:THR:CG2	2.40	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:TYR:HB3	1:A:192:PRO:HD3	1.77	0.67
1:A:374:SER:OG	1:A:377:VAL:HG23	1.96	0.66
1:A:294:ILE:CG2	1:A:294:ILE:CD1	2.73	0.66
1:A:289:MET:CE	1:A:292:ILE:HG21	2.26	0.66
1:A:263:PRO:O	1:A:266:VAL:HG11	1.96	0.66
1:A:264:LEU:CD1	1:A:296:GLN:HE21	2.11	0.64
1:A:294:ILE:CG2	1:A:294:ILE:HB	2.20	0.62
1:A:297:GLU:HG3	1:A:301:LYS:HD2	1.83	0.61
1:A:370:LEU:O	1:A:373:VAL:HG12	2.01	0.61
1:A:266:VAL:O	1:A:266:VAL:HG23	1.96	0.60
1:A:189:GLU:OE1	1:A:193:THR:HG22	2.03	0.59
1:A:294:ILE:CG2	1:A:294:ILE:HD13	2.34	0.58
1:A:256:ASN:HD21	1:A:316:LYS:HZ3	1.52	0.58
1:A:291:HIS:CG	1:A:377:VAL:HG13	2.40	0.57
1:A:289:MET:O	1:A:289:MET:CG	2.54	0.56
1:A:289:MET:CG	1:A:292:ILE:HB	2.34	0.56
1:A:191:TYR:CB	1:A:192:PRO:CD	2.84	0.56
1:A:267:ALA:HB1	1:A:286:VAL:HA	1.88	0.56
1:A:233:PHE:HB3	1:A:234:PRO:HD3	1.88	0.54
1:A:264:LEU:HD12	1:A:264:LEU:C	2.27	0.53
1:A:286:VAL:HG23	1:A:287:ALA:N	2.23	0.53
1:A:384:VAL:HA	1:A:388:GLY:O	2.09	0.53
1:A:191:TYR:HB3	1:A:192:PRO:CD	2.38	0.53
1:A:256:ASN:HD21	1:A:316:LYS:NZ	2.08	0.52
1:A:256:ASN:ND2	1:A:316:LYS:NZ	2.60	0.50
1:A:264:LEU:CD1	1:A:296:GLN:HG2	2.20	0.49
1:A:242:VAL:CG1	1:A:246:ARG:HE	2.25	0.49
1:A:388:GLY:CA	1:A:389:LYS:CB	2.82	0.49
1:A:292:ILE:O	1:A:296:GLN:HG3	2.14	0.48
1:A:347:GLU:HG2	1:A:350:ARG:HH22	1.80	0.47
1:A:391:PRO:HB2	1:A:394:THR:HG23	1.97	0.47
1:A:228:ARG:HH22	1:A:403:GLY:HA3	1.80	0.46
1:A:293:ARG:HH11	1:A:294:ILE:HG23	1.76	0.46
1:A:263:PRO:O	1:A:266:VAL:CG1	2.64	0.46
1:A:249:TRP:CH2	1:A:392:ILE:HD12	2.50	0.46
1:A:208:GLY:O	1:A:209:ILE:C	2.51	0.46
1:A:211:ASN:C	1:A:211:ASN:OD1	2.54	0.46
1:A:289:MET:HG3	1:A:289:MET:O	2.15	0.46
1:A:289:MET:CE	1:A:292:ILE:CG2	2.94	0.45
1:A:347:GLU:HG2	1:A:350:ARG:NH2	2.31	0.45
1:A:288:PHE:O	1:A:289:MET:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:ILE:CD1	1:A:294:ILE:HG21	2.44	0.45
1:A:388:GLY:CA	1:A:389:LYS:HB2	2.42	0.45
1:A:288:PHE:CD2	1:A:291:HIS:CG	3.05	0.44
1:A:297:GLU:OE1	1:A:301:LYS:NZ	2.36	0.44
1:A:393:GLU:OE2	1:A:394:THR:CG2	2.65	0.43
1:A:171:GLY:HA3	1:A:177:TYR:HB2	2.01	0.42
1:A:264:LEU:HD12	1:A:296:GLN:HE21	1.82	0.42
1:A:293:ARG:HD3	1:A:294:ILE:HG23	2.01	0.42
1:A:208:GLY:C	1:A:209:ILE:CG2	2.88	0.42
1:A:393:GLU:OE2	1:A:394:THR:HG23	2.20	0.42
1:A:267:ALA:HB1	1:A:286:VAL:CA	2.50	0.41
1:A:215:LEU:HD11	1:A:218:ARG:HH21	1.85	0.41
1:A:261:SER:HA	1:A:303:LYS:NZ	2.36	0.41
1:A:220:LEU:HD22	1:A:392:ILE:HD13	2.03	0.41
1:A:286:VAL:CG2	1:A:287:ALA:N	2.84	0.41
1:A:263:PRO:C	1:A:266:VAL:HG11	2.40	0.40
1:A:348:TYR:CE1	1:A:352:GLN:HG3	2.56	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	202/244 (83%)	188 (93%)	5 (2%)	9 (4%)	2 0

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	191	TYR
1	A	209	ILE
1	A	267	ALA
1	A	288	PHE

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Mol	Chain	Res	Type
1	A	389	LYS
1	A	405	SER
1	A	174	SER
1	A	289	MET
1	A	192	PRO

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	185/213 (87%)	167 (90%)	18 (10%)	8 0

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	172	SER
1	A	187	ARG
1	A	207	MET
1	A	209	ILE
1	A	266	VAL
1	A	268	PRO
1	A	288	PHE
1	A	289	MET
1	A	293	ARG
1	A	294	ILE
1	A	297	GLU
1	A	342	GLN
1	A	374	SER
1	A	381	LEU
1	A	385	ARG
1	A	390	THR
1	A	397	ARG
1	A	404	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	229	ASN
1	A	256	ASN
1	A	265	HIS
1	A	296	GLN
1	A	342	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 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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.